

10336256.txt

## SEQUENCE LISTING

<110> Michelle Cayouette  
 Connie Jo Hansen  
 Amy McClure  
 Mark Dyaico  
 Svetlana Gramatikova  
 May Sun  
 Nelson Barton  
 Justin Stege  
 Nahla Aboushadi

<120> Proteases, Nucleic Acids Encoding Them  
 and Methods For Making and Using Them

<130> 09010-093W01

<140> not assigned

<141> 2003-10-10

<150> 60/418,467

<151> 2002-10-10

<150> 60/471,423

<151> 2003-05-16

<160> 255

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1305

<212> DNA

<213> Bacteria

<400> 1

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cacgctgcgg	agcatgtcaa	gaagctgccc	ggcgtccttc	acgtatccga	ggatggcgag	300
gtaaaggcgt	tcgcagttag	agtctcgcga	accagccgcg	cgcagacaat	gccgtggggc	360
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ggcgtggtg	attccgagat	cgagggttgc	gtgatagact	ctggtgttga	cctagaccac	480
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gatgagaacg	ccacggtgcc	agactggagc	aaccgcaacc	cagaggtaac	agccccaggc	1020
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gccaccccac	acgtgagcgg	cacagtgcgc	ctaattcagg	cagccaggct	cgcccagggc	1140
ctaccactac	taccaccagg	cacagaggac	gacctaacca	cagacaccgt	gagaggcatc	1200
ctacacctaa	cagcggctga	cctcggagac	cccggctacg	acacgctata	cggctacggc	1260
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<210> 2

<211> 434

<212> PRT

<213> Bacteria

<220>

<221> SIGNAL

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&lt;400&gt; 2

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 20      25      30
Pro Val Ala Thr Ala Val Ser Tyr Lys Thr Leu Ile Val Lys Ile Asp
 35      40      45
Arg Ala Lys Phe Asp Pro Glu Arg Val Lys Gly Leu Gly Gly Arg Val
 50      55      60
Val Tyr Val Ala Gln Leu Ala Pro Val Ala Ile Leu Val Val Pro Ala
 65      70      75
His Ala Ala Glu His Val Lys Lys Leu Pro Gly Val Leu His Val Ser
 85      90      95
Glu Asp Gly Glu Val Lys Ala Phe Ala Val Arg Val Ser Leu Thr Gln
100      105      110
Pro Pro Gln Thr Met Pro Trp Gly Val Asp Tyr Ile Asp Ala Glu Gln
115      120      125
Val Trp Ser Ile Thr Lys Gly Phe Val Asp Val Asn Gly Asp Gly Asp
130      135      140
Ser Glu Ile Glu Val Ala Val Ile Asp Ser Gly Val Asp Leu Asp His
145      150      155
Pro Asp Leu Ala Asp Asn Ile Lys Trp Cys Val Ala Val Leu Asn Gly
165      170      175
Arg Ile Ser Asn Arg Cys Ser Asp Val Asn Gly His Gly Thr His Val
180      185      190
Thr Gly Thr Ile Ala Ala Leu Asp Asn Glu Ile Gly Val Val Gly Val
195      200      205
Ala Pro Glu Val Glu Ile Tyr Met Ile Lys Ala Leu Lys Asn Ser Gly
210      215      220
Ser Gly Ser Trp Ser Asp Leu Ile Ile Ala Ile Asp Leu Ala Val Arg
225      230      235
Gly Pro Asp Gly Val Ile Asp Ala Asp Gly Asp Gly Val Ile Val Gly
245      250      255
Asp Pro Glu Asp Asp Ala Pro Glu Val Ile Ser Met Ser Leu Gly Gly
260      265      270
Tyr Asp Pro Pro Glu Leu Gln Glu Val Ile Ala Ala Ala Tyr Ser
275      280      285
Tyr Gly Ile Val Ile Val Ala Ala Ala Gly Asn Glu Gly Leu Asp Thr
290      295      300
Pro Ala Tyr Pro Ala Ala Tyr Pro Glu Val Ile Ala Val Gly Ala Ile
305      310      315
Asp Glu Asn Ala Thr Val Pro Asp Trp Ser Asn Arg Asn Pro Glu Val
325      330      335
Thr Ala Pro Gly Val Asp Ile Leu Ser Thr Tyr Pro Asp Asp Ser Tyr
340      345      350
Ala Val Leu Ser Gly Thr Ser Met Ala Thr Pro His Val Ser Gly Thr
355      360      365
Val Ala Leu Ile Gln Ala Ala Arg Leu Ala Gln Gly Leu Pro Leu Leu
370      375      380
Pro Pro Gly Thr Glu Asp Asp Leu Thr Thr Asp Thr Val Arg Gly Ile
385      390      395
Leu His Leu Thr Ala Val Asp Leu Gly Asp Pro Gly Tyr Asp Thr Leu
405      410      415
Tyr Gly Tyr Gly Val Ile Asn Ala Tyr Asp Ala Val Leu Thr Ala Leu
420      425      430
Asn Ser

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&lt;210&gt; 3

&lt;211&gt; 1572

&lt;212&gt; DNA

&lt;213&gt; Bacteria

&lt;400&gt; 3

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60  
120

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aagatcaagc ggacctacac ctcgggcgct aacgggtacg ccgtcgaact ctccgaggcc 300
caggcgaaga agctcgcggc cgaccccgcc gtgacctcgg tcgtccagaa ccgcgtcttc 360
cacgtcgacg gcacgcagcc ctccccgccc tcctgggggtc tggaccggat cgaccagaag 420
gcccttccgc tgaaccagag ctacacctac cccgacaccg cgggccaggg cgtgacggcg 480
tacatcatcg acaccggcgt acgcatcacc cacagcgact tcggcgggcg cgctctctac 540
ggctacgacg ccatcgacaa cgacaacacc gccaggacg gccacggcca cggcaccac 600
gtcgcgggca cggtcgcggg cacctcgtag ggctcgcca agaaggcgaa gatcgtcggc 660
gtccgcgtcc tcgacaactc cggctccggc acgaccgagc aggtcgtcgc gggcatcgac 720
tgggtcacgc ggaacgccgt gaagccggcc gtcgccaaca tgagcctcgg cggtggcgtc 780
gacaccgtcc tcgacgcagc cgtccgcaac tcgatcgctt ccggcgtcac gtacgcggtc 840
gcggccggca acgacagctc caacgcctcc aactactcgc cggcgcgcg caccgaggcc 900
atcaccgtcg gctccacgac caacaccgac gcccgtctca gcttctcaa ctacggcacg 960
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gtcggcgggc gcaccaccac cccgcccggc ccgaagtctg agaacaccgc cgactacgcc 1260
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tcggacaaca tcaacaccac gtacagcgtg aacgcctcct cggaggtcgc caacggcacg 1500
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<212> PRT  
<213> Bacteria

<220>  
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35 40 45  
Glu Gly Thr Ile Ala Gly Ser Tyr Ile Val Thr Leu Asp Glu Ser Ala  
50 55 60  
Gln Ala Glu Thr Ala Lys Gly Arg Ala Val Ala Ala Lys Phe Gly Ala  
65 70 75 80  
Lys Ile Lys Arg Thr Tyr Thr Ser Ala Val Asn Gly Tyr Ala Val Glu  
85 90 95  
Leu Ser Glu Ala Gln Ala Lys Lys Leu Ala Ala Asp Pro Ala Val Thr  
100 105 110  
Ser Val Val Gln Asn Arg Val Phe His Val Asp Gly Thr Gln Pro Ser  
115 120 125  
Pro Pro Ser Trp Gly Leu Asp Arg Ile Asp Gln Lys Ala Leu Pro Leu  
130 135 140  
Asn Gln Ser Tyr Thr Tyr Pro Asp Thr Ala Gly Gln Gly Val Thr Ala  
145 150 155 160  
Tyr Ile Ile Asp Thr Gly Val Arg Ile Thr His Ser Asp Phe Gly Gly  
165 170 175  
Arg Ala Ser Tyr Gly Tyr Asp Ala Ile Asp Asn Asp Asn Thr Ala Gln  
180 185 190  
Asp Gly His Gly His Gly Thr His Val Ala Gly Thr Val Ala Gly Thr  
195 200 205  
Ser Tyr Gly Val Ala Lys Lys Ala Lys Ile Val Gly Val Arg Val Leu  
210 215 220  
Asp Asn Ser Gly Ser Gly Thr Thr Glu Gln Val Val Ala Gly Ile Asp  
225 230 235 240  
Trp Val Thr Arg Asn Ala Val Lys Pro Ala Val Ala Asn Met Ser Leu  
245 250 255

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Gly Gly Gly Val Asp Thr Val Leu Asp Ala Ala Val Arg Asn Ser Ile  
 260 265 270  
 Ala Ser Gly Val Thr Tyr Ala Val Ala Ala Gly Asn Asp Ser Ser Asn  
 275 280 285  
 Ala Ser Asn Tyr Ser Pro Ala Arg Val Thr Glu Ala Ile Thr Val Gly  
 290 295 300  
 Ser Thr Thr Asn Thr Asp Ala Arg Ser Ser Phe Ser Asn Tyr Gly Thr  
 305 310 315 320  
 Val Leu Asp Ile Phe Ala Pro Gly Ser Ser Ile Thr Ser Ser Trp Asn  
 325 330 335  
 Thr Ser Asp Ser Ala Thr Asn Thr Ile Ser Gly Thr Ser Met Ala Thr  
 340 345 350  
 Pro His Val Ala Gly Ala Ala Ala Val Tyr Leu Ala Gly Asn Pro Thr  
 355 360 365  
 Ala Thr Pro Ala Gln Val Ser Thr Ala Leu Thr Thr Ala Ala Thr Pro  
 370 375 380  
 Asn Val Val Thr Asn Pro Gly Ser Gly Ser Pro Asn Arg Leu Leu Tyr  
 385 390 395 400  
 Val Gly Gly Gly Thr Thr Thr Pro Pro Gly Pro Lys Phe Glu Asn Thr  
 405 410 415  
 Ala Asp Tyr Ala Ile Ala Asp Asn Ala Thr Val Glu Ser Pro Val Thr  
 420 425 430  
 Val Ser Gly Val Ser Gly Asn Ala Pro Ala Ala Leu Gln Val Pro Val  
 435 440 445  
 Asn Ile Val His Thr Tyr Ile Gly Asp Leu Gln Ile Gln Leu Ile Ala  
 450 455 460  
 Pro Asp Gly Ser Ala Tyr Thr Leu Lys Ala Phe Gly Thr Gly Gly Ser  
 465 470 475 480  
 Ser Asp Asn Ile Asn Thr Thr Tyr Ser Val Asn Ala Ser Ser Glu Val  
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 <211> 3684  
 <212> DNA  
 <213> Bacteria

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 <213> Bacteria  
  
 <220>  
 <221> SIGNAL  
 <222> (1)...(32)

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 35 40 45  
 Ser Thr Thr Val Thr Leu Val Thr Gly Asp Arg Val Thr Leu Thr Asp  
 50 55 60  
 Leu Gly Gly Gly Arg Lys Thr Val Thr Val Asp Arg Ala Glu Gly Ala  
 65 70 75 80  
 Thr Gly Ala Ile Arg Ser Arg Ile Asp Asp Gly Arg Val Thr Val Val  
 85 90 95  
 Pro Asp Glu Ala Arg Pro Tyr Leu Asp Ser Gly Ala Leu Asp Pro Arg  
 100 105 110  
 Leu Phe Asp Val Thr Gly Leu Val Glu Gln Gly Val Thr Gly Glu Leu  
 115 120 125  
 Pro Leu Ile Val Thr Tyr Gly Gly Lys Thr Ala Arg Thr Ala Ala Ala  
 130 135 140  
 Ala Pro Arg Gly Ala Glu Thr Val Arg Pro Leu Pro Ser Ile Gly Gly  
 145 150 155 160  
 Ala Ala Val Thr Ala Thr Asp Pro Ala Ser Phe Trp Arg Gly Phe Thr  
 165 170 175

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 Gly Arg Val 180 Lys Ala Ala Met Ala 185 Glu Ser Asn Ala Gln 190 Ile Gly Thr  
 Pro Lys 195 Ala Trp Glu Ala Gly 200 Leu Thr Gly Lys Gly 205 Val Lys Val Ala  
 Val 210 Leu Asp Thr Gly Ala 215 Asp Leu Ala His Pro 220 Leu Ala Gly Arg  
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 Asn Gly His 245 Thr His Val Ala Ser 250 Thr Val Gly Gly Ser 255 Gly Ala  
 Gly Ser Asp 260 Gly Lys Glu Lys Gly 265 Val Ala Pro Gly Ala Thr Leu Ala  
 Val Gly 275 Lys Val Leu Ser Asp 280 Glu Gly Ser Gly Ser 285 Glu Ser Glu Ile  
 Ile Ala Gly Met Glu Trp 295 Ala Lys Asp Ile Asp Ala Lys Ile Val  
 305 Ser Met Ser Leu Gly 310 Ser Arg Glu Pro Ser Asp Gly Thr Asp Pro Met  
 Ala Leu Ala Val 325 Asn Thr Leu Thr Ala 330 Glu Thr Gly Ala Leu Phe Val  
 Ile Ala Ala Gly 340 Asn Ser Gly Tyr 345 Pro Gly Ser Ile Gly Ser Pro Gly  
 Ala Ala Asp 355 Ser Ala Leu Thr 360 Ile Gly Ala Val Asp 365 Ser Ala Asp Glu  
 Ala Ala Tyr Phe Thr 375 Ser Gln Gly Pro Arg Tyr 380 Gly Asp Gln Ala Leu  
 385 Lys Pro Asp Leu Ser 390 Ala Pro Gly Val Asp 395 Ile Leu Ala Ala Arg Ser  
 Gln Leu Leu Pro Gly 405 Ser Gly Leu Tyr Thr Ser Met Ser Gly Thr Ser  
 Met Ala Thr 420 Pro His Val Ala Gly Val Ala Ala Leu Leu Ala Glu Arg  
 His Pro Asp 435 Trp Thr Gly Ala 440 Gln Leu Lys Asp Ala 445 Leu Met Ser Ser  
 Ser Lys Thr Leu Asp Ala 455 Ser Ser Tyr Ala Leu Gly Ser Gly Arg Val  
 465 Asp Val Ala Ala Ala 470 Ile Ala Ala Asn Val Thr Ala Thr Gly Ser Ala  
 Asp Leu Gly Phe Val Ala Trp Pro Tyr Ala Ser Ser Lys Pro Val Thr  
 Lys Thr Val 500 Thr Tyr Thr Asn Ser 505 Ser Asp Ala Pro Val Glu Leu Asn  
 Leu Ala Val Glu Gly Met Pro Ala Gly Val Ala Ala Leu Ala Asp Thr  
 Thr 530 Leu Thr Val Pro Ala 535 His Gly Thr Ala Ser Thr Thr Val Thr Gly  
 545 Asp Gly Thr Lys Ala 550 Pro Val Gly Gln Ser Ser Gly Arg Ile Thr Ala  
 Thr Ala Ala Gly 565 Thr Val Val Ala His 570 Thr Ala Leu Gly Leu Val Lys  
 Glu Glu Glu Arg Tyr Thr Leu Thr Val His Val Lys Asp 585 Arg Asp Gly  
 Ala Pro Thr Pro Ala His 600 Gly Val Lys Gln Leu Ala Glu Asp Thr  
 Asp 610 Pro Phe Pro Ala Ala 615 Val Gly Asp Ser Gly 620 Leu Glu Leu Arg  
 625 Leu Gln Pro Gly Thr Tyr Thr Val Asp Thr Phe Leu Asp Val Arg Gly  
 Ser His Gly Glu 645 Asp Ser Leu Gly Leu 650 Gly Phe Leu Thr Ala Pro Glu  
 Ile Thr Leu 660 Asp Arg Asp Arg Glu 665 Ile Thr Leu Asp Gly Arg Gln Leu  
 Arg Glu 675 Ile Arg Ala Glu Val 680 Asp Arg Arg Thr Glu Thr Arg Gln Leu  
 Leu Met Glu Phe Asp Arg 695 Lys Ala Asn Gly Ala Ser Tyr Gly Gly Ala  
 705 710 720

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Val	Gln	Val	Pro	Pro	Met	Tyr	Asp	Ser	Ile	Phe	Ala	Ala	Pro	Thr	Ala
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Lys	Pro	Met	Leu	Glu	Thr	Ser	Val	Asp	Gly	Ser	Arg	Leu	Ser	Gly	Ala
Thr	Pro	Gln	Ala	Gly	Ala	Thr	Leu	Leu	Glu	Gly	Arg	His	Arg	Leu	Gly
Leu	Val	Asp	Ala	Gly	Thr	Gly	Thr	Pro	Ala	Glu	Tyr	Thr	Gly	Arg	Asn
Val	Thr	Gly	Lys	Ala	Val	Leu	Val	Arg	Leu	Thr	Glu	Gly	Ala	Asp	Pro
Ala	Gln	Val	Ala	Gln	Thr	Ala	Gln	Asp	Ala	Gly	Ala	Lys	Ala	Leu	Phe
Val	Thr	Asp	Asp	Arg	Pro	Gly	Arg	Leu	Met	Glu	Trp	Phe	Gly	Thr	Ala
Asp	Tyr	Gln	Asp	Arg	Pro	Leu	Ala	Val	Ala	Thr	Val	Asn	Ala	Ala	Asp
Ala	Arg	Arg	Leu	Ala	Ala	Gly	Ala	Ala	Arg	Gly	Lys	Arg	Val	Asp	Leu
Thr	Gly	Thr	Arg	Phe	Thr	Pro	Phe	Thr	Tyr	Asp	Leu	Ser	Glu	Gly	His
Pro	Gly	Ala	Ile	Gly	Lys	Asp	Leu	Val	Phe	Arg	Pro	Asp	Glu	Asp	Glu
Leu	Ala	Thr	Val	Arg	Ser	Thr	Phe	His	Ala	Pro	Thr	Lys	Arg	Ala	Glu
Leu	Gly	Gly	Glu	Phe	Arg	Tyr	Ser	Ile	Thr	Asp	Thr	Phe	Pro	Ile	Gly
Phe	Gly	Phe	Lys	Glu	Trp	Ile	Ser	Phe	Pro	Ala	Glu	Arg	Thr	Glu	Tyr
Val	Ser	Thr	Gly	Thr	Gly	Gln	Arg	Trp	His	Glu	Ser	Val	Asp	Leu	Gly
Glu	Ser	Leu	Glu	Glu	Arg	Gly	Gly	Gln	Ser	Val	Tyr	Arg	Gly	Gly	Ser
Arg	Val	Asp	Leu	Asp	Trp	Phe	Gly	Pro	Val	Trp	His	Pro	Trp	Leu	Gly
Thr	Gly	Leu	Gly	Trp	Gly	Gln	Gln	Arg	Thr	Gly	Asn	Asp	Leu	Arg	Phe
Asn	Thr	Pro	Gly	Trp	Gly	Asp	Ser	Gly	Asn	Asp	His	Thr	Gly	Phe	Gly
Asn	Val	Trp	Ser	Asp	Asp	Ser	Met	Thr	Gln	Tyr	Thr	Glu	Val	Tyr	Val
Asn	Gly	Thr	Arg	Val	Asp	Arg	Lys	Thr	Ser	Ser	Gly	Ala	Tyr	Ala	Trp
Asp	Ala	Pro	Ala	Glu	Glu	Ala	Ala	Tyr	Lys	Val	Val	Thr	Asp	Thr	Thr
Leu	Asp	Pro	Ala	Arg	Trp	Arg	Leu	Ala	Thr	Lys	Gly	His	Ser	Glu	Trp
Thr	Phe	Arg	Ser	Ala	Glu	Thr	Pro	His	Asp	Lys	Ile	Thr	Tyr	Leu	Pro
Met	Leu	Asn	Leu	Gly	Phe	Asp	Val	Asp	Thr	Asp	Ile	Asn	Gly	Asp	Val
Arg	Ala	Gly	Ser	Arg	Leu	Pro	Val	Gly	Ile	Ser	Ala	Glu	Tyr	Val	Lys
Gly	Ala	Thr	Gly	Thr	Gly	Ser	Ile	Gly	Thr	Gly	Thr	Leu	Glu	Val	Ser
Tyr	Asp	Glu	Gly	Arg	Thr	Trp	Thr	Lys	Val	Ala	Leu	Lys	Lys	Ala	Arg
His	Gly	Ala	Ala	Trp	Asp	Gly	Glu	Leu	Arg	Val	Pro	Ser	Gly	Ala	Asp
Ser	Val	Ser	Leu	Arg	Ala	Gly	Ala	Ser	Asp	Asp	Arg	Gly	Gly	Ser	Val
Thr	Gln	Glu	Leu	Ile	Arg	Ala	Val	Gly	Val	Lys					

<210> 7  
 <211> 1332  
 <212> DNA

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&lt;213&gt; Bacteria

&lt;400&gt; 7

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aaaatgtttg	aaagattttt	taagaataga	aaaaaattat	ccgtcattat	agaatttgag	180
agtaattgct	atcaagaggg	atgcttagag	gtgaatcaag	cttttacgaa	acgcaatggt	240
tgtaaaatta	gaaacgagtt	ctctatcatt	tcttgctgta	gtgccgatat	aacaccatca	300
gtcttagaag	aggttttaac	taattgtaac	catattaaaa	aggtgtattt	aaatcatgaa	360
gtgcgagctt	tattagatac	ggctgttata	tcagcaaagt	caaaaaatat	tgtgagaaat	420
aacacgacac	tcacagggaa	aggaatcact	attgcggtta	ttgataccgg	tatctttccg	480
cacaccgacc	tttcaggaag	aattattgat	tttggttgatt	ttattaacga	cagaacggaa	540
acctacgatg	ataatgggca	tggtacgcat	tgccgaggag	atgctctcgg	agatgggtca	600
gcttcttcag	gactttatat	ggggcctgca	ccagaagcga	atgtcattgg	tgtaaagggt	660
ttaaataagg	taggatctgg	ttcattagaa	acagtcatgc	aaggggttga	ctgggtgtata	720
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cctgcacagc	gatatgagaa	tgagaacgat	gatccgatgg	tgaaaatggt	agagaaagca	840
tgggagaatg	gaattgtcgt	ttgtgttgct	gctggaaatg	aggggccgga	agcgagtacg	900
attgctagtc	ctgggggttag	tgaacaagtt	ataaccgttg	gagcgctaga	tgataaaaacg	960
acggctgata	caagatcaga	cgatgaggtc	gctagctttt	ctagtagagg	gccaacgata	1020
tatgaaaagg	tgaagcctga	tatttttagct	ccaggtgtag	atatttatatc	attacgtttcc	1080
ccaaattctt	atttagacaa	atttcaaaaa	gggaatcgag	tggggtcaga	ctatttttct	1140
ttatcaggaa	cttccatggc	aacacctatt	tgtgcagggg	tagcagcatt	aatattacaa	1200
cataatccaa	atgcaactcc	gcaagaggta	aaagacttat	taaaaagagg	aacggattta	1260
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cctgacaatt	aa					1332

&lt;210&gt; 8

&lt;211&gt; 443

&lt;212&gt; PRT

&lt;213&gt; Bacteria

&lt;400&gt; 8

Met	Phe	Gly	Phe	Ser	Met	Val	Lys	Met	Val	Arg	Ser	His	Ser	Gln	Lys
1				5					10					15	
Leu	Asp	Lys	Thr	Leu	Arg	Asp	Arg	Ile	Leu	Asn	Leu	Tyr	Lys	Pro	Phe
			20					25					30		
Lys	Trp	Thr	Pro	Cys	Phe	Leu	His	Lys	Met	Phe	Glu	Arg	Phe	Phe	Lys
			35				40					45			
Asn	Arg	Lys	Lys	Leu	Ser	Val	Ile	Ile	Glu	Phe	Glu	Ser	Asn	Cys	Tyr
			50			55					60				
Gln	Glu	Gly	Cys	Leu	Glu	Val	Asn	Gln	Ala	Phe	Thr	Lys	Arg	Asn	Gly
			65			70				75				80	
Cys	Lys	Ile	Arg	Asn	Glu	Phe	Ser	Ile	Ile	Ser	Cys	Cys	Ser	Ala	Asp
			85					90						95	
Ile	Thr	Pro	Ser	Val	Leu	Glu	Glu	Val	Leu	Thr	Asn	Cys	Asn	His	Ile
			100					105						110	
Lys	Lys	Val	Tyr	Leu	Asn	His	Glu	Val	Arg	Ala	Leu	Leu	Asp	Thr	Ala
			115				120					125			
Val	Ile	Ser	Ala	Asn	Ala	Lys	Asn	Ile	Val	Arg	Asn	Asn	Thr	Thr	Leu
			130			135					140				
Thr	Gly	Lys	Gly	Ile	Thr	Ile	Ala	Val	Ile	Asp	Thr	Gly	Ile	Phe	Pro
			145			150				155				160	
His	Thr	Asp	Leu	Ser	Gly	Arg	Ile	Ile	Asp	Phe	Val	Asp	Phe	Ile	Asn
			165						170					175	
Asp	Arg	Thr	Glu	Thr	Tyr	Asp	Asp	Asn	Gly	His	Gly	Thr	His	Cys	Ala
			180					185					190		
Gly	Asp	Ala	Leu	Gly	Asp	Gly	Ser	Ala	Ser	Ser	Gly	Leu	Tyr	Met	Gly
			195				200					205			
Pro	Ala	Pro	Glu	Ala	Asn	Val	Ile	Gly	Val	Lys	Val	Leu	Asn	Lys	Val
			210			215						220			
Gly	Ser	Gly	Ser	Leu	Glu	Thr	Val	Met	Gln	Gly	Val	Asp	Trp	Cys	Ile
			225			230				235				240	
Lys	Tyr	Asn	Asp	Gln	Asn	Pro	Asp	Gln	Lys	Ile	Asn	Ile	Ile	Asn	Met
			245						250					255	
Ser	Leu	Gly	Ala	Pro	Ala	Gln	Arg	Tyr	Glu	Asn	Glu	Asn	Asp	Asp	Pro
			260					265					270		
Met	Val	Lys	Met	Val	Glu	Lys	Ala	Trp	Glu	Asn	Gly	Ile	Val	Val	Cys

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275 280 285  
 Val Ala Gly Asn Glu Gly Pro Glu Ala Ser Thr Ile Ala Ser Pro  
 290 300  
 Gly Val Ser Glu Gln Val Ile Thr Val Gly Ala Leu Asp Asp Lys Thr  
 305 310 315 320  
 Thr Ala Asp Thr Arg Ser Asp Asp Glu Val Ala Ser Phe Ser Ser Arg  
 325 330 335  
 Gly Pro Thr Ile Tyr Glu Lys Val Lys Pro Asp Ile Leu Ala Pro Gly  
 340 345 350  
 Val Asp Ile Ile Ser Leu Arg Ser Pro Asn Ser Tyr Leu Asp Lys Phe  
 355 360 365  
 Gln Lys Gly Asn Arg Val Gly Ser Asp Tyr Phe Ser Leu Ser Gly Thr  
 370 375 380  
 Ser Met Ala Thr Pro Ile Cys Ala Gly Ile Ala Ala Leu Ile Leu Gln  
 385 390 395 400  
 His Asn Pro Asn Ala Thr Pro Gln Glu Val Lys Asp Leu Leu Lys Arg  
 405 410 415  
 Gly Thr Asp Leu Trp Thr Asn Arg Asp Pro Asn Ile Tyr Gly Ala Gly  
 420 425 430  
 Tyr Ile Asn Ala Glu Asn Ser Val Pro Asp Asn  
 435 440

&lt;210&gt; 9

&lt;211&gt; 2181

&lt;212&gt; DNA

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; obtained from an environmental sample

&lt;400&gt; 9

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ctgtcccgatc	cttatttctg	gctgcgcgat	ccgagctatc	cggtcgtcga	tgacgcggac	240
gtcctcgatt	atgtgaaggc	cgaaaatgcc	tatttcgacg	cagcaatgaa	gccgcacgca	300
aagctcgtcg	agacgttggt	tcaggagatg	aagggccgca	tcaaggaggc	cgattcctcg	360
gtgcccgcaga	aggacggcga	ctgggtctat	tggtatcgaat	atgacgaggg	cgccgaatat	420
aagaaatggt	accggaagcc	agcgtcaggc	tccggcgaga	cccagctcat	cctcgacgag	480
gtggcgatgg	cggagggcaa	ggattatttc	cgctcgccgc	aactgtcgat	cagtcccgac	540
ggccggctga	tgccctattc	gttcgacgac	aacggttccg	aacgcttcga	ggcgcgcgtc	600
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agcatcgagg	cgccggggac	atggaaaacg	ctgatcccg	ggtcggatca	cagctacatc	1080
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caggctcgata	tccgcaaata	tgacgcaccg	ctaacccccg	gccggatcga	attccccgag	1200
gccacttacg	ttgcggggct	cggcgacaaat	cccgaatatc	atcaggacaa	gctccggctc	1260
gattatgaat	cgatgggtcac	tcccgatatac	gtctatgatt	atgatatcgc	gaccggcacg	1320
ctcgaaacgc	tgaaggtaca	ggaaatccca	tcgggttatg	atgcaacgca	atatgttaacc	1380
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gtgcctttcg	tcgacgtgat	caacacgatg	gtcgacgaaa	cgctgccact	caccccggc	1860
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ctcaacgacc	cgcgctaac	ctattgggag	cccgcacaa	gggtcgccaa	gctccgcgcg	2040
acgcgaccca	gtgctgctg	gctgctgctg	cgaccaaca	tgggcgcggg	ccatgccggc	2100
aaatcgggcc	gctggggctc	gctccacgat	gatgccgagg	agttcgctt	cggtgctgacg	2160
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<210> 10  
 <211> 726  
 <212> PRT  
 <213> Unknown

<220>  
 <221> SIGNAL  
 <222> (1)...(28)

<223> obtained from an environmental sample

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 Ser Asp Leu Thr Thr Ser Pro Ala Leu Pro Ala Ala Pro Val Ala Glu  
 35 40 45  
 Gln Arg Pro His Asp Val Thr Leu His Gly Lys Thr Leu Ser Asp Pro  
 50 55 60  
 Tyr Phe Trp Leu Arg Asp Pro Ser Tyr Pro Val Val Asp Asp Ala Asp  
 65 70 75 80  
 Val Leu Asp Tyr Val Lys Ala Glu Asn Ala Tyr Phe Asp Ala Ala Met  
 85 90 95  
 Lys Pro His Ala Lys Leu Val Glu Thr Leu Phe Gln Glu Met Lys Gly  
 100 105 110  
 Arg Ile Lys Glu Ala Asp Ser Ser Val Pro Gln Lys Asp Gly Asp Trp  
 115 120 125  
 Leu Tyr Trp Ile Glu Tyr Asp Glu Gly Ala Glu Tyr Lys Lys Trp Tyr  
 130 135 140  
 Arg Lys Pro Ala Ser Gly Ser Gly Glu Thr Gln Leu Ile Leu Asp Glu  
 145 150 155 160  
 Val Ala Met Ala Glu Gly Lys Asp Tyr Phe Arg Leu Ala Glu Leu Ser  
 165 170 175  
 Ile Ser Pro Asp Gly Arg Leu Met Ala Tyr Ser Phe Asp Asp Asn Gly  
 180 185 190  
 Ser Glu Arg Phe Glu Ala Arg Val Arg Asn Leu Glu Thr Gly Glu Leu  
 195 200 205  
 Leu Pro Asp Val Ile Pro Gly Thr Leu Ser Ser Leu Val Trp Thr Ser  
 210 215 220  
 Gly Asn Asp Ala Ile Leu Tyr Gly Leu Ala Asn Glu Asn Trp Arg Thr  
 225 230 235 240  
 Asp Asn Val Arg Leu His Lys Leu Gly Thr Pro Val Gly Gln Asp Lys  
 245 250 255  
 Leu Leu Tyr Lys Glu Pro Asp Ile Gly Phe Gly Val Gly Ile Gly Lys  
 260 265 270  
 Thr Ala Ala Asp Asn Tyr Ile Val Ile Gly Thr Gly Asp Asn Glu Thr  
 275 280 285  
 Asn Glu Val Tyr Leu Leu Pro Ala Asp Asn Pro Glu Ala Glu Met Gln  
 290 295 300  
 Leu Val Ser Ala Arg Gln Lys Gly Arg Glu Tyr Ser Val Asp Glu Arg  
 305 310 315 320  
 Asp Gly Thr Leu Tyr Ile Leu Thr Asn Asp Glu His Pro Asn Phe Arg  
 325 330 335  
 Val Ala Thr Ala Ser Ile Glu Ala Pro Gly Thr Trp Lys Thr Leu Ile  
 340 345 350  
 Pro Gly Ser Asp His Ser Tyr Ile Thr Gly Phe Ser Val Phe Arg Asp  
 355 360 365  
 Tyr Phe Val Leu Glu Ala Arg Glu Asp Gly Leu Asp Gln Val Asp Ile  
 370 375 380  
 Arg Lys Tyr Asp Ala Pro Leu Thr Pro Gly Arg Ile Glu Phe Pro Glu  
 385 390 395 400  
 Ala Thr Tyr Val Ala Gly Leu Gly Asp Asn Pro Glu Tyr His Gln Asp  
 405 410 415  
 Lys Leu Arg Leu Asp Tyr Glu Ser Met Val Thr Pro Asp Thr Val Tyr  
 420 425 430  
 Asp Tyr Asp Ile Ala Thr Gly Thr Leu Glu Thr Leu Lys Val Gln Glu

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435 440 445  
 Ile Pro Ser Gly Tyr Asp Ala Thr Gln Tyr Val Thr Glu Arg Val Asn  
 450 455 460  
 Leu Pro Ser Arg Asp Gly Lys Thr Met Ile Pro Ala Ser Leu Val Tyr  
 465 470 475 480  
 Lys Lys Gly Thr Lys Arg Asp Gly Ser Ala Pro Met His Leu Tyr Ala  
 485 490 495  
 Tyr Gly Ser Tyr Gly Tyr Arg Ile Ala Pro Gly Phe Ser Thr Thr Arg  
 500 505 510  
 Leu Ser Leu Val Asp Arg Gly Met Ile Tyr Ala Ile Ala His Val Arg  
 515 520 525  
 Gly Gly Asp Asp Leu Gly Arg Ala Trp Tyr Leu Ala Gly Lys Thr Asp  
 530 535 540  
 His Arg Lys Asn Thr Phe Asn Asp Phe Ile Asp Val Ala Lys Gly Leu  
 545 550 555 560  
 Ile Ala Lys Gly Tyr Thr Ser Ala Gly Lys Ile Ser Ile Glu Gly Arg  
 565 570 575  
 Ser Ala Gly Gly Gln Val Met Gly Ala Val Thr Asn Glu Ala Pro Glu  
 580 585 590  
 Leu Trp Gly Ala Val Leu Ala Gly Val Pro Phe Val Asp Val Ile Asn  
 595 600 605  
 Thr Met Val Asp Glu Thr Leu Pro Leu Thr Pro Gly Glu Trp Pro Glu  
 610 615 620  
 Trp Gly Asn Pro Ile Thr Asp Lys Ala Ala Phe Asp Tyr Met Leu Ser  
 625 630 635 640  
 Tyr Ser Pro Tyr Asp Asn Val Thr Ala Lys Ala Tyr Pro Pro Met Leu  
 645 650 655  
 Val Ser Ala Gly Leu Asn Asp Pro Arg Val Thr Tyr Trp Glu Pro Ala  
 660 665 670  
 Lys Trp Val Ala Lys Leu Arg Ala Thr Arg Thr Asn Asp Ala Thr Leu  
 675 680 685  
 Leu Leu Arg Thr Asn Met Gly Ala Gly His Ala Gly Lys Ser Gly Arg  
 690 695 700  
 Trp Gly Ser Leu His Glu Asp Ala Glu Glu Phe Ala Phe Val Leu Thr  
 705 710 715 720  
 Gln Leu Gly Val Glu Lys 725

<210> 11  
 <211> 1374  
 <212> DNA  
 <213> Unknown

<220>  
 <223> Obtained from an environmental sample

<400> 11  
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 gctttgcccg aagatctaca gcgattaatt cgcgcgaatg cgccggatac tgccggattt 180  
 gaagccgttt gtgcacgctg tgtcaggctt ttgtaacgcg ccaaagataa ttttttgagt 240  
 gatgcggcga tgaacaaaga cggttcgtat gtgctttcga cacttttgcg gctcgaatgt 300  
 gacgaacggt ttacgggcaa gggcgtgacg atcgcgtttc tcgattcggg tttttatccg 360  
 cacgtcgatc tgactacacc gaacaatcga attatcgggt accgcagctt gatgcatgca 420  
 gaaggcgatc tgacgacact ttttcaatcg gatgtagcga gctggcacgg aatgatgacc 480  
 tcggtcgtcg cggcaggaaa cggctcgttt tccaacgggt tttatcgcgg aattgcgccc 540  
 gatccaatg ttgtgttggt gaaactggca cgaacaggac gaatcaccga gcaaaatatt 600  
 caagacggct tttagccaat tttagccaat cgaacgaaat acggcattaa agtcgtcaat 660  
 atttcggcag gcggcgattt tgaacaaagt tatctacacg atgcgctttc gcaaacggtc 720  
 gaggaatgcg ttgcgaaagg tttgacgacg gtttgcgaga tcggaacgcg gggacatttg 780  
 ccgactcatc cggttttttc gcctgcccag tcgccttcgg caattgcggt cggcggactt 840  
 gatgatcata attccatcaa ccgcgcgaat cgcgggatgt atcgtcaag ttatggtccg 900  
 accttgagcg gttttcaaaa acctgagatc atcgcgtctt cgaatctgggt tcccgcgcgg 960  
 atccttccca acaccccaac cgctaagcaa gttgattttc tggagacttt ggacaaggct 1020  
 tcggatgaag atctgcattc gataatcgaa gaaaatcgcg ggatggacgg tgagcttgaa 1080  
 gccgcgcttg accgtccgcg gtatatgctt cgcgacggga catcttttgc cgccgcgatc 1140  
 gaaagcgtaa ttaccgcgtc ttacaaatac catcttttgc cgccgcgatc 1200  
 gtttcatcag taattgctca aatgctcgaa gcaaatccga atctgacacc gcagaaaatt 1260

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aaacgaattt tgatcagttc ggcggaacgt cttccgcatt atgaagtcga tcggcaaggc 1320  
 tggggcgtga tcgatccgcg aaaagccgtt gaaatggcac tttcctttgt ttaa 1374

<210> 12  
 <211> 457  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Obtained from an environmental sample

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 35 40 45  
 Leu Ile Arg Ala Asn Ala Pro Asp Thr Ala Gly Phe Glu Ala Val Cys  
 50 55 60  
 Ala Arg Cys Val Arg Leu Phe Glu Arg Ala Lys Asp Asn Ile Leu Ser  
 65 70 75 80  
 Asp Ala Ala Met Asn Lys Asp Gly Ser Tyr Val Leu Ser Thr Pro Leu  
 85 90 95  
 Arg Leu Asp Ala Asp Glu Arg Phe Thr Gly Lys Gly Val Thr Ile Ala  
 100 105 110  
 Phe Leu Asp Ser Gly Phe Tyr Pro His Val Asp Leu Thr Thr Pro Asn  
 115 120 125  
 Asn Arg Ile Ile Gly Tyr Arg Ser Leu Met His Ala Glu Gly Asp Leu  
 130 135 140  
 Thr Thr Leu Phe Gln Ser Asp Val Ala Ser Trp His Gly Met Met Thr  
 145 150 155 160  
 Ser Val Val Ala Ala Gly Asn Gly Ser Leu Ser Asn Gly Phe Tyr Arg  
 165 170 175  
 Gly Ile Ala Pro Asp Ala Asn Val Val Leu Val Lys Leu Ala Arg Thr  
 180 185 190  
 Gly Arg Ile Thr Glu Gln Asn Ile Gln Asp Gly Leu Glu Trp Ile Leu  
 195 200 205  
 Ala Asn Arg Thr Lys Tyr Gly Ile Lys Val Val Asn Ile Ser Ala Gly  
 210 215 220  
 Gly Asp Phe Glu Gln Ser Tyr Leu His Asp Ala Leu Ser Gln Thr Val  
 225 230 235 240  
 Glu Glu Cys Val Ala Lys Gly Leu Thr Ile Val Cys Ala Ile Gly Asn  
 245 250 255  
 Ala Gly His Leu Pro Thr His Pro Val Phe Pro Pro Ala Ser Ser Pro  
 260 265 270  
 Ser Ala Ile Ala Val Gly Gly Leu Asp Asp His Asn Ser Ile Asn Arg  
 275 280 285  
 Ala Lys Arg Gly Met Tyr Arg Ser Ser Tyr Gly Pro Thr Leu Asp Gly  
 290 295 300  
 Phe Gln Lys Pro Glu Ile Ile Ala Ser Ser Ile Trp Val Pro Ala Pro  
 305 310 315 320  
 Ile Leu Pro Asn Thr Pro Thr Ala Lys Gln Val Asp Phe Leu Glu Thr  
 325 330 335  
 Leu Asp Lys Ala Ser Asp Glu Asp Leu His Arg Ile Ile Glu Glu Asn  
 340 345 350  
 Arg Gly Met Asp Gly Glu Leu Glu Ala Ala Leu Asp Arg Pro Ala Tyr  
 355 360 365  
 Met Leu Arg Gln Ile Ile Leu Leu Lys Leu Gln Arg Glu Ser Val Ile  
 370 375 380  
 Thr Arg His Tyr Lys Tyr Val Asp Gly Thr Ser Phe Ala Ala Pro Ile  
 385 390 395 400  
 Val Ser Ser Val Ile Ala Gln Met Leu Glu Ala Asn Pro Asn Leu Thr  
 405 410 415  
 Pro Gln Lys Ile Lys Arg Ile Leu Ile Ser Ser Ala Glu Arg Leu Pro  
 420 425 430  
 His Tyr Glu Val Asp Arg Gln Gly Trp Gly Val Ile Asp Pro Arg Lys  
 435 440 445

10336256.txt

Ala Val Glu Met Ala Leu Ser Phe Val  
450 455

<210> 13  
<211> 783  
<212> DNA  
<213> Bacteria

<400> 13  
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ggcaccgcgg ccgcccaggg cgagttcccg tggatggtcc ggctctccat gggctgcggc 180  
ggctcgtga tctcgcgcga ggctcgtctc accgccgccc actgctcag cggctccggc 240  
aacaacacca gcatcaccgc caccgccggg gtcgtcgacc tgcagagcag cagcgccatc 300  
aaggtccggt ccaccaaggt cctccaggcc cccggctaca acggcaaggg caaggactgg 360  
gcgctgatca agctcgccag ccccatcacc tcgctgcccc acctgaagat cgccgagacc 420  
accgctgaca acagcggcac cttcacgggt gccggctggg gcgccgcccg tgagggcggc 480  
ggccagcagc gctacctgct caaggcgaac gtgccgttcg tctccgacgc ctctgcccag 540  
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ggggctgaca cctgccaggg tgactccggc ggccccatgt tccgcaagga caacgccgga 660  
gcgtgggtcc aggtcggcat cgtgagctgg ggcgagggct gcgccgcgc cggctacccg 720  
ggcgtctaca cggagggtctc gaccttcgcc gccgccatca agtccgcggc ggccaccctg 780  
taa 783

<210> 14  
<211> 260  
<212> PRT  
<213> Bacteria

<220>  
<221> SIGNAL  
<222> (1)...(33)

<400> 14  
Met Ser Gln Asn Arg Met Val Arg Ala Leu Gln Lys Leu Ala Ala Ala  
1 5 10 15  
Gly Ala Val Val Leu Ala Ala Val Ser Leu Gln Pro Thr Thr Ala Ser  
20 25 30  
Ala Ala Pro Ala Pro Val Val Gly Thr Arg Ala Ala Gln Gly Glu  
35 40 45  
Phe Pro Trp Met Val Arg Leu Ser Met Gly Cys Gly Gly Ser Leu Ile  
50 55 60  
Ser Pro Gln Val Val Leu Thr Ala Ala His Cys Val Ser Gly Ser Gly  
65 70 75 80  
Asn Asn Thr Ser Ile Thr Ala Thr Ala Gly Val Val Asp Leu Gln Ser  
85 90 95  
Ser Ser Ala Ile Lys Val Arg Ser Thr Lys Val Leu Gln Ala Pro Gly  
100 105 110  
Tyr Asn Gly Lys Gly Lys Asp Trp Ala Leu Ile Lys Leu Ala Ser Pro  
115 120 125  
Ile Thr Ser Leu Pro Asn Leu Lys Ile Ala Glu Thr Thr Ala Tyr Asn  
130 135 140  
Ser Gly Thr Phe Thr Val Ala Gly Trp Gly Ala Arg Glu Gly Gly  
145 150 155 160  
Gly Gln Gln Arg Tyr Leu Leu Lys Ala Asn Val Pro Phe Val Ser Asp  
165 170 175  
Ala Ser Cys Gln Ser Ser Tyr Gly Ser Asp Leu Val Pro Ala Glu Glu  
180 185 190  
Ile Cys Ala Gly Tyr Ser Gln Gly Gly Val Asp Thr Cys Gln Gly Asp  
195 200 205  
Ser Gly Gly Pro Met Phe Arg Lys Asp Asn Ala Gly Ala Trp Val Gln  
210 215 220  
Val Gly Ile Val Ser Trp Gly Glu Gly Cys Ala Arg Ala Gly Tyr Pro  
225 230 235 240  
Gly Val Tyr Thr Glu Val Ser Thr Phe Ala Ala Ala Ile Lys Ser Ala  
245 250 255  
Ala Ala Thr Leu  
260

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<210> 15  
 <211> 900  
 <212> DNA  
 <213> Bacteria

<400> 15  
 atgcgcacca cccccacgag aaccgtccgg ctgctcgccg tcgcggcagg cctcgccgcc 60  
 gccgccgcgc tcgccgcccc caccgcgagc gcgggcaccg ccgactccgc gcggagcacc 120  
 cgcaccttcg acgccgccgc cctctcggcg accggcgacg ccgtccgcgc cgccgacgtg 180  
 gccggcaccg cctggtacgc cgacacggcc accggcgagc tggtcgtcac cgccgactcc 240  
 accgtcaccc ccgccgggat cgcgaagatc aagcggcagg cgggggcgaa cgcgacgcc 300  
 atccgggtcg agcggacccc gggcaagtcc accaagctga tctccggcgg cgacgcgatc 360  
 tacggcacca gctggcgctg ctgcgtgggt ttcaacgtcc gggacagtgc gggcaactac 420  
 tacttcctga ccgccggcca ctgcaccgac ggcgcgggca cctggtactc caactcctcc 480  
 cggaccaccg tcctcggcac caccgcgggg tccagcttcc ccggcaacga ctacggtctg 540  
 gtgcgtaca ccaactcctc cgtcaccaag tccggcacgg tcggcagcgt ggacatcacc 600  
 agcggccgca acgccaccgt cggcatgtcg gtcacccgcc gcggctccac caccggcatc 660  
 cacagcggct ccgtgacggg cctgaacgcc accgtgaact acggcggcgg tgacatcgtc 720  
 tccgggctga tccgtacgaa cgtgtgcgcc gagcccggcg actccggcgg tccgctctac 780  
 tcgggcagcc gggcgtcgg cctcacctcg ggcggcagcg gcaactgctc cacgggcggc 840  
 acgaccttct tccagcccgt gaccgagggc ctgagcgcgt acggggtcag cgtcttctag 900

<210> 16  
 <211> 299  
 <212> PRT  
 <213> Bacteria

<220>  
 <221> SIGNAL  
 <222> (1)...(31)

<400> 16  
 Met Arg Thr Thr Pro Thr Arg Thr Val Arg Leu Leu Ala Val Ala Ala  
 1 5 10 15  
 Gly Leu Ala Ala Ala Ala Leu Ala Pro Thr Ala Ser Ala Gly  
 20 25 30  
 Thr Ala Asp Ser Ala Arg Ser Thr Arg Thr Phe Asp Ala Ala Ala Leu  
 35 40 45  
 Ser Ala Thr Gly Asp Ala Val Arg Ala Ala Asp Val Ala Gly Thr Ala  
 50 55 60  
 Trp Tyr Ala Asp Thr Ala Thr Gly Glu Leu Val Val Thr Ala Asp Ser  
 65 70 75 80  
 Thr Val Thr Pro Ala Gly Ile Ala Lys Ile Lys Arg Gln Ala Gly Ala  
 85 90 95  
 Asn Ala Asp Ala Ile Arg Val Glu Arg Thr Pro Gly Lys Phe Thr Lys  
 100 105 110  
 Leu Ile Ser Gly Gly Asp Ala Ile Tyr Ala Thr Ser Trp Arg Cys Ser  
 115 120 125  
 Leu Gly Phe Asn Val Arg Asp Ser Ala Gly Asn Tyr Tyr Phe Leu Thr  
 130 135 140  
 Ala Gly His Cys Thr Asp Gly Ala Gly Thr Trp Tyr Ser Asn Ser Ser  
 145 150 155 160  
 Arg Thr Thr Val Leu Gly Thr Thr Ala Gly Ser Ser Phe Pro Gly Asn  
 165 170 175  
 Asp Tyr Gly Leu Val Arg Tyr Thr Asn Ser Ser Val Thr Lys Ser Gly  
 180 185 190  
 Thr Val Gly Ser Val Asp Ile Thr Ser Ala Ala Asn Ala Thr Val Gly  
 195 200 205  
 Met Ser Val Thr Arg Arg Gly Ser Thr Thr Gly Ile His Ser Gly Ser  
 210 215 220  
 Val Thr Gly Leu Asn Ala Thr Val Asn Tyr Gly Gly Asp Ile Val  
 225 230 235 240  
 Ser Gly Leu Ile Arg Thr Asn Val Cys Ala Glu Pro Gly Asp Ser Gly  
 245 250 255  
 Gly Pro Leu Tyr Ser Gly Ser Arg Ala Val Gly Leu Thr Ser Gly Gly  
 260 265 270  
 Ser Gly Asn Cys Ser Thr Gly Gly Thr Thr Phe Phe Gln Pro Val Thr

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275 280 285  
 Glu Ala Leu Ser Ala Tyr Gly Val Ser Val Phe  
 290 295

<210> 17  
 <211> 1137  
 <212> DNA  
 <213> Bacteria

<400> 17  
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 gtagactaca gcgtcgaggt taagcgcggc gaccgtgtcg ttataaggac gtggcttgag 120  
 gctctcccc tcgcaaggct cgtctaccgc gaggtgctga ggagggcgcg gcaccccgca 180  
 ctatacctgg aggatgatat cctcgccgag atattctacc gcgaggctag cgacgagcag 240  
 atcgatttcg ttgacgccct ccgccgcagc atatacaccg agttcgacgt cgtgataacc 300  
 ctctttgccc cgagccactt gaagaatctt gtgagtatcc cgccggagaa gcaggctagg 360  
 aggagcaagg ccctcgagcc ctacttcacg aggttcctcc aggaggccgc tgagggcaag 420  
 aagaggtggg ttctcgccgc ctaccgcagc ctgcgatgg cccaggaggc tggcatgacg 480  
 cctatcgagt tcgaggagtt cgtggcaaga gcagtgaagg tcacggagga cgaccgggtc 540  
 gccgcgtgga ggaggcaagc cgagtaccag aggaggatag tcgacgagat cctctcgaag 600  
 cgtgatgagc ttgtcttcaa gggcccgggc atcgacctaa ccgtgaaggt cgggtggccgc 660  
 cgctggatcg ttgacgacgg ccacgagaat atgccgggtg gcgaggtgtt cacgggcccc 720  
 gtcgaggata gcgtggaggg ctgtgtacgc ttcgacttcc cgagcgtcta tcgcggcgtg 780  
 gaggtagagg gcgtcaagct gtgcttcaag aggggcgagg ttgtagagta tgacgccgtc 840  
 aagggccgcg acttcctcgc taagatgctg agtgtggacg agggcgccaa gaggctagga 900  
 gagctggcct tcgggtcgaa ctatggcata accagggcga cgcgagagat actcttcgac 960  
 gagaagatag ggggtaccat ccacatggcg cttggaaacg gctacccgga gaccggctcg 1020  
 agaaacaaga gcgccatcca ctgggacctg ataaaagaca tgagggaccc agaggcacgc 1080  
 gtctatgccg atggcgagct tatctacaag gctggcaggt tcctactaga ggagtga 1137

<210> 18  
 <211> 378  
 <212> PRT  
 <213> Bacteria

<400> 18  
 Met Lys Arg Pro Val Ser Ile Val Phe Pro Ala Tyr Leu Glu Lys Tyr  
 1 5 10 15  
 Ala Arg Leu Leu Val Asp Tyr Ser Val Glu Val Lys Arg Gly Asp Arg  
 20 25 30  
 Val Val Ile Arg Thr Trp Leu Glu Ala Leu Pro Leu Ala Arg Leu Val  
 35 40 45  
 Tyr Arg Glu Val Leu Arg Arg Gly Ala His Pro Ala Leu Tyr Leu Glu  
 50 55 60  
 Asp Asp Ile Leu Ala Glu Ile Phe Tyr Arg Glu Ala Ser Asp Glu Gln  
 65 70 75 80  
 Ile Asp Phe Val Asp Ala Leu Arg Arg Ser Ile Tyr Thr Glu Phe Asp  
 85 90 95  
 Val Val Ile Thr Leu Phe Ala Pro Ser His Leu Lys Asn Leu Val Ser  
 100 105 110  
 Ile Pro Pro Glu Lys Gln Ala Arg Arg Ser Lys Ala Leu Glu Pro Tyr  
 115 120 125  
 Phe Thr Arg Phe Leu Gln Glu Ala Ala Glu Gly Lys Lys Arg Trp Val  
 130 135 140  
 Leu Ala Ala Tyr Pro Thr Leu Ala Met Ala Gln Glu Ala Gly Met Thr  
 145 150 155 160  
 Pro Ile Glu Phe Glu Phe Val Ala Arg Ala Val Lys Val Thr Glu  
 165 170 175  
 Asp Asp Pro Val Ala Ala Trp Arg Arg Gln Ala Glu Tyr Gln Arg Arg  
 180 185 190  
 Ile Val Asp Glu Ile Leu Ser Lys Ala Asp Glu Leu Val Phe Lys Gly  
 195 200 205  
 Pro Gly Ile Asp Leu Thr Val Lys Val Gly Gly Arg Arg Trp Ile Val  
 210 215 220  
 Asp Asp Gly His Glu Asn Met Pro Gly Gly Glu Val Phe Thr Gly Pro  
 225 230 235 240  
 Val Glu Asp Ser Val Glu Gly Cys Val Arg Phe Asp Phe Pro Ser Val  
 245 250 255

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Tyr Arg Gly Val Glu Val Glu Gly Val Lys Leu Cys Phe Lys Arg Gly  
 260 265 270  
 Glu Val Val Glu Tyr Asp Ala Val Lys Gly Arg Asp Phe Leu Ala Lys  
 275 280 285  
 Met Leu Ser Val Asp Glu Gly Ala Lys Arg Leu Gly Glu Leu Ala Phe  
 290 295 300  
 Gly Leu Asn Tyr Gly Ile Thr Arg Ala Thr Arg Glu Ile Leu Phe Asp  
 305 310 315 320  
 Glu Lys Ile Gly Gly Thr Ile His Met Ala Leu Gly Asn Gly Tyr Pro  
 325 330 335  
 Glu Thr Gly Ser Arg Asn Lys Ser Ala Ile His Trp Asp Leu Ile Lys  
 340 345 350  
 Asp Met Arg Asp Pro Glu Ala Arg Val Tyr Ala Asp Gly Glu Leu Ile  
 355 360 365  
 Tyr Lys Ala Gly Arg Phe Leu Leu Glu Glu  
 370 375

<210> 19  
 <211> 2298  
 <212> DNA  
 <213> Unknown

<220>  
 <223> obtained from an environmental sample.

<400> 19  
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 actctctgct acagccttgc ggcttaccct tcatctcaaa acacagaagc cttggcgcaa 120  
 attcaagata agattgctca aaatgacagc actctagtct tggtagaatt acttctaccg 180  
 agcactgcgg ccaatttgag cggcggcaat ctggcatctc acactgaaca gctcagaaat 240  
 attcagttga gtgtattggg tgacctaaact accggagcca gcaccaactc aaacctgatc 300  
 aatgccactt tatttgatta cgtcaatggg atggctctga cagttgatgc aaacctgctg 360  
 gatcagctgt tgcagcacc tctgtgtggc cgcatttcgc caaatgatgt tagttatcca 420  
 atgctaaccg atagcatgcc cttgattggc gctgatccca caggcggctt ttccggacac 480  
 ggcggtcaag gtcaagcggg agccatttgg gatacaggcg ttgataaata tcaccccgct 540  
 tttaaggtta gagttatctc agaagcctgt tattctgctg ctgcttatac tgatgactgg 600  
 ttgattcagt ctttttctact atgccctgga ggggttgctg aatcagtatt gccaggctct 660  
 ggcatacact gcgagaacca ccgtgattgc ggccacggta cacacgtagc gggcatagca 720  
 actggtcaag cggttaagcgt caataatcaa tctgtctttg gtgttgctcc gtcggccgac 780  
 ataactcgcca ttcttaaagg gttggagcgc cacactccca accagaccac aggcctggatt gcaggcccac 840  
 actttggata ttcttaaagg gttggagcgc gtcatagcct tgcacgacgc aggcaccctt 900  
 atcgctgcgg ctaatatgag tttagggttc tcattatttc aggaactcat cgatgatcac 960  
 caacctctga tgactcaagc cattgagaac ttgctgagtc gtggcattgc aacctatgtc 1020  
 gccagcggtg actattgggt tagagaccgc ataagctggc cggcatgtat atccagcgct 1080  
 atcagtggtg gtagcacaac gaaagatgat gaagtatccg attttagcaa tcacacctct 1140  
 cttgtaaatt tactagcgcc tggcagtgaa attcttgag ccgtgccggg taacgctttt 1200  
 gaggtttata gcggtacatc tatggccgca ccccatgttg ccggtgcctg ggctgtgctt 1260  
 aaaggcgctt acccagagtc aagtgtggag gacattttta ctgctgtaga cgctacaggt 1320  
 attcccgat tggatacacg gcatggcgcc attgatcatg ccatacctcg catacaggtt 1380  
 gaccaagcac ttttgccctt aggcaccccc aattacgatt caacttatcc aagcatgcac 1440  
 attcgcgcca ctttcaacgc ctgggacaac gccagcatga gacttgtaga tgactttaca 1500  
 tgggaagcaa atcttgctact gcaacctagc aacggtgctg ctacaccttt caagtttgat 1560  
 gcatacggtg attggcttag aaattatggg tccagtgcg aagcaggagt agcttcactt 1620  
 tacggcgctg atcttgaaac acagtgcacc ggagaagtga cggttaagggt caacgatgcc 1680  
 aacctttcat actctgtaga aggtgagggc tgtactgatt ccaactggcg ccgactgtt 1740  
 attttcatct atggtcaaac ccaagtaggg caagacatgt ttattcgtgg cggaatagac 1800  
 caggtttacg ccagcagtggt attgggcatt aattgcacgc aggaaaacat gctttgcgcc 1860  
 ataccatttc taacctttgaa agcacgacaa acccctggaa agtgaacgac 1920  
 caccacctgg attggtatgg tgctgagcct gggcaaagta gtagcgcggc aggcacacca 1980  
 tttgattgga ccacaaacct ctggccatcc agctggggca ccagaagaac ggttgaagtt 2040  
 gatggttacg gcgaaacacc tctcaatcaa tggggggatc attactggat gctggacggt 2100  
 gaaatggatt gctccagagt ggtgaatgga ttggttgaag taaaatcctt tataacaaat 2160  
 gggcccggtt gggaaagcga tgtgaatcaa cccggacgcc cttgggtatc tggcaatcac 2220  
 tttgctcaat gtggaacgct taatgtcttt aggcgcaatg aagatcaacc cgtattggtt 2280  
 ggtcagccaa ttccgtga

<210> 20  
 <211> 765

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&lt;212&gt; PRT

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; Obtained from an environmental sample.

&lt;221&gt; SIGNAL

&lt;222&gt; (1)...(39)

&lt;400&gt; 20

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Met Lys Leu Lys Pro Phe Pro Leu Arg Leu Gln Ala Lys Thr Trp Leu
1      5      10      15
Leu Phe Ile Leu Thr Leu Cys Tyr Ser Leu Ala Ala Tyr Pro Ser Ser
20      25      30
Gln Asn Thr Glu Ala Leu Ala Gln Ile Gln Asp Lys Ile Ala Gln Asn
35      40      45
Asp Ser Thr Leu Val Leu Val Glu Leu Leu Leu Pro Ser Thr Ala Ala
50      55      60
Asn Leu Ser Gly Gly Asn Leu Ala Ser His Thr Glu Gln Leu Arg Asn
65      70      75      80
Ile Gln Leu Ser Val Leu Gly Asp Leu Thr Thr Gly Ala Ser Thr Asn
85      90      95
Ser Asn Leu Ile Asn Ala Thr Leu Phe Asp Tyr Val Asn Gly Met Ala
100      105      110
Leu Thr Val Asp Ala Asn Leu Leu Asp Gln Leu Leu Gln His Pro Ser
115      120      125
Val Gly Arg Ile Ser Pro Asn Asp Val Ser Tyr Pro Met Leu Thr Asp
130      135      140
Ser Met Pro Leu Ile Gly Ala Asp Pro Thr Gly Gly Phe Ser Gly His
145      150      155      160
Gly Gly Gln Gly Gln Ala Val Ala Ile Leu Asp Thr Gly Val Asp Lys
165      170      175
Tyr His Pro Ala Phe Gln Gly Arg Val Ile Ser Glu Ala Cys Tyr Ser
180      185      190
Ala Ser Ala Tyr Thr Asp Asp Trp Leu Ile Gln Ser Phe Ser Leu Cys
195      200      205
Pro Gly Gly Val Ala Glu Ser Val Leu Pro Gly Ser Gly Ile His Cys
210      215      220
Glu Asn His Arg Asp Cys Gly His Gly Thr His Val Ala Gly Ile Ala
225      230      235      240
Thr Gly Gln Ala Val Ser Val Asn Asn Gln Ser Val Phe Gly Val Ala
245      250      255
Pro Ser Ala Asp Ile Ile Ala Ile Gln Val Phe Thr Leu Pro Thr Arg
260      265      270
Pro Gln Ala Gly Leu Gln Ala His Thr Leu Asp Ile Leu Lys Gly Leu
275      280      285
Glu Arg Val Ile Ala Leu His Asp Ala Gly Thr Pro Ile Ala Ala Ala
290      295      300
Asn Met Ser Leu Gly Phe Ser Leu Phe Gln Asp Ser Cys Asp Asp His
305      310      315      320
Gln Pro Leu Met Thr Gln Ala Ile Glu Asn Leu Arg Ser Arg Gly Ile
325      330      335
Ala Thr Ile Val Ala Ser Gly Asn Tyr Gly Phe Arg Asp Arg Ile Ser
340      345      350
Trp Pro Ala Cys Ile Ser Ser Ala Ile Ser Val Gly Ser Thr Thr Lys
355      360      365
Asp Asp Glu Val Ser Asp Phe Ser Asn His Thr Ser Leu Val Asn Leu
370      375      380
Leu Ala Pro Gly Ser Glu Ile Leu Ala Ala Val Pro Gly Asn Ala Phe
385      390      395      400
Glu Val Tyr Ser Gly Thr Ser Met Ala Ala Pro His Val Ala Gly Ala
405      410      415
Trp Ala Val Leu Lys Gly Ala Tyr Pro Glu Ser Ser Val Asp Asp Ile
420      425      430
Leu Thr Ala Leu Asp Ala Thr Gly Ile Pro Val Leu Asp Thr Arg His
435      440      445
Gly Ala Ile Asp His Ala Ile Pro Arg Ile Gln Val Asp Gln Ala Leu
450      455      460

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## 10336256.txt

Leu Ala Leu Gly Thr Pro Asn Tyr Asp Ser Thr Tyr Pro Ser Met His  
 465 470 475 480  
 Ile Arg Gly Thr Phe Asn Ala Trp Asp Asn Ala Ser Met Arg Leu Val  
 485 490 495  
 Asp Asp Phe Thr Trp Glu Ala Asn Leu Val Leu Gln Pro Ser Asn Gly  
 500 505 510  
 Ala Ala His Leu Phe Lys Phe Asp Ala Tyr Gly Asp Trp Leu Arg Asn  
 515 520 525  
 Tyr Gly Ser Ser Ala Glu Ala Gly Val Ala Ser Leu Tyr Gly Ala Asp  
 530 535 540  
 Leu Glu Thr Gln Cys Thr Gly Glu Val Thr Val Arg Phe Asn Asp Ala  
 545 550 555 560  
 Asn Leu Ser Tyr Ser Val Glu Gly Glu Gly Cys Thr Asp Ser Asn Trp  
 565 570 575  
 Arg Arg Thr Val Ile Phe Ile Tyr Gly Gln Thr Gln Val Gly Gln Asp  
 580 585 590  
 Met Phe Ile Arg Gly Gly Ile Asp His Gly Tyr Ala Ser Ser Val Leu  
 595 600 605  
 Gly Ile Asn Cys Thr Gln Glu Asn Met Leu Cys Ala Ile Pro Ile Arg  
 610 615 620  
 His Leu Asn Asn Leu Asn Ser Thr Thr Asn Pro Trp Lys Val Asn Asp  
 625 630 635 640  
 His His Leu Asp Trp Tyr Gly Ala Glu Pro Gly Gln Ser Ser Ser Ala  
 645 650 655  
 Ala Gly Thr Pro Phe Asp Trp Thr Thr Asn Leu Trp Pro Ser Ser Trp  
 660 665 670  
 Gly Thr Arg Arg Thr Val Glu Val Asp Gly Tyr Gly Glu Thr Pro Leu  
 675 680 685  
 Asn Gln Trp Gly Asp His Tyr Trp Met Leu Asp Val Glu Met Asp Cys  
 690 695 700  
 Ser Arg Thr Val Asn Gly Trp Phe Glu Val Lys Ser Phe Ile Thr Asn  
 705 710 715 720  
 Gly Pro Gly Trp Glu Ser Asp Val Asn Gln Pro Gly Arg Pro Trp Val  
 725 730 735  
 Ser Gly Asn His Phe Ala Gln Cys Gly Thr Leu Asn Val Phe Arg Arg  
 740 745 750  
 Asn Glu Asp Gln Pro Val Leu Val Gly Gln Pro Ile Pro  
 755 760 765

<210> 21  
 <211> 867  
 <212> DNA  
 <213> Unknown

<220>  
 <223> Obtained from an environmental sample.

<400> 21  
 atgaataaca taaaaaagat aataatgtta ctgttaacga tagcaaacgg tttatatatta 60  
 agttctcaaa atatagattt tgacaaccaa tccaaattaa acataacctca attgcaactt 120  
 cccaacgttc aaccggccat aggaaccgaa gaaaagggtt cgaaaatagt cggcggagtg 180  
 acaacgacaa actcgggaatt tcctttcata gtttccttac aacattctta ctacggccat 240  
 ttctgcgagg gctcattaat agcaaaggat tgggttttaa ccgcggtca ctgctagac 300  
 ggaataactc cttcttacat agtaacgggc ataagcaagc tcacggatac cgtcgggtcaa 360  
 agatttactc cggttaaaat aataaaacat ccttcctgga attcccagac aatggactac 420  
 gactacgctt taatcaaatt aagcggacaa tcctccgctc cgattataga attaaacacg 480  
 ctggaattaa acgccggaac caatctaacg gtagcggggt ggggacttac caaagaaaac 540  
 ggagacatct ccaatacgct tcaaaaagta actcttccgc tcgtatccaa aacaacctgc 600  
 ttaaaagctt atcctaacgc cataaccgac agaatgatag gcgcgggtta cgccaccggc 660  
 gggaaagact catgtcaggg agatagcggc ggtccttgg tatacaaaac ctcttcaaaa 720  
 cgtatcttg tcggtgtggt tagctggggg gagggatgcg cgagagaagg gaaatatgga 780  
 atttattcaa aggttaagcg cgtaaagcgc tggatagaaa acaccgtaaa aacgggaagt 840  
 tcaagctcac ttatactcga ttattga 867

<210> 22  
 <211> 288  
 <212> PRT  
 <213> Unknown

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&lt;220&gt;

&lt;223&gt; Obtained from an environmental sample.

&lt;221&gt; SIGNAL

&lt;222&gt; (1)...(22)

&lt;400&gt; 22

```

Met Asn Asn Ile Lys Lys Ile Ile Met Leu Leu Leu Thr Ile Ala Asn
 1      5      10      15
Gly Leu Tyr Leu Ser Ser Gln Asn Ile Asp Phe Asp Asn Gln Ser Lys
 20      25      30
Leu Asn Ile Pro Gln Leu Gln Leu Pro Asn Val Gln Pro Ala Ile Gly
 35      40      45
Thr Glu Glu Lys Val Ser Lys Ile Val Gly Gly Val Thr Thr Thr Asn
 50      55      60
Ser Glu Phe Pro Phe Ile Val Ser Leu Gln His Ser Tyr Tyr Gly His
 65      70      75      80
Phe Cys Gly Gly Ser Leu Ile Ala Lys Asp Trp Val Leu Thr Ala Ala
 85      90      95
His Cys Val Asp Gly Ile Thr Pro Ser Tyr Ile Val Thr Gly Ile Ser
100      105      110
Lys Leu Thr Asp Thr Val Gly Gln Arg Phe Thr Pro Val Lys Ile Ile
115      120      125
Lys His Pro Ser Trp Asn Ser Gln Thr Met Asp Tyr Asp Tyr Ala Leu
130      135      140
Ile Lys Leu Ser Gly Gln Ser Ser Ala Pro Ile Ile Glu Leu Asn Thr
145      150      155      160
Leu Glu Leu Asn Ala Gly Thr Asn Leu Thr Val Ala Gly Trp Gly Leu
165      170      175
Thr Lys Glu Asn Gly Asp Ile Ser Asn Thr Leu Gln Lys Val Thr Leu
180      185      190
Pro Leu Val Ser Lys Thr Thr Cys Leu Lys Ala Tyr Pro Asn Ala Ile
195      200      205
Thr Asp Arg Met Ile Cys Ala Gly Tyr Ala Thr Gly Lys Asp Ser
210      215      220
Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Tyr Lys Thr Ser Ser Lys
225      230      235      240
Ala Tyr Leu Val Gly Val Val Ser Trp Gly Glu Gly Cys Ala Arg Glu
245      250      255
Gly Lys Tyr Gly Ile Tyr Ser Lys Val Ser Ala Val Lys Asn Trp Ile
260      265      270
Glu Asn Thr Val Lys Thr Gly Ser Ser Ser Leu Ile Leu Asp Tyr
275      280      285

```

&lt;210&gt; 23

&lt;211&gt; 1647

&lt;212&gt; DNA

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; Obtained from an environmental sample.

&lt;400&gt; 23

```

atgaatcggt cgcaagtga gttgctggcc gcgtcgctgc tgctggccct cagcctgccg      60
gccgcggcgg aagacatctc cggcaatacc cggttcgacc tcagttcggt gcaggaaggc      120
gccacctatg accgcttcat cgtggtctac cgcaatggca gcacggagca cgccagcccc      180
gtcggcgggc tccaggcgct gtcggcgggc gccggcaagg cgacgcttct cgacgcggga      240
acggggcgct cgcccaatac ccttcgcgcc ggcggccgcg cgctgggcct gaactacaag      300
cgcaagctcg ccagcggcgg cgacctggtc accacctcgc gccgcctgag cgcgtccgag      360
gcccggcagt tcgtgcagca gatcgcggcc gatccggccg tcgagttcgt gcagccggac      420
tacatgcgcc acgcgctggg caagccggtc aaggtgcagc ccgagggcgc ggccaccttc      480
accacgccga atgaccagta ctacgccggc tatcagtggg attacctgcc cgccgacggc      540
gcagccttca acgacaacag cctgggcaag gccgtggcca actggggcgg cgccaacatc      600
cagaaggcat ggagcctggc cgacggcacc ggcacgtcga tcgccagcct cgataccggc      660
gtgaccaacc atccggacct ggacctgacc ctggccgacg ccggctacga cttcatcagg      720
accgcgctgg tgtcggggcg ctccaccgac ggcgcggctt cgggcggctg ggatctgggc      780
gactggacca ccggcagcaa gtacctggcc agcaacggcg gctgcgtgga ctccacccat      840

```

## 10336256.txt

ccggccgagg	acagcagctg	gcacggcact	catgtgttcg	gcaccgccgg	cggcgagaag	900
accaacaaca	gcaccggcat	ggtcgggtacc	gccttcggcg	ccaagggtgct	gccgggtccgc	960
gtgctggggc	actgcggcgg	ctacgacagc	gacatcgccg	acgccatcac	ctgggcttcc	1020
ggcgggccacg	tggacggcgt	gccggacaac	acccatccgg	cgcagggtgat	cagcatgagc	1080
ctgggcgggca	gcggcacctg	cacctccagc	acgggtgaccg	gtcgcgccat	cagtggcgcg	1140
atcagcccg	gcgcgaccgt	ggtcgtggcg	gccggcaaca	gcaacgcca	cgtgtccaac	1200
ttctcgccgg	ccagctgccc	cggcgtgatc	gcgggtcgcg	ccaccggcat	caccagccgc	1260
cgcgcgtact	actccaacta	cggcaagggc	atcaccttgg	ccgcgccggg	cggcggcgtg	1320
tacgccaacg	acggctccag	cggttcgag	gcgaccaccg	gcttcacatc	gtcgaccatc	1380
gactcgggca	ccaccacgcc	ggccgggttcc	acctacggcg	gcatggcggg	tacctcgag	1440
gccacgcccgc	acgtggccgg	cgcggtggcg	ctgatgcaga	gctaccgcct	ggcgtgggc	1500
aagtcgtgc	tgagctccgc	gcaggtgacg	tcgctgctga	agtccacggc	caccgtgccg	1560
cacgtggccg	ccagcggcag	caagccgatc	ggcgcgggca	tcctcaacgc	ctacgccgcg	1620
gtgcaggccg	cgggcgcgca	gccctga				1647

<210> 24  
 <211> 548  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Obtained from an environmental sample.

<221> SIGNAL  
 <222> (1)...(23)

<400> 24

Met	Asn	Arg	Ser	Gln	Val	Lys	Leu	Leu	Ala	Ala	Ser	Leu	Leu	Leu	Ala
1				5					10					15	
Leu	Ser	Leu	Pro	Ala	Ala	Ala	Glu	Asp	Ile	Ser	Gly	Asn	Thr	Arg	Phe
			20					25					30		
Asp	Leu	Ser	Ser	Val	Gln	Glu	Gly	Ala	Thr	Tyr	Asp	Arg	Phe	Ile	Val
		35					40					45			
Val	Tyr	Arg	Asn	Gly	Ser	Thr	Glu	His	Ala	Ser	Pro	Ala	Ala	Ala	Ile
	50					55					60				
Gln	Ala	Leu	Ser	Ala	Ala	Ala	Gly	Lys	Ala	Gln	Leu	Ser	Asp	Ala	Gly
65					70					75				80	
Thr	Gly	Ala	Ser	Pro	Asn	Thr	Leu	Arg	Ala	Gly	Gly	Arg	Ala	Leu	Gly
			85						90					95	
Leu	Asn	Tyr	Lys	Arg	Lys	Leu	Ala	Ser	Gly	Gly	Asp	Leu	Val	Thr	Thr
			100					105					110		
Ser	Arg	Arg	Leu	Ser	Ala	Ser	Glu	Ala	Arg	Gln	Phe	Val	Gln	Gln	Ile
		115					120					125			
Ala	Ala	Asp	Pro	Ala	Val	Glu	Phe	Val	Gln	Pro	Asp	Tyr	Leu	Arg	His
	130					135					140				
Ala	Leu	Gly	Lys	Pro	Val	Lys	Val	Gln	Pro	Glu	Gly	Ala	Ala	Thr	Phe
145					150					155				160	
Thr	Thr	Pro	Asn	Asp	Gln	Tyr	Tyr	Ala	Gly	Tyr	Gln	Trp	Asp	Tyr	Leu
			165						170				175		
Pro	Ala	Asp	Gly	Ala	Ala	Phe	Asn	Asp	Asn	Ser	Leu	Gly	Lys	Ala	Val
			180					185					190		
Ala	Asn	Trp	Gly	Gly	Ala	Asn	Ile	Gln	Lys	Ala	Trp	Ser	Leu	Ala	Asp
	195						200					205			
Gly	Thr	Gly	Ile	Val	Ile	Ala	Ser	Leu	Asp	Thr	Gly	Val	Thr	Asn	His
	210					215					220				
Pro	Asp	Leu	Asp	Leu	Thr	Leu	Ala	Asp	Ala	Gly	Tyr	Asp	Phe	Ile	Ser
225					230					235				240	
Thr	Ala	Leu	Val	Ser	Gly	Arg	Ser	Thr	Asp	Gly	Arg	Ala	Ser	Gly	Gly
			245						250					255	
Trp	Asp	Leu	Gly	Asp	Trp	Thr	Thr	Gly	Ser	Lys	Tyr	Leu	Ala	Ser	Asn
			260					265					270		
Gly	Gly	Cys	Val	Asp	Ser	Thr	His	Pro	Ala	Glu	Asp	Ser	Ser	Trp	His
	275						280					285			
Gly	Thr	His	Val	Phe	Gly	Thr	Ala	Gly	Gly	Glu	Lys	Thr	Asn	Asn	Ser
	290					295					300				
Thr	Gly	Met	Val	Gly	Thr	Ala	Phe	Gly	Ala	Lys	Val	Leu	Pro	Val	Arg
305					310					315				320	
Val	Leu	Gly	His	Cys	Gly	Gly	Tyr	Asp	Ser	Asp	Ile	Ala	Asp	Ala	Ile

10336256.txt

```

      325      330      335
Thr Trp Ala Ser Gly Gly His Val Asp Gly Val Pro Asp Asn Thr His
      340      345      350
Pro Ala Gln Val Ile Ser Met Ser Leu Gly Gly Ser Gly Thr Cys Thr
      355      360      365
Ser Ser Thr Val Thr Gly Arg Ala Ile Ser Gly Ala Ile Ser Arg Gly
      370      375      380
Ala Thr Val Val Val Ala Ala Gly Asn Ser Asn Ala Asn Val Ser Asn
      385      390      395
Phe Ser Pro Ala Ser Cys Pro Gly Val Ile Ala Val Ala Ala Thr Gly
      400      405      410
Ile Thr Ser Arg Arg Ala Tyr Tyr Ser Asn Tyr Gly Lys Gly Ile Thr
      415      420      425
Leu Ala Ala Pro Gly Gly Gly Val Tyr Ala Asn Asp Gly Ser Ser Gly
      430      435      440
Ser Gln Ala Thr Thr Gly Phe Ile Trp Ser Thr Ile Asp Ser Gly Thr
      445      450      455
Thr Thr Pro Ala Gly Ser Thr Tyr Gly Gly Met Ala Gly Thr Ser Gln
      460      465      470
Ala Thr Pro His Val Ala Gly Ala Val Ala Leu Met Gln Ser Tyr Arg
      475      480      485
Leu Ala Leu Gly Lys Ser Leu Leu Ser Ser Ala Gln Val Thr Ser Leu
      490      495      500
Leu Lys Ser Thr Ala Thr Val Pro His Val Ala Ala Ser Gly Ser Lys
      505      510      515
Pro Ile Gly Ala Gly Ile Leu Asn Ala Tyr Ala Ala Val Gln Ala Ala
      520      525      530
Gly Ala Gln Pro
      535      540      545

```

<210> 25  
 <211> 1323  
 <212> DNA  
 <213> Unknown

<220>  
 <223> Obtained from an environmental sample.

<400> 25

atgagcagca	tcgcagtgtc	tccagcgccc	cagccgacag	gcaatatgct	ggttatgttc	60
catccggacc	ggaagcccag	ggatgtcgag	cggctggtgt	ccaatgtcgt	cggcgcgaa	120
gtcgtgcatt	cgcgcgattt	ccgggcccga	acgcccggga	tcgcccgaag	cttcgcggat	180
gccggtgcgc	tcaaccttga	ccgggtcggc	atcgcggtcg	tgaaggcgcc	ggaggacgac	240
ggcttctcgg	tgcccgccga	gacgcttcgc	aaccgcaagg	aggctcgtcg	ggtgctccg	300
gagttctgga	tgcacatgct	ggccgggtgg	gacgatcgct	acgccgcctg	ggtgctcgac	360
ggcctctccc	tgctggccga	ccaggcgctg	cgcggtcgtc	tgccgcccgc	tcccggcgcc	420
atcgcgccgg	gaccgggcgt	tgccggtcgc	tcccagctct	ctgcgacctg	ggggcttgcc	480
gccaccggcg	tcgatcgtct	gtcctatacg	ggcgctcgga	tcaaggctcg	ggtgctggac	540
accgggttcg	acttcaccca	tcccgacttc	gccgggcgca	cgctcgtgtc	aaaaagcttc	600
gtgcccggcg	aggacgtcca	ggatgtgcag	ggccacggca	cccattgcat	cggcacggcc	660
tgcgggcccgc	tgctcgccggc	cgaacagggtc	cgctacggcg	tcgcctacga	agccgagatc	720
tatgcgggca	aggttttgga	caacaacggc	tccggcgccg	aacgctgggt	gctcgccggc	780
atggaatggg	cgatcgagca	gaagtgcgag	gtcatatcca	tgctcgtcgg	ccgcgcccgt	840
cagccgggtg	aggcgccgga	cgatttctat	gagcgcgccg	gcgaatacgc	gctcgagaac	900
ggctcgtgta	tcatcgccgc	ggccggcaat	aacagctggc	ggcaatacaa	cgacatcaag	960
ccggtcggct	cgccggccaa	tgccccctcg	atcatggcgg	tgccggcggt	cgacgccaag	1020
atgaaggctc	cgaacttctc	ctgcccggcg	gtcaatccgg	caggcggtga	ggtcaacatc	1080
gccgggcctg	gcgtccctcc	gtgcccgatgc	gtgcccgatgc	cgcgcaaata	tgaccgcttc	1140
tccggcacct	cgatggcgac	gccgcatgtc	gccggcatgc	ccgccctcct	cgcccagtcg	1200
gacaagagcc	tgcgcggcaa	ggcgctgtgg	acggcgctgg	aacaaggcgc	gcgcaatatc	1260
gggcatcccc	cgcgcgacgt	gggcgcgggg	ctcgtgatgg	cgccgggaag	cgcctgtcga	1320
tag						1323

<210> 26  
 <211> 440  
 <212> PRT  
 <213> Unknown

10336256.txt

&lt;220&gt;

&lt;223&gt; obtained from an environmental sample.

&lt;400&gt; 26

```

Met Ser Ser Ile Ala Val Ser Pro Ala Pro Gln Pro Thr Gly Asn Met
 1      5      10      15
Leu Val Met Phe His Pro Asp Arg Lys Pro Arg Asp Val Glu Arg Leu
 20      25      30
Val Ser Asn Val Val Gly Ala Lys Val Val His Ser Arg Asp Phe Arg
 35      40      45
Ala Asp Thr Pro Gly Ile Ala Glu Ala Phe Ala Asp Ala Gly Ala Leu
 50      55      60
Asn Leu Asp Arg Leu Gly Ile Ala Val Val Lys Ala Pro Glu Asp Asp
 65      70      75      80
Gly Phe Ser Val Ala Ala Glu Thr Leu Arg Asn Arg Lys Glu Val Val
 85      90      95
Glu Val Arg Pro Glu Phe Trp Met His Met Leu Ala Gly Trp Asp Asp
 100      105      110
Arg Tyr Ala Ala Trp Val Arg Asp Gly Leu Ser Leu Leu Ala Asp Gln
 115      120      125
Ala Leu Arg Gly Val Leu Pro Pro Pro Gly Gly Ile Ala Ala Gly
 130      135      140
Pro Gly Val Ala Val Ala Ser Gln Leu Ser Ala Thr Trp Gly Leu Ala
 145      150      155      160
Ala Thr Gly Val Asp Arg Ser Ser Tyr Thr Gly Val Gly Ile Lys Val
 165      170      175
Ala Val Leu Asp Thr Gly Phe Asp Phe Thr His Pro Asp Phe Ala Gly
 180      185      190
Arg Ser Val Val Ser Lys Ser Phe Val Pro Gly Glu Asp Val Gln Asp
 195      200      205
Val Gln Gly His Gly Thr His Cys Ile Gly Thr Ala Cys Gly Pro Leu
 210      215      220
Ser Pro Ala Glu Gln Val Arg Tyr Gly Val Ala Tyr Glu Ala Glu Ile
 225      230      235      240
Tyr Ala Gly Lys Val Leu Gly Asn Asn Gly Ser Gly Ala Glu Arg Trp
 245      250      255
Val Leu Ala Gly Met Glu Trp Ala Ile Glu Gln Lys Cys Glu Val Ile
 260      265      270
Ser Met Ser Leu Gly Arg Ala Val Gln Pro Gly Glu Ala Pro Asp Ala
 275      280      285
Phe Tyr Glu Arg Ala Gly Glu Tyr Ala Leu Glu Asn Gly Ser Leu Ile
 290      295      300
Ile Ala Ala Ala Gly Asn Asn Ser Trp Arg Gln Tyr Asn Asp Ile Lys
 305      310      315      320
Pro Val Gly Ser Pro Ala Asn Ala Pro Ser Ile Met Ala Val Ala Ala
 325      330      335
Val Asp Ala Lys Met Lys Val Ala Asn Phe Ser Cys Gly Gly Val Asn
 340      345      350
Pro Ala Gly Gly Glu Val Asn Ile Ala Gly Pro Gly Val Asp Val Leu
 355      360      365
Ser Ser Val Pro Met Pro Arg Lys Tyr Asp Arg Phe Ser Gly Thr Ser
 370      375      380
Met Ala Thr Pro His Val Ala Gly Ile Ala Ala Leu Leu Ala Gln Ser
 385      390      395      400
Asp Lys Ser Leu Arg Gly Lys Ala Leu Trp Thr Ala Leu Glu Gln Gly
 405      410      415
Ala Arg Asn Ile Gly His Pro Ala Arg Asp Val Gly Ala Gly Leu Val
 420      425      430
Met Ala Pro Gly Ser Ala Cys Arg
 435      440

```

&lt;210&gt; 27

&lt;211&gt; 1893

&lt;212&gt; DNA

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; Obtained from an environmental sample.

10336256.txt

```

<400> 27
gtgatcaaga agcagaacct tcgcatcaat gtgttgccag ccgccgtgct gtcgctgacc 60
gggtgtggcc tggcacaggc cgccgacctg aaagcaaatg cgccgttgct cggcccgaag 120
acgcagcagg tggatggcat catcgtgaaa taccgcgctg gcagcgccgc agctgccgat 180
gcgaacgcca agctggccgt ggtcaactcg gccatcgccc gcgcccgtgcc ggcaggtacc 240
aacgcggctg cgcgcagtgc cgcgctgcgc ccgcaggtgg cccgcaagct gggcatcggt 300
gccgatctga tccgcctgca gggagggatc gcgcgcgccc aactggacaa ggtgctgggc 360
gaactgaagg ctgacccgac cgtcgaatat gcggtggccg acgccatcat gtatccgatc 420
gatgtgcgt cgtcgccgcg tgcggacgcc gtcgcgaagt ccgatgcgtc gccaggttc 480
gtgcccaacg atccgtacta ccagagccac aactggcact tccacaaccc ggtcggtggtc 540
gtgaacgcac cggccgcatg ggacgtctcg cagggcgagg gcatcggtgt ggccgtgctc 600
gataccggga tcctgcccga gcacccggat ttccgcccgc gcaccctgct ggagggtac 660
gacttcacat gccaggccag ccgctcgctg cgtgccgccc atggccgctg gccgggtgca 720
ctcgactacg gtgactggat gccccaccgc aatgcctgct acgacggttc gccggtacgt 780
gacagcagct ggcacggtac ccattgtgacc ggcaccatcg ccgaggccac caacaacggc 840
ctgcataacc cgggcctggc ctacaaggcc aaggtgttgc cggtgccgct gctcggctac 900
tgcggtggca ccctgtcgga catcacccgac gccatcacct gggcctcggg cggtgccgtg 960
gccggcatcc ctgccaacca gaatccggcc gagatcatca acatgagcct gggcggctcc 1020
ggcagctgcg atccggccta ccaggcggcc atcaccggtg ccaccaaccg cggtagccctg 1080
gtggtggtgg cagccggcaa cgactcgatg aatgtggcca acgcccgcgc ggccaactgc 1140
gatggcgtgg tctcggtcgg cgcgaccgga atcaccggcg ccatggccta ctactccaac 1200
ttcggtagcc gcacatgatc gtccggcccg ggcgggtggc tcaccgacgg caatccgaac 1260
ggctatgtct ggcaggcggt gtccagcagc aagacgtcgc cgcgggcagc cggttccacc 1320
gaggggtaca cccttgccgg caaggccggc acgtcgatgg cggcaccgca tgtggctgcc 1380
gtcgcgcgcg tggtcagag cgcgctgatc gccgccaacc ggcacccgct cgcgcccggc 1440
ggcatgctga ccctgctgaa ggaaacggca cgtccgttcc cggtcagcat tccgtccgac 1500
accccgatcg gtaccggcat cgtcgatgcc aaggccgcgc tggacaaggc cctggaagag 1560
ccatgcaccg agaactgcgg gccggtggcc aagccgctga ccaacaaggg ggccatcggc 1620
gggttgagtg gtgccgccc cagcagcgct ctttacagct tcgaagccgc ggcaggcaag 1680
cagctcagcg tcatcaccta tgggtggcacc ggcaacgtgt cgggtctacct ggccaagggc 1740
cgcgagccga gtgccaccga caacgatgcg cgctcgaccc gtccggggcac ctcggaacgc 1800
gtcggggtga cggcaccgac tgccggcacc tactacatca aggtggtggg cgaggcggtc 1860
tacagcgggtg tgagcattct cgccacgcag taa 1893

```

```

<210> 28
<211> 630
<212> PRT
<213> Unknown

```

```

<220>
<223> Obtained from an environmental sample.

```

```

<221> SIGNAL
<222> (1)...(27)

```

```

<400> 28
Met Ile Lys Lys Gln Asn Leu Arg Ile Asn Val Leu Ala Ala Ala Val
1      5      10      15
Leu Ser Leu Thr Gly Val Gly Leu Ala Gln Ala Ala Asp Leu Lys Ala
20     25     30
Asn Ala Pro Leu Ser Gly Pro Lys Thr Gln Gln Val Asp Gly Ile Ile
35     40     45
Val Lys Tyr Arg Ala Gly Ser Ala Ala Ala Ala Asp Ala Asn Ala Lys
50     55     60
Leu Ala Val Val Asn Ser Ala Ile Ala Arg Ala Val Pro Ala Gly Thr
65     70     75     80
Asn Ala Ala Ala Arg Ser Ala Ala Leu Arg Pro Gln Val Ala Arg Lys
85     90     95
Leu Gly Ile Gly Ala Asp Leu Ile Arg Leu Gln Gly Gly Ile Ala Arg
100    105    110
Ala Glu Leu Asp Lys Val Leu Gly Glu Leu Lys Ala Asp Pro Thr Val
115    120    125
Glu Tyr Ala Val Ala Asp Ala Ile Met Tyr Pro Ile Asp Ala Ala Ser
130    135    140
Ser Pro Arg Ala Asp Ala Val Ala Lys Ser Asp Ala Ser Pro Ser Phe
145    150    155    160
Val Pro Asn Asp Pro Tyr Tyr Gln Ser His Asn Trp His Phe His Asn

```

## 10336256.txt

Pro Val Gly Gly Val Asn Ala Pro Ala Ala Trp Asp Val Ser Gln Gly  
 Glu Gly Ile Val Val Ala Val Leu Asp Thr Gly Ile Leu Pro Glu His  
 Pro Asp Phe Ala Ala Gly Thr Leu Leu Glu Gly Tyr Asp Phe Ile Ser  
 Gln Ala Ser Arg Ser Arg Arg Ala Ala Asp Gly Arg Val Pro Gly Ala  
 Leu Asp Tyr Gly Asp Trp Met Pro Thr Ala Asn Ala Cys Tyr Asp Gly  
 Ser Pro Val Arg Asp Ser Ser Trp His Gly Thr His Val Thr Gly Thr  
 Ile Ala Glu Ala Thr Asn Asn Gly Leu His Thr Ala Gly Leu Ala Tyr  
 Lys Ala Lys Val Leu Pro Val Arg Val Leu Gly Tyr Cys Gly Gly Thr  
 Leu Ser Asp Ile Thr Asp Ala Ile Thr Trp Ala Ser Gly Gly Ala Val  
 Ala Gly Ile Pro Ala Asn Gln Asn Pro Ala Glu Ile Ile Asn Met Ser  
 Leu Gly Gly Ser Gly Ser Cys Asp Pro Ala Tyr Gln Ala Ala Ile Thr  
 Gly Ala Thr Asn Arg Gly Thr Leu Val Val Val Ala Ala Gly Asn Asp  
 Ser Met Asn Val Ala Asn Ala Arg Pro Ala Asn Cys Asp Gly Val Val  
 Ser Val Gly Ala Thr Gly Ile Thr Gly Ala Met Ala Tyr Tyr Ser Asn  
 Phe Gly Thr Arg Ile Asp Leu Ser Gly Pro Gly Gly Gly Val Thr Asp  
 Gly Asn Pro Asn Gly Tyr Val Trp Gln Ala Val Ser Ser Ser Lys Thr  
 Ser Pro Pro Ala Ala Gly Ser Thr Glu Gly Tyr Thr Leu Gly Gly Lys  
 Ala Gly Thr Ser Met Ala Ala Pro His Val Ala Ala Val Ala Ala Leu  
 Val Gln Ser Ala Leu Ile Ala Ala Asn Arg Asp Pro Leu Ala Pro Ala  
 Gly Met Arg Thr Leu Lys Glu Thr Ala Arg Pro Phe Pro Val Ser  
 Ile Pro Ser Ala Thr Pro Ile Gly Thr Gly Ile Val Asp Ala Lys Ala  
 Ala Leu Asp Lys Ala Leu Glu Glu Pro Cys Thr Glu Asn Cys Gly Pro  
 Val Ala Lys Pro Leu Thr Asn Lys Val Ala Ile Gly Gly Leu Ser Gly  
 Ala Ala Gly Ser Ser Val Leu Tyr Ser Phe Glu Ala Ala Ala Gly Lys  
 Gln Leu Ser Val Ile Thr Tyr Gly Gly Thr Gly Asn Val Ser Val Tyr  
 Leu Ala Lys Gly Arg Glu Pro Ser Ala Thr Asp Asn Asp Ala Arg Ser  
 Thr Arg Pro Gly Thr Ser Glu Thr Val Arg Val Thr Ala Pro Thr Ala  
 Gly Thr Tyr Tyr Ile Lys Val Val Gly Glu Ala Ala Tyr Ser Gly Val  
 Ser Ile Leu Ala Thr Gln  
 625 630

<210> 29  
 <211> 1506  
 <212> DNA  
 <213> Unknown

<220>  
 <223> obtained from an environmental sample.

## 10336256.txt

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<400> 29
atgcgtacgt cgcttcgggt ttcccttgcc agtgccatca ccctggtcct ggccagcgcc      60
cccgccttcg cccaacccac cgaacgggta tggacgcgag gcatggccag caacgagcag      120
tacagcagtt tcatcgtcaa gtaccgggac ggacgcagca agcgcgcttc cgccgacacc      180
gcccaggacg cgctgaagaa ggcgcctcggc gcccagcagc gcagcaagcg ttcgatcggc      240
agtgcgcccgc cagcggccgc gtccgtgacc catcaacgcc gcatgggagg cggcgcccgc      300
gtgggtcacca cggacaagcc actggaccgt ccggaggccg agatcctgat gcagcgcac      360
gccgacgatc cggacgtcga gtatgtgcag ccgaactaca tgatgagtgc attcgctacg      420
ccgaacgacc cgcgctacgg cgagcagtgg cactacagca atccgaccag tggcgcgcgc      480
ctgccaggcg catgggatcg ctctaccggc cagggtgtgg tgggtggccg ggtcgattcg      540
ggctacctca acaacaacga cctgcaggcc aatctgttgc cgggttacga catgatctcg      600
tcaacccgtc cgttcagtga ctggcagtgc atcatcgggg gcatgaatcc cggctgtggg      660
ggctccgacg atgggtgacgg acgcgacgcc gatgcattcg atgcctcggg cattgcacac      720
ggcaccacag tcgccggaac ggtcgctgcg gtgaccaaca accagatcgg cgtggccggc      780
gtggcctaca acgcaaaagt cgtaccgggt cgcgctactgg gaaaccaggg caatgggtggc      840
tccgcccgata tcatcgacgg catgctctgg agtgccggta tcaacgtgcc caacgtcccg      900
gccaatgcc aacccggccga ggtcatcaat ctgagcctgg gtggccgccc cgcctgctcg      960
ccggccgagc aggatgcaat cgacgacatc acggcccagg gcacgatcgt ggtgggtcgcc      1020
gccggcaaca gcaatcttga tgtgtccgag ttgccccggc cgaactgcaa gggcgatgc      1080
gcgggttgctg ccaacgatca gggcggtcgt cgcgcgcttct actccaacta tgggtgcaggc      1140
atccacatca ccgcaccggg tggcgagacc tgggtcgtgcc gtgcgtcggg ggggtgagttc      1200
ctgccgctgg ccacgcccgc gagccaggcc aactgcgacc ccacccgcca gcatccggcg      1260
cagggcatcc tgtccaccgt gggttaacaac gccttcgact tcatgtccgg cacctcgatg      1320
gcggcgcccc acgtcgctgg catcgtcgcg ctgatgcagg cgggtggcgcc ggtgccgaag      1380
accaccgacc aggtcaagga catcctgcgt cgaaccgcgc acccgatcgc agcggcgaac      1440
tggccgggagc gttgcggacc gggcattgtc gacgctgcag aagcggtgaa ggccgcccagc      1500
aactga                                     1506

```

```

<210> 30
<211> 501
<212> PRT
<213> Unknown

```

```

<220>
<223> Obtained from an environmental sample.

```

```

<221> SIGNAL
<222> (1)...(24)

```

```

<400> 30
Met Arg Thr Ser Leu Arg Val Ser Leu Ala Ser Ala Ile Thr Leu Val
1      5      10      15
Leu Ala Ser Ala Pro Ala Phe Ala Gln Pro Thr Glu Arg Val Trp Thr
20      25      30
Arg Gly Met Ala Ser Asn Glu Gln Tyr Ser Ser Phe Ile Val Lys Tyr
35      40      45
Arg Asp Gly Ser Ser Lys Arg Val Ser Ala Asp Thr Ala Gln Asp Ala
50      55      60
Leu Lys Lys Arg Leu Gly Ala Gln Gln Arg Ser Lys Arg Ser Ile Gly
65      70      75      80
Ser Ala Pro Pro Ala Ala Ala Ser Val Thr His Gln Arg Arg Met Gly
85      90      95
Gly Gly Ala Asp Val Val Thr Thr Asp Lys Pro Leu Asp Arg Pro Glu
100      105      110
Ala Glu Ile Leu Met Gln Arg Ile Ala Asp Asp Pro Asp Val Glu Tyr
115      120      125
Val Gln Pro Asn Tyr Met Met Ser Ala Phe Ala Thr Pro Asn Asp Pro
130      135      140
Arg Tyr Gly Glu Gln Trp His Tyr Ser Asn Pro Thr Ser Gly Ala Arg
145      150      155      160
Leu Pro Gly Ala Trp Asp Arg Ser Thr Gly Gln Gly Val Val Val Ala
165      170      175
Val Val Asp Ser Gly Tyr Leu Asn Asn Asn Asp Leu Gln Ala Asn Leu
180      185      190
Leu Pro Gly Tyr Asp Met Ile Ser Ser Thr Arg Pro Phe Ser Asp Trp
195      200      205
Gln Cys Ile Ile Gly Gly Met Asn Pro Gly Cys Gly Gly Ser Asp Asp
210      215      220

```

## 10336256.txt

Gly Asp Gly Arg Asp Ala Asp Ala Phe Asp Ala Ser Gly Ile Ala His  
 225 230 235 240  
 Gly Thr His Val Ala Gly Thr Val Ala Val Thr Asn Asn Gln Ile  
 245 250 255  
 Gly Val Ala Gly Val Ala Tyr Asn Ala Lys Val Val Pro Val Arg Val  
 260 265 270  
 Leu Gly Asn Gln Gly Asn Gly Gly Ser Ala Asp Ile Ile Asp Gly Met  
 275 280 285  
 Leu Trp Ser Ala Gly Ile Asn Val Pro Asn Val Pro Ala Asn Ala Asn  
 290 295 300  
 Pro Ala Glu Val Ile Asn Leu Ser Leu Gly Gly Arg Arg Ala Cys Ser  
 305 310 315 320  
 Pro Ala Glu Gln Asp Ala Ile Asp Asp Ile Thr Ala Gln Gly Thr Ile  
 325 330 335  
 Val Val Val Ala Ala Gly Asn Ser Asn Leu Asp Val Ser Glu Phe Ala  
 340 345 350  
 Pro Ala Asn Cys Lys Gly Val Ile Ala Val Ala Ala Asn Asp Gln Gly  
 355 360 365  
 Gly Arg Arg Ala Phe Tyr Ser Asn Tyr Gly Ala Gly Ile His Ile Thr  
 370 375 380  
 Ala Pro Gly Gly Glu Thr Trp Ser Cys Arg Ala Ser Val Gly Glu Phe  
 385 390 395 400  
 Leu Pro Leu Ala Thr Pro Pro Ser Gln Ala Asn Cys Ala Pro Thr Arg  
 405 410 415  
 Gln His Pro Ala Gln Gly Ile Leu Ser Thr Val Gly Asn Asn Ala Phe  
 420 425 430  
 Asp Phe Met Ser Gly Thr Ser Met Ala Ala Pro His Val Ala Gly Ile  
 435 440 445  
 Val Ala Leu Met Gln Ala Val Ala Pro Val Pro Lys Thr Thr Asp Gln  
 450 455 460  
 Val Lys Asp Ile Leu Arg Arg Thr Ala His Pro Ile Ala Ala Ala Asn  
 465 470 475 480  
 Cys Pro Gly Gly Cys Gly Pro Gly Ile Val Asp Ala Ala Glu Ala Val  
 485 490 495  
 Lys Ala Ala Ser Asn  
 500

<210> 31  
 <211> 1929  
 <212> DNA  
 <213> Unknown

<220>  
 <223> obtained from an environmental sample.

<400> 31  
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 gccagcctcg gcgatcagca gatcttccgc cgcttcgctcg tgcagtaccg cgacggcacg 180  
 cgcgagaaga ccgaccgcaa tgccggcgctc gccacgttca gccgcgcgtt gtcgcgctcg 240  
 ggcctgtcga agagccgcg cggccgacgcc aagcacgtgc gtacgctcgc caacggccac 300  
 cagctgtcga agctctcgc cggcctcgat cgcgcggaag ccgaggccct gctgcgccag 360  
 ctcaaggccg acccgaacgt ggtctcggtg cgccccgatc gcctgcgcca gatcgcgcgc 420  
 ctgccaacg tgcagccggc ctacgtgccc aacgatccgc tgttccagga ataccagtgg 480  
 cacatgcgtg cgccggacgg cggcgcgacc ttcgacggcg gcccacacg cggcggcatc 540  
 aacgcgcccg cgccctggga cctcgccgac ggcaacggca tcaccatcgc cgtgctcgac 600  
 accggcatca cgcgcgatcc tgacgtcgat acctcgatgg ccgatgccgg ctacgacttc 660  
 atcagcgacg ccttcgtctc cggccgcgac accgacgacc gcgtgcccgg cggctgggac 720  
 ctgggcgact ggaccatcgg ctatccgggc gcggaaacct gcatccagcg ctacagctcc 780  
 tggcacggcg cccacgtcgc cggcaccgcc ggcgcgcagc tgacggacaa cggcgtaggc 840  
 ctgaccggcg tcgcctacaa cgccaacgtc gtgcccgatcc gcgtgctcgg ccactgcggc 900  
 ggctacgaca cgcgcatcg cgacgcgatc gtctgggcgg ccggcgcgca ggtggaaggc 960  
 atgccgtcga acgagaacct ggcgcacgtg atcaacctga gcctgggccc ctcgggcccgc 1020  
 tgcaccgact acgaggccga tgcgatcgcg caggccaacg ccctgggccc cgtggctcgtg 1080  
 gtgcggcgcc gcaaccagaa cgccaatacc tcgggctatt cgccgggcaa ctgcccgggc 1140  
 gtgatcacgg tggcgtcgaa cggcgtgacc agccgtccgc cctactactc caactacggc 1200  
 gacggcatcg agatcgccgc gcccgggcgc gcggtcaacc ccaacgacgg cagcggcgcc 1260  
 gcgcagatct acgacggcct cgtctggcag gcggtcaacc ccagcgacac cgagccgatg 1320

## 10336256.txt

ccggccgacg	agatcgcgcc	cgacggctcc	aacggcggct	acggcggatc	ggccggtact	1380
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gcgggcatgc	cgctgctcac	tccggaggag	gtgctggacg	tgctgcagtc	gacggtgacg	1500
ccgttcgcgg	tcgcgccctc	gacctcgag	ccgatcggcc	cgggcatcgt	gaacgcggcc	1560
gccgccgtgg	ccaaggcgat	cgagccgccc	tcgagggtcg	actgcgcgcc	ggatgccacg	1620
ccgatcgtca	acggcgctgc	gctcaccggc	ctgaccggca	ccgcgggcag	cgaaacgctc	1680
tacagcatca	ccgtgcccga	gggcgcgcgc	ggtcgcgtca	gcacagcac	caccggcggc	1740
agcggcgacg	tgaacctgct	ggtgagcttc	gaggccgagc	ccaccgacgc	ggacgcggac	1800
ttccgctcgg	cgcgccggg	caacaacgag	acgggtgcga	tcaacgcgcc	gcaggcaggc	1860
acctactaca	tcaagctggt	cggcgcccgc	gcctacagca	acgtgcgtct	gctggtccgt	1920
cacaactga						1929

<210> 32  
 <211> 642  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Obtained from an environmental sample.

<221> SIGNAL  
 <222> (1)...(26)

<400> 32

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			20					25					30		
Ala	Thr	Asp	Thr	Ala	Ala	Leu	Ser	Ala	Ser	Leu	Gly	Asp	Gln	Gln	Ile
		35					40					45			
Phe	Arg	Arg	Phe	Val	Val	Gln	Tyr	Arg	Asp	Gly	Thr	Arg	Glu	Lys	Thr
50					55					60					
Asp	Arg	Asn	Ala	Gly	Val	Ala	Thr	Phe	Ser	Arg	Ala	Leu	Ser	Arg	Ser
65				70					75					80	
Gly	Leu	Ser	Lys	Ser	Arg	Ala	Ala	Asp	Ala	Lys	His	Val	Arg	Thr	Leu
			85					90					95		
Ala	Asn	Gly	His	Gln	Leu	Leu	Lys	Leu	Ser	Arg	Gly	Leu	Asp	Arg	Ala
		100						105					110		
Glu	Ala	Glu	Ala	Leu	Leu	Arg	Gln	Leu	Lys	Ala	Asp	Pro	Asn	Val	Val
		115					120					125			
Ser	Val	Arg	Pro	Asp	Arg	Leu	Arg	Gln	Ile	Ala	Arg	Leu	Pro	Asn	Val
130						135					140				
Gln	Pro	Ala	Tyr	Val	Pro	Asn	Asp	Pro	Leu	Phe	Gln	Glu	Tyr	Gln	Trp
145					150					155					160
His	Met	Arg	Ala	Pro	Asp	Gly	Gly	Ala	Thr	Phe	Asp	Gly	Gly	Pro	Asn
			165					170						175	
Arg	Gly	Gly	Ile	Asn	Ala	Pro	Ala	Ala	Trp	Asp	Leu	Ala	Asp	Gly	Asn
			180					185					190		
Gly	Ile	Thr	Ile	Ala	Val	Leu	Asp	Thr	Gly	Ile	Ser	Ala	His	Pro	Asp
		195					200					205			
Val	Asp	Thr	Ser	Met	Ala	Asp	Ala	Gly	Tyr	Asp	Phe	Ile	Ser	Asp	Ala
210					215						220				
Phe	Val	Ser	Gly	Arg	Asp	Thr	Asp	Asp	Arg	Val	Pro	Gly	Gly	Trp	Asp
225					230					235					240
Leu	Gly	Asp	Trp	Thr	Ile	Gly	Tyr	Pro	Gly	Ala	Glu	Thr	Cys	Ile	Gln
			245						250					255	
Arg	Tyr	Ser	Ser	Trp	His	Gly	Thr	His	Val	Ala	Gly	Thr	Ala	Gly	Ala
			260					265					270		
Gln	Leu	Thr	Asp	Asn	Gly	Val	Gly	Leu	Thr	Gly	Val	Ala	Tyr	Asn	Ala
		275					280					285			
Asn	Val	Val	Pro	Ile	Arg	Val	Leu	Gly	His	Cys	Gly	Gly	Tyr	Asp	Thr
		290				295					300				
Asp	Ile	Ala	Asp	Ala	Ile	Val	Trp	Ala	Ala	Gly	Gly	Glu	Val	Glu	Gly
305					310					315					320
Met	Pro	Leu	Asn	Glu	Asn	Pro	Ala	His	Val	Ile	Asn	Leu	Ser	Leu	Gly
			325						330					335	
Gly	Ser	Gly	Ala	Cys	Thr	Asp	Tyr	Glu	Ala	Asp	Ala	Ile	Ala	Gln	Ala
			340					345					350		

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Asn	Ala	Leu	Gly	Ala	Val	Val	Val	Val	Ala	Ala	Gly	Asn	Gln	Asn	Ala
355		355					360					365			
Asn	Thr	Ser	Gly	Tyr	Ser	Pro	Gly	Asn	Cys	Pro	Gly	Val	Ile	Thr	Val
370						375					380				
Ala	Ser	Asn	Gly	Val	Thr	Ser	Arg	Arg	Ala	Tyr	Tyr	Ser	Asn	Tyr	Gly
385					390					395					400
Asp	Gly	Ile	Glu	Ile	Ala	Ala	Pro	Gly	Gly	Gly	Val	Tyr	Ala	Asn	Asp
			405						410					415	
Gly	Ser	Gly	Gly	Ala	Gln	Ile	Tyr	Asp	Gly	Phe	Val	Trp	Gln	Ala	Val
			420					425					430		
Asn	Pro	Ser	Asp	Thr	Glu	Pro	Met	Pro	Ala	Asp	Glu	Ile	Ala	Pro	Asp
		435					440					445			
Gly	Ser	Asn	Gly	Gly	Tyr	Gly	Gly	Ser	Ala	Gly	Thr	Ser	Gln	Ala	Ala
450						455					460				
Pro	His	Val	Ala	Gly	Val	Ile	Ala	Leu	Met	Gln	Gly	Ala	Arg	Leu	Asp
465					470					475					480
Ala	Gly	Met	Pro	Leu	Leu	Thr	Pro	Glu	Glu	Val	Leu	Asp	Val	Leu	Gln
			485						490					495	
Ser	Thr	Val	Thr	Pro	Phe	Ala	Val	Ala	Pro	Ser	Thr	Ser	Gln	Pro	Ile
			500					505					510		
Gly	Pro	Gly	Ile	Val	Asn	Ala	Ala	Ala	Val	Ala	Lys	Ala	Ile	Glu	
		515					520				525				
Pro	Pro	Cys	Glu	Val	Asp	Cys	Ala	Pro	Asp	Ala	Thr	Pro	Ile	Val	Asn
530						535					540				
Gly	Val	Ala	Leu	Thr	Gly	Leu	Thr	Gly	Thr	Ala	Gly	Ser	Glu	Thr	Leu
545					550					555					560
Tyr	Ser	Ile	Thr	Val	Pro	Glu	Gly	Ala	Arg	Gly	Pro	Leu	Ser	Ile	Ser
			565					570						575	
Thr	Thr	Gly	Gly	Ser	Gly	Asp	Val	Asn	Leu	Leu	Val	Ser	Phe	Glu	Ala
			580					585					590		
Glu	Pro	Thr	Asp	Ala	Asp	Ala	Asp	Phe	Arg	Ser	Ala	Arg	Pro	Gly	Asn
		595					600					605			
Asn	Glu	Thr	Val	Arg	Ile	Asn	Ala	Pro	Gln	Ala	Gly	Thr	Tyr	Tyr	Ile
610						615					620				
Lys	Leu	Val	Gly	Ala	Arg	Ala	Tyr	Ser	Asn	Val	Arg	Leu	Leu	Val	Arg
625					630					635					640
His	Asn														

<210> 33  
 <211> 981  
 <212> DNA  
 <213> Unknown

<220>  
 <223> obtained from an environmental sample.

<400> 33

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tttgggtccct	ctggcgggccc	gcgccccgac	gacatcgtcc	agggcccgat	cggcgactgc	180
tacttcctcg	cggcgctcgc	ctccttcgcg	cagcagcagc	cccagctgat	ccgcaacgcg	240
atcgcttcg	atgccaaacac	cgaaaacttc	aacgtgacgc	tgacacaagga	tgcgcaaccc	300
tggaatccgt	tcaatcgcca	cgagaagggtg	accgtccggg	tcacgcagca	ggaaatcgac	360
agccatgtca	tgaacgacaa	gggcgcccag	ctgggcaacg	acggcgcgcg	gtggccgggtg	420
gtcatggaga	tcgcgcgcgc	caagatgctc	gacagcaatc	cgaagaacgg	cttggacgaa	480
ggctacaatg	cactcgagca	tcagacgcgg	ttcggcttgc	ttcagggcgg	catgccgtca	540
tcggccatgg	agaccatctc	cggccaaccc	ggcgacacgg	catacacgac	gccgctcggc	600
atcttcggag	acgcgacgca	aggacccttg	cagccgtggc	tctcgctcgt	ctcgcccggg	660
caggcggttag	cgccggaggc	ggcaaaccat	cactatagcc	aggtcaaagc	cgcgctggag	720
gacggacggc	ccgtgacgct	gggtaccggc	ttgtccagcc	cgcaggacgg	cctcgttcgc	780
gggcacgcct	atcagggtcga	ggatatccag	cgcaacgccg	acggcagcgt	taacgtcacg	840
gttcgcaatc	catggggaac	caatcagggt	gtcggcgaa	gcaccaatcc	ggccgacccg	900
cgtgtcacca	tcaggatggg	agccgcgggc	ctgtcgtgtg	tcgcaatcgg	ttcaagcgcg	960
caggagacca	gcgccggata	g				981

<210> 34  
 <211> 326

10336256.txt

&lt;212&gt; PRT

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; Obtained from an environmental sample.

&lt;400&gt; 34

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Met Ile Pro Pro Ile Gly Gly Lys Ser Asp Pro Ile Asp Thr Ser Ser
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Thr Trp Gln Ser Ser Leu Ser Gln Ala Ala Asn Thr Asn Gln Pro Gln
20
Gln Gln Tyr Asn Ala Ser Gly Leu Phe Gly Pro Ser Gly Gly Pro Arg
35      40      45
Pro Asp Asp Ile Val Gln Gly Pro Ile Gly Asp Cys Tyr Phe Leu Ala
50      55      60
Ala Leu Ala Ser Phe Ala Gln Gln Gln Pro Gln Leu Ile Arg Asn Ala
65      70      75      80
Ile Ala Phe Asp Ala Asn Thr Gly Asn Phe Asn Val Thr Leu His Lys
85      90      95
Asp Ala Gln Pro Trp Asn Pro Phe Asn Arg His Glu Lys Val Thr Val
100      105      110
Arg Val Thr Gln Gln Glu Ile Asp Ser His Val Met Asn Asp Lys Gly
115      120      125
Ala Arg Leu Gly Asn Asp Gly Ala Arg Trp Pro Val Val Met Glu Ile
130      135      140
Ala Arg Ala Lys Met Leu Asp Ser Asn Pro Lys Asn Gly Leu Asp Glu
145      150      155      160
Gly Tyr Asn Ala Leu Glu His Gln Thr Pro Phe Gly Leu Leu Gln Gly
165      170      175
Gly Met Pro Ser Ala Met Glu Thr Ile Ser Gly Gln Pro Gly Asp
180      185      190
Thr Ala Tyr Thr Thr Pro Leu Gly Ile Phe Gly Asp Ala Thr Gln Gly
195      200      205
Pro Leu Gln Pro Trp Leu Ser Leu Val Ser Pro Gly Gln Ala Leu Ala
210      215      220
Pro Glu Ala Ala Asn His Tyr Ser Gln Val Lys Ala Ala Leu Glu
225      230      235      240
Asp Gly Arg Pro Val Thr Leu Gly Thr Gly Leu Ser Ser Pro Gln Asp
245      250      255
Gly Leu Val Arg Gly His Ala Tyr Gln Val Glu Asp Ile Gln Arg Asn
260      265      270
Ala Asp Gly Ser Val Asn Val Thr Val Arg Asn Pro Trp Gly Thr Asn
275      280      285
Gln Gly Val Gly Glu Gly Thr Asn Pro Ala Asp Pro Arg Val Thr Ile
290      295      300
Arg Met Gly Ala Ala Gly Leu Ser Leu Phe Ala Ile Gly Ser Ser Ala
305      310      315      320
Gln Glu Thr Ser Ala Gly
325

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&lt;210&gt; 35

&lt;211&gt; 1854

&lt;212&gt; DNA

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; Obtained from an environmental sample.

&lt;400&gt; 35

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gccgtcgggtg ccgtccacgc cgccgggttg ccgaccctgtg aaccgggtgcg ccaggccagc 120
accgccgagc cgggcaccca gcgcatcatc gtcaagtacc gtgccggcac cgctgcggcg 180
ggcgaccggt cggccaagct gtccaccgtg cagtccgcgc tgaccgcgcg cagcctgtcc 240
ggtggcacta cccgcgccag cgcgctcggc ccgcaggctc tgccgaggct gggcgctcgg 300
gccgacctga tccgcctgca ggggcgcctg gcgcctgccg aactgcagcg cgtgctgaag 360
gaactgaagg ccgatccgct cgtgcagtac gccgaggccg atgtgaagct gcgccgtacc 420
gagctgcgtg ccggtgacgt gcagccggcg ctggcgccga atgatcccta ctaccagcag 480
taccagtggc acctgcacaa cgccaccggc ggcacacacg caccgtcggc gtgggatgta 540

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## 10336256.txt

tcgcagggcg	aaggcgtggt	ggtggcggta	ctcgcacccg	gcatcctgcc	gcagcacccg	600
gacctgggtcg	gcaacctgct	ggaaggctac	gacttcatca	gcgatgccga	gacgtcgcgc	660
cgtgccacca	acgaccgcgt	gccggggcgcg	caggactatg	gtgactgggt	cgagaacgac	720
aacgagtgtct	acaccggctc	cgtcgccgag	gacagctcct	ggcacgggtac	ccatgtggcc	780
ggtaccgtgg	ccgagcagac	caacaacggg	gtcggcatgg	ccgggtgtcg	gcacaaggcc	840
aaggtgtctgc	cggtccgcgt	gctcggcaag	tgcggtggtc	acctttccga	tatagccgac	900
gccatcacct	gggcctccgg	cggcacgggtg	gccggcggtac	ccgccaatgc	caaccgggcc	960
gaagtcatca	acatgagcct	cggcggcagc	ggcagctgcg	acgggacctta	ccaggaagcg	1020
atcaatggcg	cgatctcgcg	tggcaccacg	gtggctgtgg	cggccggcaa	cgagaccgac	1080
aacgcctcca	aataccgtcc	agccagttgc	gacggcggtg	tgaccgtcgg	cgccaccgcg	1140
attaccggcg	gcatcaccta	ctactccaac	tacggcaccc	gcgtggacct	gtccgggtccg	1200
ggtgggtgggtg	gcagcgtcga	tggcaatccc	ggcgggtacg	tctggcagtc	cggttccgat	1260
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gcctcgccgc	acgtgggtgc	cgctcggtgca	ctgggtgcaga	gcgcgctgat	gcgcaagggc	1380
aaggatccgc	tggcccccgc	cgcgatgcgc	accctgtgta	aggaaaccgc	gcgtccgttc	1440
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ctggccaagg	cgctggaaga	gccgtgcacc	gagaactgtg	gaccgggtgg	gacgccgctg	1560
accaacaagg	ccgccgtggg	ggggctgaac	ggcacggccg	gcagcagccg	cctgtacagc	1620
ttcgaggcag	ccgctggcaa	gcagctcagc	gtgatcacct	acgggtggcac	cggaacagtg	1680
tcgggtctaca	tcgcccaggg	tcgcgagccg	agcgccagcg	acaacgatgg	caagtcgacc	1740
cgtcccggga	cgtccgaaac	ggtacgggtg	aacaagccgg	tggcaggcac	ctactacatc	1800
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<210> 36  
 <211> 617  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Obtained from an environmental sample.

<221> SIGNAL  
 <222> (1)...(27)

<400> 36

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		20						25				30			
Arg	Glu	Pro	Val	Arg	Gln	Ala	Ser	Thr	Ala	Glu	Pro	Gly	Thr	Gln	Arg
		35					40					45			
Ile	Ile	Val	Lys	Tyr	Arg	Ala	Gly	Thr	Ala	Ala	Ala	Gly	Asp	Arg	Ser
	50					55					60				
Ala	Lys	Leu	Ser	Thr	Val	Gln	Ser	Ala	Leu	Thr	Arg	Ala	Ser	Leu	Ser
65					70					75				80	
Gly	Gly	Thr	Thr	Arg	Ala	Ser	Ala	Leu	Gly	Pro	Gln	Val	Val	Arg	Arg
				85				90						95	
Leu	Gly	Val	Gly	Ala	Asp	Leu	Ile	Arg	Leu	Gln	Gly	Arg	Leu	Ala	Pro
		100						105					110		
Ala	Glu	Leu	Gln	Arg	Val	Leu	Lys	Glu	Leu	Lys	Ala	Asp	Pro	Ser	Val
		115					120					125			
Gln	Tyr	Ala	Glu	Ala	Asp	Val	Lys	Leu	Arg	Arg	Thr	Glu	Leu	Arg	Ala
	130					135					140				
Gly	Asp	Val	Gln	Pro	Ala	Leu	Ala	Pro	Asn	Asp	Pro	Tyr	Tyr	Gln	Gln
145					150					155				160	
Tyr	Gln	Trp	His	Leu	His	Asn	Ala	Thr	Gly	Gly	Ile	Asn	Ala	Pro	Ser
			165						170					175	
Ala	Trp	Asp	Val	Ser	Gln	Gly	Glu	Gly	Val	Val	Val	Ala	Val	Leu	Asp
		180						185					190		
Thr	Gly	Ile	Leu	Pro	Gln	His	Pro	Asp	Leu	Val	Gly	Asn	Leu	Leu	Glu
		195					200					205			
Gly	Tyr	Asp	Phe	Ile	Ser	Asp	Ala	Glu	Thr	Ser	Arg	Arg	Ala	Thr	Asn
	210					215					220				
Asp	Arg	Val	Pro	Gly	Ala	Gln	Asp	Tyr	Gly	Asp	Trp	Val	Glu	Asn	Asp
225					230					235				240	
Asn	Glu	Cys	Tyr	Thr	Gly	Ser	Val	Ala	Glu	Asp	Ser	Ser	Trp	His	Gly
			245						250					255	
Thr	His	Val	Ala	Gly	Thr	Val	Ala	Glu	Gln	Thr	Asn	Asn	Gly	Val	Gly

## 10336256.txt

Met Ala Gly Val Ala His Lys Ala Lys Val Leu Pro Val Arg Val Leu  
 260 265 270  
 Gly Lys 275 Cys Gly Gly Tyr Leu 280 Ser Asp Ile Ala Asp 285 Ile Thr Trp  
 290  
 Ala Ser Gly Gly Thr Val Ala Gly Val Pro Ala Asn Ala Asn Pro Ala  
 305 310 315 320  
 Glu Val Ile Asn Met 325 Ser Leu Gly Gly Ser Gly Ser Cys Asp Gly Thr  
 330 335  
 Tyr Gln Glu Ala Ile Asn Gly Ala Ile Ser Arg Gly Thr Thr Val Val  
 340 345 350  
 Val Ala Ala Gly Asn Glu Thr Asp Asn Ala Ser Lys Tyr Arg Pro Ala  
 355 360 365  
 Ser Cys Asp Gly Val Val Thr Val Gly Ala Thr Arg Ile Thr Gly Gly  
 370 375 380  
 Ile Thr Tyr Tyr Ser Asn Tyr Gly Thr Arg Val Asp Leu Ser Gly Pro  
 385 390 395 400  
 Gly Gly Gly Gly Ser Val Asp Gly Asn Pro Gly Gly Tyr Val Trp Gln  
 405 410 415  
 Ser Gly Ser Asp Ala Ala Thr Thr Pro Glu Ser Gly Ser Tyr Ser Tyr  
 420 425 430  
 Met Gly Met Gly Gly Thr Ser Met Ala Ser Pro His Val Ala Ala Val  
 435 440 445  
 Ala Ala Leu Val Gln Ser Ala Leu Ile Ala Lys Gly Lys Asp Pro Leu  
 450 455 460  
 Ala Pro Ala Ala Met Arg Thr Leu Leu Lys Glu Thr Ala Arg Pro Phe  
 465 470 475 480  
 Pro Val Ser Ile Pro Thr Ala Thr Pro Ile Gly Thr Gly Ile Val Asp  
 485 490 495  
 Ala Lys Ala Ala Leu Ala Lys Ala Leu Glu Glu Pro Cys Thr Glu Asn  
 500 505 510  
 Cys Gly Pro Val Ala Thr Pro Leu Thr Asn Lys Ala Ala Val Gly Gly  
 515 520 525  
 Leu Asn Gly Thr Ala Gly Ser Ser Arg Leu Tyr Ser Phe Glu Ala Ala  
 530 535 540  
 Ala Gly Lys Gln Leu Ser Val Ile Thr Tyr Gly Gly Thr Gly Asn Val  
 545 550 555 560  
 Ser Val Tyr Ile Ala Gln Gly Arg Glu Pro Ser Ala Ser Asp Asn Asp  
 565 570 575  
 Gly Lys Ser Thr Arg Pro Gly Thr Ser Glu Thr Val Arg Val Asn Lys  
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 Asn Gly Val Ser Ile Leu Ala Thr Gln  
 610 615

<210> 37  
 <211> 3582  
 <212> DNA  
 <213> Unknown

<220>  
 <223> obtained from an environmental sample.

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 accgatgtcc tgcagcgta ccagcagcag cgcgcagagc agtcgctcgc gttcgcgcgt 180  
 gacctgcaca gcgcttcgct ggcggcgacc tttgttgctc cgatcggcgc caacgaccag 240  
 accgtttcct tcacggggcc gcgcaccagc gccgaggccg ccggcccat tctgggcaag 300  
 ccgggtgatg tggaaagctg gcatagcgat gagttcaatg ccgactgggg tctggccgcg 360  
 atgggggccc attacgcgta tgcgcgcggc ctaccgggtc agggcgctgc cttgggcgtg 420  
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&lt;211&gt; 1193

&lt;212&gt; PRT

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; Obtained from an environmental sample.

&lt;221&gt; SIGNAL

&lt;222&gt; (1)...(37)

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Gly	Asn	Ser	Phe	Ala	Val	Ser	Gly	Ala	Ala	Ile	Ala	Asp	Asn	Ala	Val
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 Arg Gln Ala Glu Ser Leu Val Ala Asn Leu Ala Gly Leu Gly Ile Glu  
 35 40 45  
 Leu Asp Glu Leu Ser Val Pro Val Pro Met Phe Ala Gln Gly Asn Glu  
 50 55 60  
 Gly Asp Arg Thr Ile Leu Ser Arg Phe Ala Ala Phe Ala Ala Pro Thr  
 65 70 75 80  
 Pro Asn Pro Glu Thr Ala Arg Ala Val Val Leu Pro Val Glu Val  
 85 90 95  
 Asp Arg Ala Arg Leu Glu Glu Leu Glu His Arg Pro Gly Val Thr Val  
 100 105 110  
 Trp Pro Asn Ser Glu Leu Ser Leu Phe Asn Thr Gly Asn Glu Asp Pro  
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 Ile Asp Leu Ala Trp Ser Lys Gly Gly Leu Asp Cys Arg Pro Phe Arg  
 130 135 140

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Val Trp Leu Glu Gly Tyr Arg Gly Gln Asn Ile Ile Val Gly Ile Ile
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Asp Glu Gly Ile Ser Gly Glu His Tyr Pro Val Val Gly Gly Phe Ser
180 185 190
Arg Pro Asn Ala Arg Arg Pro Gly Thr Ala Pro Ile Thr Ser His Gly
195 200 205
Ser Met Cys Ala Ala Asp Val Leu Ile Ala Ala Pro Ala Ala Arg Leu
210 215 220
Tyr Asp Tyr Pro Phe Leu Gly Val Pro Asn Ser Gly Gly Ala Leu Gln
225 230 235
Met Phe Gln Ala Val Leu Asp Gln Arg Arg Leu Asp Gly Thr Pro His
240 245 250 255
Leu Thr Asn Asn Ser Tyr Gly Phe Val Gly Val Pro Asp Pro Arg Gln
260 265 270
Trp Pro Asn His Glu Val His Asn Ile Asn His Pro Leu His Arg Lys
275 280 285
Val Arg Glu Val Val Ala Ala Gly Val Ala Cys Phe Phe Ala Ala Gly
290 295 300
Asn Cys Gly Ala Asp Cys Pro Ser Gly Asn Cys His Pro Ser Gly Ile
305 310 315 320
Gly Ala Gly Lys Ser Ile His Ala Ser Asn Ser Leu Ala Glu Val Val
325 330 335
Thr Val Ala Ala Val Asn Ser Arg His Glu Arg Ile Gly Tyr Ser Ser
340 345 350
Gln Gly Pro Gly Met Phe Glu Pro Arg Lys Pro Asp Leu Ala Ser Tyr
355 360 365
Ser His Ile Phe Ala Asn Phe Gly Pro Gly Arg Pro Ala Gly Thr Gly
370 375 380
Ser Gln Pro Phe Asp Asn Gly Thr Ser Ala Ala Thr Pro Val Ala Ala
385 390 395 400
Gly Val Ala Ala Leu Leu Leu Ser Ala Phe Pro Asp Val Asp Pro Asp
405 410 415
Arg Leu Lys Arg Val Leu Thr Ala Thr Ala Thr Arg Leu Gly Glu Thr
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gacgaggttg	cacgcctggc	ccatgagaac	ggctcagccc	gcgccaacct	gcccgaagtc	240
gcccagggtg	cacaggccat	ggcccgcggc	catggggctc	aactcgagcg	cagctttacc	300
catgccctgc	gtggcttcgt	ggtcgaagcc	gacgaccgcg	cgctggcccc	actgctgctg	360
gacgaacgcg	tcgccttcac	cgaagaagac	ggcatcgtca	gcatttccca	gaccaccag	420
ccgaacgcaa	cctggggcct	ggaccggatc	gaccagcgcg	atcgccccct	tgatggcaac	480
tacatctacg	acacgaccgc	gtcgaacgtg	tacacctaca	tcgtcgacac	cgggtgtgcg	540
accaaccaca	acgacttcgg	tggccgcgta	ctgagtggat	ttaccagcat	caatgacggc	600
aacggcacca	acgactgcaa	cgggcacggc	acctatgtgg	ccggcacctg	agccggcagc	660
acctgggggtg	tggccaaggc	cgcccgcctc	gtgcccgttc	gcgtgctggg	ctgccagggc	720
aacggcacca	acgcgggcgt	cattgccggc	atggactgga	tcgcccgaac	ccacgtcaag	780
cccgcctgtg	ccaacatgag	cctcgggtgg	ggcgccctga	ccgcaacgga	caacgccgtg	840
accaacatgc	gcaatgccgg	cgtcaccgtg	gtcgtcgcag	ctggcaacga	aaaccagaat	900
gcctgcaatg	tttcacccgg	tcgctctggc	aatgccatga	ccgtgggttc	aaccaccagc	960
accgatgcac	gctcgaactt	ctccaactgg	ggcaactcgc	tggtatctct	tgctccgggc	1020
agcagcatcc	gttcggcctg	gcacaccagc	aacaccgcag	ccaacaccat	cagtgggtacc	1080

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```

tcgatggccg ctccgcacgt tgctggcgta gccgccttgt tcctggccaa caacccgaac 1140
gccaccccg ccaggttga aaacgcgac tacagcaacg gtagcaccgg caagctcagc 1200
ggcctgaatg gttcgccaa cctgctggtc tactcgcgct tcggcggcgg cggcggcccg 1260
gatccagatc gaggcggatg a 1281

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<210> 42  
 <211> 426  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Obtained from an environmental sample.

<221> SIGNAL  
 <222> (1)...(22)

<400> 42  
 Met Ser Trp Lys Thr Leu Ser Thr Ser Leu Thr Gly Ala Ala Val Leu  
 1 5 10 15  
 Ala Leu Ser Ser Phe Ala Ala Ser Asp Ala Ala Ala Asn Asn Arg Ser  
 20 25 30  
 Asn Ser Glu Thr Arg Ala Gln Thr Ser Ala Asp Phe Arg His Ala Glu  
 35 40 45  
 Arg Pro Val Glu Gly Arg Tyr Ile Val Val Leu Lys Asp Glu Val Ala  
 50 55 60  
 Arg Leu Ala His Glu Asn Gly Ser Ala Arg Ala Asn Leu Pro Glu Val  
 65 70 75 80  
 Ala Gln Val Ala Gln Ala Met Ala Arg Gly His Gly Ala Gln Leu Glu  
 85 90 95  
 Arg Ser Phe Thr His Ala Leu Arg Gly Phe Val Val Glu Ala Asp Asp  
 100 105 110  
 Arg Ala Leu Ala Arg Leu Leu Leu Asp Glu Arg Val Ala Phe Ile Glu  
 115 120 125  
 Glu Asp Gly Ile Val Ser Ile Ser Gln Thr Thr Gln Pro Asn Ala Thr  
 130 135 140  
 Trp Gly Leu Asp Arg Ile Asp Gln Arg Asp Arg Pro Leu Asp Gly Asn  
 145 150 155 160  
 Tyr Ile Tyr Asp Thr Thr Ala Ser Asn Val Tyr Thr Tyr Ile Val Asp  
 165 170 175  
 Thr Gly Val Arg Thr Asn His Asn Asp Phe Gly Gly Arg Val Leu Ser  
 180 185 190  
 Gly Phe Thr Ser Ile Asn Asp Gly Asn Gly Thr Asn Asp Cys Asn Gly  
 195 200 205  
 His Gly Thr His Val Ala Gly Thr Val Ala Gly Ser Thr Trp Gly Val  
 210 215 220  
 Ala Lys Ala Ala Arg Ile Val Pro Val Arg Val Leu Gly Cys Gln Gly  
 225 230 235 240  
 Asn Gly Thr Asn Ala Gly Val Ile Ala Gly Met Asp Trp Ile Ala Ala  
 245 250 255  
 Asn His Val Lys Pro Ala Val Ala Asn Met Ser Leu Gly Gly Gly Ala  
 260 265 270  
 Ser Thr Ala Thr Asp Asn Ala Val Thr Asn Met Arg Asn Ala Gly Val  
 275 280 285  
 Thr Val Val Val Ala Ala Gly Asn Glu Asn Gln Asn Ala Cys Asn Val  
 290 295 300  
 Ser Pro Ala Arg Ser Gly Asn Ala Ile Thr Val Gly Ser Thr Thr Ser  
 305 310 315 320  
 Thr Asp Ala Arg Ser Asn Phe Ser Asn Trp Gly Asn Cys Val Asp Ile  
 325 330 335  
 Phe Ala Pro Gly Ser Ser Ile Arg Ser Ala Trp His Thr Ser Asn Thr  
 340 345 350  
 Ala Ala Asn Thr Ile Ser Gly Thr Ser Met Ala Ala Pro His Val Ala  
 355 360 365  
 Gly Val Ala Ala Leu Phe Leu Ala Asn Asn Pro Asn Ala Thr Pro Ala  
 370 375 380  
 Gln Val Glu Asn Ala Ile Tyr Ser Asn Gly Ser Thr Gly Lys Leu Ser  
 385 390 395 400  
 Gly Leu Asn Gly Ser Pro Asn Leu Leu Val Tyr Ser Arg Phe Gly Gly

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405 410 415  
 Gly Gly Gly Pro Asp Pro Asp Arg Gly Gly  
 420 425

<210> 43  
 <211> 1881  
 <212> DNA  
 <213> Unknown

<220>  
 <223> obtained from an environmental sample.

<400> 43  
 atgaacaaga catccatcag cgtggccctg gccgcggttc tggccggcgc gctcggcgcg 60  
 caggtcgccg atgctgcccg tacccccgcg aagatcgtgc cgcgcacatcga tgtggcgccg 120  
 ccggccgagg ccgctgccga ccgtatcgtc gtgcgctacg cgcaagcgcg catcgccagc 180  
 accgatcgca ccggcaagct gcaggtcgcg accgcgcga tccgccgcgc cgggctcgag 240  
 cgtccggtcg cctccggccg cgcggccaag gcgctgccgg cgttgcaagg cgcccatctg 300  
 cgcacgaccg cggctcggtt cgacgtgctc cggctgtcgc ggccgctgcc cgcgcgcgac 360  
 ttgcaggcgc tggtagccga actggccgcc gatccggcgg tggcgtcggg gcacgtggat 420  
 cggcgcacgc gcgcgaccgg tgtggacaag cgcaccgtca cgccgcagtt caccctcaac 480  
 gacgagttct tcgccagcca ccagtggcac ctgcagggtc cgcccggcgc gatcaacgtt 540  
 gccaacgcct gggaccgctc gaccggtgcc ggcacgtggt tcgcggtgct cgacaccggc 600  
 atcctggccg agcaccggga cttcgcgcac aacatcctgc ccggctacga cttcatcacc 660  
 gatcctttcg tgtcccggcg cgagaccgcc gaccgtgtgc ccggcgact ggaccacggc 720  
 gactggaaac cggtagcggg cgagtgtac agcggctcgc cggtagatcga cagcacctgg 780  
 catggcacc atgtggccgg cacggctgcc gaggcgacc acaacggcat cggtaggtgct 840  
 ggctgtcgcc acgacgcgca ggtgttgccg gtgcgcgtgc tcggccgctg cgggggctat 900  
 gactctgaca tcgccgatgc gatcgtctgg gcctcgggcg gcgcggtcga gggcgtgccg 960  
 gaaaacgtgc acccggtga ggtcatcaat ctacgcctcg gcggacaagg cacgtgcgag 1020  
 gcgatgaccc aggcggcgat cgacagtgcg gtcgcgcgcg gcagcgtggg cgtggtcgcg 1080  
 gccggcaact acaacgacga tgcccagcgc tattcgccag ccaactgcaa gaacgtgatc 1140  
 acggctcggcg ccaaccgcat caacagcggg cgcgcgact actccaactt cggtagcggg 1200  
 gtcgacgttt ttggccccgg cggtagcggc gagttcgaca ccggcaatgg cggctggaat 1260  
 ggctacgtgc tcgagaccgg ttacgacggc aagaccacgc cgacctccgg gcagtacctc 1320  
 tacaccgggc tgatgggcac ctcgatggcg gccccgcag tgtcgggcat cgccgcgctg 1380  
 gtgcagagcg cgtggtcgc ccaggaccgt ccgccgctga cgccggccga gatggagctc 1440  
 ctgctcaagc gcaccgcgcg tccgttcaat gtgccgcgc cgccaatac gccgatcggc 1500  
 gtgggcatcg ttgatgcgac ccgcgcgtg gagaaggcgc tggagacccc ctgcgatccg 1560  
 gccaccgaga cctgcgagct cggcaccag ctgttcaatg gcgccgacgt cactggcctg 1620  
 gcctccaacg gcgagggcgc gctgttccgc ttcgaggccc aggcgggtcg cacgttgacg 1680  
 ctgatgacgc tggccggccg cggcgacgtc actctgcac cgcgctatgg cgcaccgccg 1740  
 acctcgaccg actacgagtt ccgctcggcg cgtgcgggca gcaacatcga gacgatccgc 1800  
 atcaccgcgc ccaaggccgg cacgtactac ctgcagttga gcggcagcta cacaggcctg 1860  
 actgtcgtcg cccgtcagta g 1881

<210> 44  
 <211> 626  
 <212> PRT  
 <213> Unknown

<220>  
 <223> obtained from an environmental sample.

<221> SIGNAL  
 <222> (1)...(25)

<400> 44  
 Met Asn Lys Thr Ser Ile Ser Val Ala Leu Ala Ala Val Leu Ala Gly  
 1 5 10 15  
 Ala Leu Gly Ala Gln Val Ala Asp Ala Arg Thr Pro Ala Lys Ile  
 20 25 30  
 Val Pro Arg Ile Asp Val Ala Pro Pro Ala Glu Ala Ala Ser Asp Arg  
 35 40 45  
 Ile Val Val Arg Tyr Ala Gln Ala Arg Ile Ala Ser Thr Asp Arg Thr  
 50 55 60  
 Gly Lys Leu Gln Val Ala Thr Ala Ala Ile Arg Arg Ala Gly Leu Glu  
 65 70 75 80

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Arg Pro Val Ala Ser Gly Arg Ala Ala Lys Ala Leu Pro Ala Leu Gln  
 Val Gly His Leu Arg Thr Thr Ala Val Gly Phe Asp Val Leu Arg Leu  
 Ser Arg Pro Leu Pro Ala Arg Asp Leu Gln Ala Leu Val Thr Glu Leu  
 Ala Ala Asp Pro Ala Val Ala Ser Val His Val Asp Arg Arg Met Arg  
 Ala Thr Gly Val Asp Lys Arg Thr Val Thr Pro Gln Phe Thr Pro Asn  
 Asp Glu Phe Phe Ala Ser His Gln Trp His Leu Gln Gly Ser Ala Gly  
 Ala Ile Asn Val Ala Asn Ala Trp Asp Arg Ser Thr Gly Ala Gly Ile  
 Val Val Ala Val Leu Asp Thr Gly Ile Leu Ala Glu His Pro Asp Phe  
 Ala Asp Asn Ile Leu Pro Gly Tyr Asp Phe Ile Thr Asp Pro Phe Val  
 Ser Arg Arg Glu Thr Ala Asp Arg Val Pro Gly Ala Leu Asp His Gly  
 Asp Trp Asn Pro Val Ala Gly Glu Cys Tyr Ser Gly Ser Pro Val Ile  
 Asp Ser Thr Trp His Gly Thr His Val Ala Gly Thr Val Ala Glu Ala  
 Thr His Asn Gly Ile Gly Gly Ala Gly Val Ala Tyr Asp Ala Gln Val  
 Leu Pro Val Arg Val Leu Gly Arg Cys Gly Gly Tyr Asp Ser Asp Ile  
 Ala Asp Ala Ile Val Trp Ala Ser Gly Gly Ala Val Glu Gly Val Pro  
 Glu Asn Val His Pro Ala Glu Val Ile Asn Leu Ser Leu Gly Gly Gln  
 Gly Thr Cys Glu Ala Met Thr Gln Ala Ala Ile Asp Ser Ala Val Ala  
 Arg Gly Ser Val Val Val Val Ala Ala Gly Asn Tyr Asn Asp Asp Ala  
 Gln Arg Tyr Ser Pro Ala Asn Cys Lys Asn Val Ile Thr Val Gly Ala  
 Asn Arg Ile Asn Ser Gly Arg Ala Tyr Tyr Ser Asn Phe Gly Ala Val  
 Val Asp Val Ser Gly Pro Gly Gly Gly Gly Glu Phe Asp Thr Gly Asn  
 Gly Gly Trp Asn Gly Tyr Val Leu Gln Thr Gly Tyr Asp Gly Lys Thr  
 Thr Pro Thr Ser Gly Gln Tyr Leu Tyr Thr Gly Leu Met Gly Thr Ser  
 Met Ala Ala Pro His Val Ser Gly Ile Ala Ala Leu Val Gln Ser Ala  
 Leu Val Ala Gln Asp Arg Pro Pro Leu Thr Pro Ala Glu Met Glu Leu  
 Leu Leu Lys Arg Thr Ala Arg Pro Phe Asn Val Pro Pro Pro Ala Asn  
 Thr Pro Ile Gly Val Gly Ile Val Asp Ala Thr Arg Ala Leu Glu Lys  
 Ala Leu Glu Thr Pro Cys Asp Pro Ala Thr Glu Thr Cys Glu Leu Gly  
 Thr Gln Leu Phe Asn Gly Ala Asp Val Thr Gly Leu Ala Ser Asn Gly  
 Glu Gly Ala Leu Phe Arg Phe Glu Ala Gln Ala Gly Arg Thr Leu Thr  
 Leu Met Thr Leu Ala Gly Arg Gly Asp Val Thr Leu His Ala Arg Tyr  
 Gly Ala Pro Pro Thr Ser Thr Asp Tyr Glu Phe Arg Ser Ala Arg Ala  
 Gly Ser Asn Ile Glu Thr Ile Arg Ile Thr Ala Pro Lys Ala Gly Thr  
 Tyr Tyr Leu Gln Leu Ser Gly Ser Tyr Thr Gly Leu Thr Val Val Ala  
 610 615 620

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Arg Gln  
625

<210> 45  
 <211> 1875  
 <212> DNA  
 <213> Unknown

<220>  
 <223> Obtained from an environmental sample.

<400> 45  
 atgcaacgctc gttcagtcct gaccgctgcg gtcagcaccg ccctcgtgtg cgcattcgggt 60  
 gccacgctcgg tcctcgtctc cgagctgctc ttccgagaga acccgatcga gggccaatac 120  
 atcgtcgtcc tcaaggagga cgcggccacg ctccgagggc agacctcgat cgcgtccaac 180  
 cgtcccaacg tggccaatgc cgcgcgcaac ctggcccgcg cccaccgcgc cgaggctcgc 240  
 cacacctaca accgcgccct gcgcggcttc gtggcccgcg ccgacgagcg tgccctggcc 300  
 cgctgctgc aggaacccggc cgtggcctac gtcgaggagg acggcatcgt ctccatcggc 360  
 gccacccaga ccggcgccac ctggggcatc gaccgcatcg accagcgcg cctgccgctg 420  
 aaccagacct acgtctacga caccaccgca tccaacgtcc acgtctacat cgtcgacacc 480  
 ggcacccgtt cggcgacaa cgacttcggc ggccgcgtcg gttccggcta caccgccatc 540  
 aacgacggcc agggcacaa cgactgcaac ggccacggca cccatgtcgc ctccaccgcc 600  
 gccggtgcca cctacggcgt ggccaaggcc gccgcctct atccgggtgcg cgtgctcggc 660  
 tgccaggggca acggctccaa ttccggcggtg atcgccggca tggactgggt cgccagcaac 720  
 caggtcaagc cggccgtggc caacatgagc ctggggcgcg gcgcctcgca ggccaccgat 780  
 gatgccgtga cgcgcatgca caacgccggc gtcaccgtcg tgggtggcgc gggcaacgac 840  
 aacgccaacg cctgcaacta ctgcggcgcg cgtgcagcct cggcgatcac cgtgggctcg 900  
 accaccaaca ccgacgcacg ctccagcttc tccaacttcg gcacctgctg gaacatcttc 960  
 gcgcggggct ccaacatcac cgccgcctgg cacaccagca acaccgcgac caacaccatc 1020  
 agcggcacct cgtggtggc gccgcacgtc gccggcggtg ccgcgtgtg gctggccaac 1080  
 aacccaacg ccaccccgcc ccaggctcag caggcgctgt acaacaacgc cagcccaac 1140  
 aaggtgacca atgcccgcac cggctcggcc aaccgcctgc tgtactcgcg ctggggcgcc 1200  
 ggcaccaacc cggatcccga tccggatccg acgcccggca gcctgaccaa cggcgtgccg 1260  
 gtcaccggcc tctccggcgc agccggctcc gagcgtcgct acaccatgac cgtcccggcc 1320  
 ggcggccaca acctgtcgtt cgccatcagc ggccgacggt gtgatgccga cctgtacgtg 1380  
 cgcttcgggtt cggcgccgac caccacgacc tacgactgcc gtccgtacct caacggcaac 1440  
 aacgagacct gcaacatcag caacgtgcag gccggcacgt accacgtgct ggtccgtggc 1500  
 tacagccagt acagcggcgt gagcctggtg ggcaacttca cccggcctc cggcggtggc 1560  
 gcgccttgca ccggctgcac caagtacacc ggctccctca gcggcacccg ccaggcccag 1620  
 gtccagccca acggcaccta ctaccagtc caccgctccg gcacgcaccg cggctggctg 1680  
 cgtggcccgt ccaacgccga cttcgacctg gagctgtacc gctggaacgg cagcagctgg 1740  
 gccgcggtgg ccagctcgac cggcggcacc agcaacgagg agatcagcta caacggcacg 1800  
 gctggctact actactggcg catcgtgtcc tacagcggca gcggcagcta cgacttctac 1860  
 ctgaccggcc cgtga 1875

<210> 46  
 <211> 624  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Obtained from an environmental sample.

<221> SIGNAL  
 <222> (1)...(26)

<400> 46  
 Met Gln Arg Arg Ser Val Leu Thr Ala Ala Val Ser Thr Ala Leu Val  
 1 5 10 15  
 Cys Ala Phe Gly Ala Thr Ser Val Leu Ala Ser Glu Leu Arg Phe Ala  
 20 25 30  
 Glu Asn Pro Ile Glu Gly Gln Tyr Ile Val Val Leu Lys Glu Asp Ala  
 35 40 45  
 Ala Thr Leu Glu Gly Glu Thr Ser Ile Ala Ser Asn Arg Pro Asn Val  
 50 55 60  
 Ala Asn Ala Ala Arg Asn Leu Ala Arg Ala His Arg Ala Glu Val Arg  
 65 70 75 80  
 His Thr Tyr Asn Arg Ala Leu Arg Gly Phe Val Ala Arg Ala Asp Glu

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Arg	Ala	Leu	Ala	Arg	Leu	Leu	Gln	Asp	Pro	Ala	Val	Ala	Tyr	Val	Glu
Glu	Asp	Gly	Ile	Val	Ser	Ile	Gly	Ala	Thr	Gln	Thr	Gly	Ala	Thr	Trp
Gly	Ile	Asp	Arg	Ile	Asp	Gln	Arg	Asp	Leu	Pro	Leu	Asn	Gln	Thr	Tyr
Val	Tyr	Asp	Thr	Thr	Ala	Ser	Asn	Val	His	Val	Tyr	Ile	Val	Asp	Thr
Gly	Ile	Arg	Ser	Ala	His	Asn	Asp	Phe	Gly	Gly	Arg	Val	Gly	Ser	Gly
Tyr	Thr	Ala	Ile	Asn	Asp	Gly	Gln	Gly	Thr	Asn	Asp	Cys	Asn	Gly	His
Gly	Thr	His	Val	Ala	Ser	Thr	Ala	Ala	Gly	Ala	Thr	Tyr	Gly	Val	Ala
Lys	Ala	Ala	Arg	Leu	Tyr	Pro	Val	Arg	Val	Leu	Gly	Cys	Gln	Gly	Asn
Gly	Ser	Asn	Ser	Gly	Val	Ile	Ala	Gly	Met	Asp	Trp	Val	Ala	Ser	Asn
His	Val	Lys	Pro	Ala	Val	Ala	Asn	Met	Ser	Leu	Gly	Gly	Gly	Ala	Ser
Gln	Ala	Thr	Asp	Asp	Ala	Val	Thr	Arg	Met	Arg	Asn	Ala	Gly	Val	Thr
Val	Val	Val	Ala	Ala	Gly	Asn	Asp	Asn	Ala	Asn	Ala	Cys	Asn	Tyr	Ser
Pro	Ala	Arg	Ala	Ala	Ser	Ala	Ile	Thr	Val	Gly	Ser	Thr	Thr	Asn	Thr
Asp	Ala	Arg	Ser	Ser	Phe	Ser	Asn	Phe	Gly	Thr	Cys	Val	Asn	Ile	Phe
Ala	Pro	Gly	Ser	Asn	Ile	Thr	Ala	Ala	Trp	His	Thr	Ser	Asn	Thr	Ala
Thr	Asn	Thr	Ile	Ser	Gly	Thr	Ser	Met	Ala	Ser	Pro	His	Val	Ala	Gly
Val	Ala	Ala	Leu	Trp	Leu	Ala	Asn	Asn	Pro	Asn	Ala	Thr	Pro	Ala	Gln
Val	Glu	Gln	Ala	Leu	Tyr	Asn	Asn	Ala	Thr	Pro	Asn	Lys	Val	Thr	Asn
Ala	Gly	Thr	Gly	Ser	Ala	Asn	Arg	Leu	Leu	Tyr	Ser	Arg	Trp	Gly	Gly
Gly	Thr	Asn	Pro	Asp	Pro	Asp	Pro	Asp	Pro	Thr	Pro	Gly	Ser	Leu	Thr
Asn	Gly	Val	Pro	Val	Thr	Gly	Leu	Ser	Gly	Ala	Ala	Gly	Ser	Glu	Arg
Arg	Tyr	Thr	Met	Thr	Val	Pro	Ala	Gly	Ala	Thr	Asn	Leu	Ser	Phe	Ala
Ile	Ser	Gly	Gly	Ser	Gly	Asp	Ala	Asp	Leu	Tyr	Val	Arg	Phe	Gly	Ser
Ala	Pro	Thr	Thr	Thr	Thr	Tyr	Asp	Cys	Arg	Pro	Tyr	Leu	Asn	Gly	Asn
Asn	Glu	Thr	Cys	Asn	Ile	Ser	Asn	Val	Gln	Ala	Gly	Thr	Tyr	His	Val
Leu	Val	Arg	Gly	Tyr	Ser	Gln	Tyr	Ser	Gly	Val	Ser	Leu	Val	Gly	Asn
Phe	Thr	Pro	Ala	Ser	Gly	Gly	Gly	Ala	Pro	Cys	Thr	Gly	Cys	Thr	Lys
Tyr	Thr	Gly	Ser	Leu	Ser	Gly	Thr	Gly	Gln	Ala	Gln	Val	Gln	Pro	Asn
Gly	Thr	Tyr	Tyr	Gln	Ser	Thr	Arg	Ser	Gly	Thr	His	Arg	Gly	Trp	Leu
Arg	Gly	Pro	Ser	Asn	Ala	Asp	Phe	Asp	Leu	Glu	Leu	Tyr	Arg	Trp	Asn
Gly	Ser	Ser	Trp	Ala	Arg	Val	Ala	Ser	Ser	Thr	Gly	Gly	Thr	Ser	Asn
Glu	Glu	Ile	Ser	Tyr	Asn	Gly	Thr	Ala	Gly	Tyr	Tyr	Tyr	Trp	Arg	Ile
Val	Ser	Tyr	Ser	Gly	Ser	Gly	Ser	Tyr	Asp	Phe	Tyr	Leu	Thr	Arg	Pro

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<210> 47  
 <211> 1506  
 <212> DNA  
 <213> Unknown

<220>  
 <223> Obtained from an environmental sample.

<400> 47  
 atgctgtacgt cgcttcgggt ttcccttgcc agtgccatca ccctgggtcct ggccagcgcc 60  
 cccgccttcg cccaaccac cgaacgggta tggacgcgag gcatggccag caacgagcag 120  
 tacagcagtt tcacgtcaa gtaccgggac ggcagcagca agcgcgtctc cgccgacacc 180  
 gccagggacg cgctgaagaa gcgcctcggc gtccagcagc gcagcaagcg ttcgatcggc 240  
 agtgcgcccgc cggcggccgc gtccgtgacc catcaacgcc gcatggggcg cgccgcccgc 300  
 gtgggtcacca cggacaagcc actggaccgt ccggaggccg agatcctgat gcagcgcac 360  
 gccgacgatc ctgacgtcga gtatgtgcag ccgaactaca tgatgagtg attcgccacg 420  
 ccgaacgacc cgcgctacgg cgagcagtg cgagggcggt tgggtgcggg ggtcgattcg 480  
 ctgcccggcg cgtgggatcg ctccaccggc cagggcggtg tgggtgcggg ggtcgattcg 540  
 ggctatctca acaacaacga cctgcaggcg aacctgctgc cgggttacga catgatctcg 600  
 tcaacccgctc cgttcagtga ctggcagtg atcatcgggg gcatgaatcc cggctgtggg 660  
 ggctccgacg atggtgacgg acgcgacgac gatgcattcg atgcctcggg cattgcacac 720  
 ggacccacg tcgcccgaac ggtcgctgag gtgaccaaca accagattgg cgtggccggc 780  
 gtggcctaca acgcgaaagt cgtaccgggt cgcgtactgg gaaaccaggg caatggtggc 840  
 tccgcccgata tcacgcgacg catgctctgg agtgccggta tcaacgtgcc caacgtcccg 900  
 gccaatgcc aaccggccga ggtcatcaat ctgagcctgg gtggccgccc cgccctgctcg 960  
 ccggcccagc aggatgcaat cgacgacatc acggcccagg gcacgatcgt ggtggtcgcc 1020  
 gccggcaaca gcaatcttga tgtgtccgag ttcgcccgg cgaactgcaa gggcggtgac 1080  
 gcggttgctg ccaacgatca gggcggtcgt cgcgcgttct actccaacta tgggtgcaggc 1140  
 atccacatca ccgcaccggg tggcgagacc tggctgtgcc gtgctgcggg gggtgagttc 1200  
 ctgcccgtgg ccacgcccgc gagccaggcc aactgcgcac ccacccgcca gcatccggcg 1260  
 cagggcatcc tgtccaccgt ggttaacaac gccttcggct tcatgtccgg cacctcgatg 1320  
 gcggcgccctc acgtcgctgg catcgtcgcg ctgatgcagg cgggtggcgc ggtgccgaag 1380  
 accactgacc aggtcaagga catcctgctg cgaaccgcgc acccgatcgc agcggcgaac 1440  
 tgcccgggcg gttgcggacc gggcattgtc gacgtgcag aagcggtgaa ggccgcccagc 1500  
 aactga 1506

<210> 48  
 <211> 501  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Obtained from an environmental sample.

<221> SIGNAL  
 <222> (1)...(24)

<400> 48  
 Met Arg Thr Ser Leu Arg Val Ser Leu Ala Ser Ala Ile Thr Leu Val  
 1 5 10 15  
 Leu Ala Ser Ala Pro Ala Phe Ala Gln Pro Thr Glu Arg Val Trp Thr  
 20 25 30  
 Arg Gly Met Ala Ser Asn Glu Gln Tyr Ser Ser Phe Ile Val Lys Tyr  
 35 40 45  
 Arg Asp Gly Ser Ser Lys Arg Val Ser Ala Asp Thr Ala Gln Asp Ala  
 50 55 60  
 Leu Lys Lys Arg Leu Gly Val Gln Gln Arg Ser Lys Arg Ser Ile Gly  
 65 70 75 80  
 Ser Ala Pro Pro Ala Ala Ala Ser Val Thr His Gln Arg Arg Met Gly  
 85 90 95  
 Gly Gly Ala Asp Val Val Thr Thr Asp Lys Pro Leu Asp Arg Pro Glu  
 100 105 110  
 Ala Glu Ile Leu Met Gln Arg Ile Ala Asp Asp Pro Asp Val Glu Tyr  
 115 120 125  
 Val Gln Pro Asn Tyr Met Met Ser Ala Phe Ala Thr Pro Asn Asp Pro  
 130 135 140  
 Arg Tyr Gly Glu Gln Trp His Tyr Ser Asn Ser Thr Ser Gly Ala Arg  
 145 150 155 160

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Leu Pro Gly Ala Trp Asp Arg Ser Thr Gly Gln Gly Val Val Val Ala  
 Val Val Asp Ser 165 Gly Tyr Leu Asn Asn Asn Asp Leu Gln Ala Asn Leu  
 Leu Pro Gly Tyr Asp Met Ile Ser Ser Thr Arg Pro Phe 175 Ser Asp Trp  
 Gln Cys 180 Ile Ile Gly Gly Met Asn Pro Gly Cys Gly 190 Gly Ser Asp Asp  
 Gly Asp Gly Arg Asp Ala Asp Ala Phe Asp Ala 205 Ser Gly Ile Ala His  
 Gly Thr His Val 210 Ala Gly Thr Val Ala Val Thr Asn Asn Gln Ile  
 Gly Val Ala Gly 225 Val Ala Tyr Asn Ala Lys Val Val Pro Val Arg Val  
 Leu Gly Asn 230 Gln Gly Asn Gly Gly Ser Ala Asp Ile Ile Asp Gly Met  
 Leu Trp 245 Ser Ala Gly Ile Asn Val Pro Asn Val Pro Ala Asn Ala Asn  
 Pro Ala Glu Val Ile Asn Leu Ser Leu Gly Gly Arg Arg Ala Cys Ser  
 Pro Ala Glu Gln Asp 255 Ala Ile Asp Asp Ile Thr Ala Gln Gly Thr Ile  
 Val Val Val Ala Ala Gly Asn Ser Asn Leu Asp Val Ser Glu Phe Ala  
 Pro Ala Asn 260 Cys Lys Gly Val Ile Ala Val Ala Ala Asn Asp Gln Gly  
 Gly Arg Arg Ala Phe Tyr Ser Asn Tyr Gly Ala Gly 270 Ile His Ile Thr  
 Ala Pro Gly Gly Glu Thr Trp Ser Cys Arg Ala Ser Val Gly Glu Phe  
 Leu Pro Leu Ala Thr 285 Pro Pro Ser Gln Ala Asn Cys Ala Pro Thr Arg  
 Gln His Pro Ala 290 Gln Gly Ile Leu Ser Thr Val Gly Asn Asn Ala Phe  
 Gly Phe Met 300 Ser Gly Thr Ser Met Ala Ala Pro His Val Ala Gly Ile  
 Val Ala Leu Met Gln Ala Val Ala Pro Val Pro Lys Thr Thr Asp Gln  
 Val Lys Asp Ile Leu Arg Arg Thr Ala His Pro Ile Ala Ala Ala Asn  
 Cys Pro Gly Gly Cys 310 Gly Pro Gly Ile Val Asp Ala Ala Glu Ala Val  
 Lys Ala Ala Ser Asn 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 495 500

&lt;210&gt; 49

&lt;211&gt; 1545

&lt;212&gt; DNA

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; Obtained from an environmental sample.

&lt;400&gt; 49

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gcactaagcc	tgacatcggt	agcggtagca	gaaggtataa	aaaaagcaga	gccggcagca	120
gagcgtgaac	ttagcctggt	tgacctggca	gaagataaaa	ccaaccgtta	cattattaaa	180
tttaaagagc	cggctcgca	gatgagtgca	accggcacag	agcagcgcg	tgagttctcg	240
gtacaacgtg	cacagcaagt	gctgcaaaaa	gccaacgtta	acgcactgtc	acatttaaaa	300
tcagtgcattg	ccagtgtagc	cgagctgact	cctaaccagc	tgaagttact	gcaggctaata	360
cctgacgttg	aatacattga	agaagatcat	aaacgttacc	tgatggatgt	gatcacgcct	420
atggcacaaa	ccacacctta	tggtattacc	atggtgcagg	ctaatacagg	aagtgatggc	480
agtgtctggca	atacaaaagt	gtgctgtatt	gataccggtt	ggacttcagg	ccatgaagat	540
ttacaaaact	cgggcgtgac	gggatattct	ttttccggcc	acggtaactg	gtatcaggac	600
ggtaacggcc	acgggtactca	tggtgcccgt	actatggttg	cgctgaacaa	taacagcggt	660
gtagtgggcg	ttattgggttc	cgccaggcc	ggggtgcaca	ttgttaaaa	tttcaataat	720
tctggcaact	ggaccacagc	ttcaaatctg	atcacggcta	ttcagtcctg	ttaaagatgcc	780
ggtgctaaag	tagtcaatat	gagtcctgggt	ggcagctcgt	ctaaccagac	tgaaaatacg	840

## 10336256.txt

gcatgacca	atttctacaa	cggtggtatg	ttgctggtgg	ctgcagcggg	taatgccggc	900
aataccagtt	tctcctaccc	ggcgtcatac	aacgccgtgg	tgctcggttg	tgccggtaaac	960
tcaagtgggtg	cttttagccag	cttttcacag	cgtaactctc	aggtagaaat	ttccggcccg	1020
ggcgtttaacg	ttaactctac	ctggaacaac	gggtggctaca	acagcattag	cggtacctct	1080
atggcatcgc	ctcatgttgc	gggtgttgcc	gcgctggtgt	ggagtaatca	cccgcaatgt	1140
actgcagcac	aaattcgtaa	tgactttaat	gctacggctg	aagatcgtgg	tgctgttgcc	1200
cgtgatacgt	cttacgggtg	gggtattgtc	aaagccaaag	ctgcacatga	ttacttaacc	1260
aacaatggct	gcggcggtgg	cggcagtaac	ccaccaccaa	caggtggcgc	aacattccct	1320
aacctgtcag	caaccagtgg	ccagtgggta	agaggcagtt	accagatccc	ttcaggtgta	1380
tcaacggtaa	ctttccagat	atccggcggt	agcggtgatg	ccgatctata	tggttaactat	1440
ggtactgaac	cgagcacaac	aacctataac	tgccggcctt	acctgaatgg	taacaatgaa	1500
gtttgtacca	ttaataatcc	gcaagccggt	acctggcatg	tgggg		1545

<210> 50  
 <211> 515  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Obtained from an environmental sample.

<221> SIGNAL  
 <222> (1)...(30)

<400> 50

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Ala	Gly	Cys	Phe	Ala	Leu	Ser	Leu	Thr	Ser	Val	Ala	Val	Ala	Glu	Gly
			20					25					30		
Ile	Lys	Lys	Ala	Glu	Pro	Ala	Ala	Glu	Arg	Glu	Leu	Ser	Leu	Val	Asp
		35					40					45			
Leu	Ala	Glu	Asp	Lys	Thr	Asn	Arg	Tyr	Ile	Ile	Lys	Phe	Lys	Glu	Pro
	50					55					60				
Val	Ala	Gln	Met	Ser	Ala	Thr	Gly	Thr	Glu	Gln	Arg	Ala	Glu	Phe	Ser
65					70					75					80
Val	Gln	Arg	Ala	Gln	Gln	Val	Leu	Gln	Lys	Ala	Asn	Val	Asn	Ala	Leu
			85						90					95	
Ser	His	Leu	Lys	Ser	Val	His	Ala	Ser	Val	Ala	Glu	Leu	Thr	Pro	Lys
			100					105					110		
Gln	Leu	Lys	Leu	Leu	Gln	Ala	Asn	Pro	Asp	Val	Glu	Tyr	Ile	Glu	Glu
		115					120					125			
Asp	His	Lys	Arg	Tyr	Leu	Met	Asp	Val	Ile	Thr	Pro	Met	Ala	Gln	Thr
	130					135					140				
Thr	Pro	Tyr	Gly	Ile	Thr	Met	Val	Gln	Ala	Asn	Gln	Val	Ser	Asp	Gly
145					150					155					160
Ser	Ala	Gly	Asn	Thr	Lys	Val	Cys	Val	Ile	Asp	Thr	Gly	Trp	Thr	Ser
			165						170					175	
Gly	His	Glu	Asp	Leu	Gln	Asn	Ser	Gly	Val	Thr	Gly	Tyr	Ser	Phe	Ser
		180						185					190		
Gly	His	Gly	Asn	Trp	Tyr	Gln	Asp	Gly	Asn	Gly	His	Gly	Thr	His	Val
		195					200					205			
Ala	Gly	Thr	Met	Val	Ala	Leu	Asn	Asn	Asn	Ser	Gly	Val	Val	Gly	Val
	210					215					220				
Ile	Gly	Ser	Gly	Gln	Ala	Gly	Val	His	Ile	Val	Lys	Ile	Phe	Asn	Asn
225					230					235					240
Ser	Gly	Asn	Trp	Thr	Ala	Ser	Asn	Leu	Ile	Thr	Ala	Ile	Gln	Ser	
			245					250						255	
Cys	Lys	Asp	Ala	Gly	Ala	Lys	Val	Val	Asn	Met	Ser	Leu	Gly	Gly	Ser
		260						265					270		
Ser	Ser	Asn	Gln	Thr	Glu	Asn	Thr	Ala	Met	Thr	Asn	Phe	Tyr	Asn	Gly
		275					280					285			
Gly	Met	Leu	Leu	Val	Ala	Ala	Gly	Asn	Ala	Gly	Asn	Thr	Ser	Phe	
	290					295				300					
Ser	Tyr	Pro	Ala	Ser	Tyr	Asn	Ala	Val	Val	Ser	Val	Ala	Ala	Val	Asn
305					310					315					320
Ser	Ser	Gly	Ala	Leu	Ala	Ser	Phe	Ser	Gln	Arg	Asn	Ser	Gln	Val	Glu
			325						330					335	
Ile	Ser	Gly	Pro	Gly	Val	Asn	Val	Asn	Ser	Thr	Trp	Asn	Asn	Gly	Gly

## 10336256.txt

Tyr Asn Ser 340 Ile Ser Gly Thr Ser 345 Met Ala Ser Pro His 350 Val Ala Gly  
 Val Ala 355 Leu Val Trp Ser 360 His Pro Gln Cys 365 Thr Ala Ala Gln  
 Ile Arg Asn Ala Leu Asn Ala Thr Ala Glu Asp Arg Gly Ala Val Gly  
 385 Arg Asp Thr Ser Tyr 390 Gly Trp Gly Ile Val Lys Ala Lys Ala Ala His  
 Asp Tyr Leu Thr Asn Asn Gly Cys Gly Gly Gly Gly Ser Asn 415 Pro  
 Pro Thr Gly 420 Ala Thr Phe Pro Asn Leu Ser Ala Thr Ser Gly Gln  
 Trp Leu Arg Gly Ser Tyr Gln Ile Pro Ser Gly Val Ser Thr Val Thr  
 450 Phe Gln Ile Ser Gly Gly Ser Gly Asp Ala Asp Leu Tyr Val Asn Tyr  
 465 Gly Thr Glu Pro Ser 470 Thr Thr Tyr Asn Cys Arg Pro Tyr Leu Asn  
 Gly Asn Asn Glu Val Cys Thr Ile Asn Asn Pro Gln Ala Gly Thr Trp  
 His Val Gly 500 505 510 515

&lt;210&gt; 51

&lt;211&gt; 2874

&lt;212&gt; DNA

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; Obtained from an environmental sample.

&lt;400&gt; 51

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ggcggcgctc	ccgtcgccga	tgtggtggcg	ctgcctgcac	tgctggccaa	ggcgcaggct	180
gaaggccgct	cgatccgcga	agtcgtgctg	cgaacgtcca	acggtggcgc	gctgatcgcc	240
ggcgaagtgg	tgcaggcggg	gatccgtacc	cagggcctgg	acaccatcgt	gtccggccac	300
tgcatttcgt	cctgctcgat	catgcagtc	gggtggcgta	accgttacct	cgccggcgat	360
ctgccgctgg	tcgactcggg	gcagatccat	gccgccagca	gtggtggcag	gatcacctat	420
gcgccgctcg	cgcgcatgac	ccagatctac	acaggcaact	acggcggtgg	catggatgcg	480
ggcctgttgc	acaaggccat	gtatgaagtg	gtgcagccca	atggcctgct	ggatttccgc	540
gacccggcgc	gtaccacggg	tacgtcggtt	accttcgatc	cggatggcag	tgaggagcaag	600
ctggagtcac	tcccgggcca	ggacatccgc	agcaacagca	tcataaacac	ggcgggctat	660
cgcgatccgg	gtgacaccc	tcgtgtcacc	agcaacgtca	gcggcgacac	caacccgggc	720
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gatgaactgc	gcggccagct	gcggctggcg	gatctggatg	cctcgaccct	ggccaactcc	960
gccggcgctg	tccgtgtcag	caatggcgcc	acctggcgca	ccgctgaaac	caccggcgcc	1020
gatttcattc	tgggtggacaa	cggcaccatc	gcactggagg	gtggtgcgct	gcgcaccccc	1080
gagctgcggg	tgatgccggg	cagcatcgct	gttgcccgcg	gtgatatcgc	atcggtcggc	1140
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cgcttgcgcg	tggttcggcac	gctgatggcg	cgcggtgggg	atctggtgac	ccacggctac	1260
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cagtcggcca	tgcgcagcgg	cggtgatgcc	gatggcctgg	cctcgagggt	ggcgagtcg	1920
gtctcctccc	agccgggcat	gcgccatggc	agcctgttca	accagctggc	gatgcacctg	1980
gtcgaagccg	cgtcgggcag	cgttgcgggc	agcgtgtagt	ctggacgcag	ccacggcatc	2040
tgggcacgctg	gtttcgccag	ccatggctgc	atcgatgctg	acgggtggcgt	ggccggcctg	2100

## 10336256.txt

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agccacacca tcggtggcat cgtggtcggt gccgataccc gcgtggccga tgaccgcgtg 2160
accctgggcg tcagcgtggc cgcgggcgac atgtcgacca aggccagcga tggctctggg 2220
ttcactgggt acgtgcgtgc gctggacgtg ggcggtacc tcgatgcgac gtacgcgcgc 2280
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aacggcatcg atggcctgca gcagccactg cgcgccaagt acagcaacga tgcgatctcc 2400
gcacgggtgg aacatgcgtt ctccttcacc accgccaagg gcctgggtgat ccagccgttg 2460
ctgcccgtgg tggactacgc gcgcacctcg gccacccgct tcaacgaagg gcagggcgcc 2520
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tggcagaagg aactgggcga ttcgcaggcc cgctacagca ccggcttcgc cgcggtctcg 2700
gatctggtgt tcggcgccag cagccaggcg gtgggcgagc aggtgctggc ctggaacctg 2760
gggtgtgacca gccgtgccag cgagcggctg tccatcatgg ccgattatgt gggtgagcgc 2820
cgcgacgggc agatccagaa cggcgtgatg ctgggcctgg gctacaagtt ctaa 2874

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<210> 52  
 <211> 957  
 <212> PRT  
 <213> Unknown

<220>  
 <223> obtained from an environmental sample.

<221> SIGNAL  
 <222> (1)...(27)

<400> 52

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Met Lys Tyr Ser Lys Leu Ser Leu Ala Leu Ala Gly Leu Met Gly Val
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Gly Ala Ile Ala Ala Asp Asp Val Met Ala Met Ser Tyr His Val
20      25      30
Gln Asp Asp Arg Val Phe Leu Ser Gly Gly Val Thr Val Ala Asp Val
35      40      45
Val Ala Leu Pro Ala Leu Leu Ala Lys Ala Gln Ala Glu Gly Arg Pro
50      55      60
Ile Arg Glu Val Val Leu Arg Thr Ser Asn Gly Gly Ala Leu Ile Ala
65      70      75      80
Gly Glu Trp Leu Gln Ala Val Ile Arg Thr Gln Gly Leu Asp Thr Ile
85      90      95
Val Ser Gly His Cys Ile Ser Ser Cys Ser Ile Met Gln Ser Gly Gly
100     105     110
Val Asn Arg Tyr Leu Gly Gly Asp Leu Pro Leu Val Asp Ser Val Gln
115     120     125
Ile His Ala Ala Ser Ser Gly Arg Ile Thr Tyr Ala Pro Ser Ala
130     135     140
Arg Met Thr Gln Ile Tyr Thr Gly Asn Tyr Gly Gly Met Asp Ala
145     150     155     160
Gly Leu Leu His Lys Ala Met Tyr Glu Val Val Gln Pro Asn Gly Leu
165     170     175
Leu Val Phe Arg Asp Pro Ala Arg Thr Thr Gly Thr Ser Val Thr Phe
180     185     190
Asp Pro Asp Gly Ser Gly Ser Lys Leu Glu Ser Phe Pro Gly Gln Asp
195     200     205
Ile Arg Ser Asn Ser Ile Ile Asn Thr Ala Gly Tyr Arg Asp Pro Gly
210     215     220
Asp Thr Leu Arg Val Thr Ser Asn Val Ser Gly Asp Ile Asn Pro Gly
225     230     235     240
Tyr Leu Arg Thr Ala Arg Gln Leu Gln Ala Phe Val Asp Asp Asp Phe
245     250     255
Ala Arg Trp Asn Thr Asp Trp Ala Ser Thr Tyr Ile Asn Tyr Ala Val
260     265     270
Ser Leu Tyr Asn Phe Ser Thr Arg Gly Ala Asn Gly Ile Gly Ala Gln
275     280     285
Ser Leu Gln Gln Leu Leu Ala Asp Pro Asp Leu Gln Asp Glu Leu Arg
290     295     300
Gly Gln Leu Arg Leu Ala Asp Leu Asp Ala Ser Thr Leu Ala Asn Ser
305     310     315     320
Ala Gly Val Ile Arg Val Ser Asn Gly Ala Thr Trp Arg Thr Ala Glu
325     330     335

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10336256.txt

Thr	Thr	Gly	Ala	Asp	Phe	Ile	Leu	Val	Asp	Asn	Gly	Thr	Ile	Ala	Leu
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Glu	Gly	Gly	Ala	Leu	Arg	Thr	Pro	Glu	Leu	Arg	Val	Met	Pro	Gly	Ser
		355					360					365			
Ile	Val	Val	Gly	Arg	Gly	Asp	Ile	Ala	Ser	Val	Gly	Thr	Asp	Ser	Asp
	370					375					380				
Ala	Leu	Leu	Asp	Gly	Thr	Gly	Pro	Ser	Tyr	Arg	Glu	Asp	Gly	Phe	Asn
385					390					395					400
Arg	Leu	Arg	Val	Phe	Gly	Thr	Leu	Met	Pro	Arg	Gly	Gly	Asp	Leu	Val
				405					410					415	
Thr	His	Gly	Tyr	Val	Asn	Ile	Met	Pro	Gly	Gly	Gln	Val	Leu	Phe	Asp
			420					425					430		
Val	Thr	Glu	Thr	Gly	Gly	Thr	Gly	Ser	Gly	Arg	Leu	Arg	Val	Gly	Ser
		435					440					445			
Phe	Tyr	Asp	Gly	Gly	Ala	Glu	Glu	Gly	Ala	Leu	Val	Ile	Ala	Gln	Gly
	450					455					460				
Ala	His	Leu	Ala	Leu	Asn	Val	Ala	Gln	Gly	Phe	Tyr	Ala	Gly	Ala	Tyr
465					470					475					480
Arg	Arg	Asp	Leu	Val	Glu	Gly	Pro	Ile	Tyr	Gln	Gly	Gly	Phe	Gln	Asp
				485					490					495	
Val	Val	Arg	Leu	Gly	Asp	Ala	Gly	Tyr	Ser	Ala	Ser	Ile	Thr	Ala	Gly
			500					505					510		
Glu	Val	Phe	Arg	Pro	Arg	His	Asn	Ser	Leu	Leu	Ser	Phe	Asn	Val	Lys
		515					520					525			
Gln	Thr	Ala	Asp	Gly	Leu	Trp	Leu	Thr	Ala	Asn	Pro	Gly	Phe	Asp	Gln
	530					535					540				
Leu	Gly	Leu	Phe	Ala	Asn	Gly	Thr	Ser	Gly	Asp	Gly	Leu	Gly	Arg	Ala
545					550					555					560
Leu	Ala	Thr	Ala	Ser	Asp	Arg	Gln	Asp	Lys	Gly	Leu	Arg	Ser	Leu	Leu
				565					570					575	
Gly	Ala	Leu	Gln	Phe	Ala	Asp	Arg	Asp	Val	Ile	Ala	Gln	Gln	Ala	Gly
			580					585					590		
Ala	Leu	Arg	Gly	Asp	Ala	His	Ala	Ser	Leu	Arg	Leu	Ala	Asp	Thr	Ala
		595					600					605			
Leu	Val	Gly	Ser	Ile	Gly	Asn	Val	Val	Gln	Gln	His	Gln	Ser	Ala	Met
	610					615						620			
Arg	Ser	Gly	Gly	Asp	Ala	Asp	Gly	Leu	Ala	Ser	Gln	Val	Ala	Gln	Ser
625					630					635					640
Val	Ser	Ser	Gln	Pro	Gly	Met	Arg	His	Gly	Ser	Leu	Phe	Asn	Gln	Leu
				645					650					655	
Ala	Met	His	Leu	Val	Glu	Pro	Ala	Ser	Gly	Ser	Val	Ala	Gly	Ser	Ala
			660					665					670		
Asp	Ala	Gly	Arg	Ser	His	Gly	Ile	Trp	Ala	Arg	Gly	Phe	Ala	Ser	His
		675					680					685			
Gly	Arg	Ile	Asp	Ala	Asp	Gly	Gly	Val	Ala	Gly	Leu	Ser	His	Thr	Ile
	690					695					700				
Gly	Gly	Ile	Val	Val	Gly	Ala	Asp	Thr	Arg	Val	Ala	Asp	Asp	Arg	Val
705					710					715					720
Thr	Leu	Gly	Val	Ser	Val	Ala	Ala	Ala	Asp	Met	Ser	Thr	Lys	Ala	Ser
				725					730					735	
Asp	Gly	Ser	Gly	Phe	Thr	Gly	Asp	Val	Arg	Ala	Leu	Asp	Val	Gly	Gly
			740					745					750		
Tyr	Leu	Asp	Ala	Thr	Tyr	Ala	Arg	Gly	Tyr	Leu	Ser	Ala	Ala	Val	Arg
		755					760					765			
Tyr	Thr	Asp	Leu	Arg	His	Asp	Thr	Arg	Arg	Ser	Ile	Asn	Gly	Ile	Asp
	770					775					780				
Gly	Leu	Gln	Gln	Pro	Leu	Arg	Ala	Lys	Tyr	Ser	Asn	Asp	Ala	Ile	Ser
785					790					795					800
Ala	Arg	Val	Glu	His	Ala	Phe	Ser	Phe	Thr	Thr	Ala	Lys	Gly	Leu	Val
				805					810					815	
Ile	Gln	Pro	Leu	Leu	Pro	Val	Val	Asp	Tyr	Ala	Arg	Thr	Ser	Ala	Thr
			820					825					830		
Arg	Phe	Asn	Glu	Gly	Gln	Gly	Ala	Gly	Ala	Leu	Val	Gly	Arg	Ser	Gly
		835					840					845			
Ser	Leu	Glu	Ser	Ile	Arg	Val	Gly	Ala	Gly	Leu	Gln	Leu	Phe	Lys	Thr
	850					855					860				
Phe	Glu	Gly	Asn	Asn	Gly	Glu	Arg	Ile	Thr	Pro	Arg	Ala	Arg	Val	Val
865					870					875					880

## 10336256.txt

Trp Gln Lys Glu Leu Gly Asp Ser Gln Ala Arg Tyr Ser Thr Gly Phe  
 885 890 895  
 Ala Ala Ala Pro Asp Leu Val Phe Gly Ala Ser Ser Gln Ala Val Gly  
 900 905 910  
 Glu Gln Val Leu Ala Trp Asn Leu Gly Val Thr Ser Arg Ala Ser Glu  
 915 920 925  
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 945 950 955

<210> 53  
 <211> 2580  
 <212> DNA  
 <213> Unknown

<220>  
 <223> obtained from an environmental sample.

<400> 53  
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 gggctcagccc tcaccgcacc gacgaccgagc ttccgagca caccctgccac agctcccacc 120  
 cagcagcact ccgaagcggc gccgtcgtac atctcaggac tcgtcgaccc gcagagcgaa 180  
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 ggcgaggcggt atgccgagcc ggagcgtccc tcgatgcaga cccgcgcgac cgcaagagt 300  
 atcgcggtgt tctgcaccgc agcagacttc gcgcaggcct caggagaggc cctggtcact 360  
 ttgatcaagg gcagcacgac cgactgcgtc aacacgctgt tctcgggtcaa gggctcgag 420  
 gcggcatcca ttttcaccga ggcaagatg gtcacggcgg cgaatggcct tcgtgccgtc 480  
 gctcagtcct acaccggcga caactccggg tcggccgccc agctcgtgct gttcctgcgg 540  
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 agcgccgtca gcgcagcgt ggatgagttc ttcaacagcc cgcggtccaa agacgtcacc 660  
 gacgccaacg gcgagaccct gtctgaggcg gtcacactga tcgactcggc agagctcaac 720  
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 tcgtgggtgga tgatgaacgc ggtcaacggc acgttcaccg tgctgttccg aggtcaccag 840  
 gtgctcgtct tctgtcagaa ggtcgctcgc gacacctcac ttctcaccac gctccgggac 900  
 ttgcgactcg gacacaccga cctgctcgcc ggggagaaac cctacctggg cacaacgcg 960  
 ggccgcgaac tcggacgggt cctcggcgac gcgcccatac aggtcgcggg gaagccgatg 1020  
 gtgaaggctg tgctcgacca gacctcgctc gacggaccca cctcgggtct gtgggtggcg 1080  
 ctgcagaga tggcggactg gtacgacaag accgactgca gctactacgg cactgtcaac 1140  
 ctgcaggagc gtatcgaagc caaggtgctc cccaccactc acgtgtgcag cccgagcatc 1200  
 acgatccgcg cccaggacat gaacgcccag cagctgaccg ccagctgcgc gagcctgaac 1260  
 gtcaggagc cactattcca cgcggtcgcc aaggaccctg gccctgtgcc cggagacgtg 1320  
 aacacgaaga tcgaggttgt cgtgttcgac tcgagcacgg agtaccaggc ctacgcgggc 1380  
 acgtgttctc gcatcgacac caacaatggc ggcatgtacc tcgaggggtga cccgaccaag 1440  
 acgaacaaca aggcccgctt catcgcttac gaggccgagt ggctgcgccc tgagttcgcg 1500  
 atctggaacc tgaaccacga gtacacgcac tacctcgacg gtcgcttcaa catgcacggc 1560  
 gacttcaccg agaacatctc gactcccacg atctgggtggg tcgagggcct cgccgagtac 1620  
 atctcgtacc actaccgtca gatgccgtat acggcggcgc agcagctggc agcaacaggg 1680  
 cagtacaagc tcagccagct gttcgacacc acgtacgacc acgacaccga tcgcatctac 1740  
 cgggtggggct acctggcggg gagcttcatg ctgaacaagc acccgatcga gatgcaggcg 1800  
 gtgctgggca actaccgggtc aggaactgg aatgcagccc gcagctatct gaagaacagc 1860  
 atcggcacca cgtacgacgc cgaggtgag cgcccccggg accaggcgcc gacggcgcg 1920  
 tgctctgctg acctcggcgg cggcgggtgag accttcacgg acgggtcgag cgacccggac 1980  
 ttaccgctcg cgaccaacgg tctcactgag ccttcacgg acgggtcgag cgacccggac 2040  
 ggtagatcg cgagccgcgc ctgggacttc ggcaacggca gaacgtcgac cgagaagaac 2100  
 ccgtcgggtga cctacgcgca ggccggatca ttaccgctcg cttgacagt gaaggatgac 2160  
 aagggcgcg ccgccacgac gacgcgcacg gtcaccgtga agatgcccga caccggcaat 2220  
 cctgaccccc ctggcgacac ctggagcgta ccggtgtgag ccgacgcaga caccgcttg 2280  
 ctcggtcagg cgtgtggacg gatgggactg acggccaaga aggggtgaatc ccgctacctc 2340  
 atgggtctggg tgcccgcggg cactccccgc ctgaccgtca cgtcgggtgg cgggagcggg 2400  
 gacgccaacc tgtacgtcag ccactacggc tggccgagcc cgagaacca cgtggcgcg 2460  
 tcgaccaact cgggcaacgg cgaacaggtg gtggtcgagt ggcggcatc gggctggaac 2520  
 tacgtcgcgc tgcacggagt caaggacttc gcgaacgtga gcgcggtcgc ccactactga 2580

<210> 54  
 <211> 859  
 <212> PRT  
 <213> Unknown

10336256.txt

&lt;220&gt;

&lt;223&gt; Obtained from an environmental sample.

&lt;221&gt; SIGNAL

&lt;222&gt; (1)...(32)

&lt;400&gt; 54

```

Met Thr Gln Arg Met Met Gln Arg Gly Ala Thr Met Leu Leu Ser Ile
 1      5      10      15
Ala Val Cys Ala Gly Leu Ala Leu Thr Ala Pro Thr Thr Ala Phe Ala
 20      25      30
Ser Thr Pro Ala Thr Ala Pro Thr His Asp Asp Ser Glu Ala Ala Pro
 35      40      45
Ser Tyr Ile Ser Gly Leu Val Asp Pro Gln Ser Glu Glu Glu Val Ser
 50      55      60
Ala Thr Pro Pro Ile Ser Ala Asn Thr Asp Ala Leu His Thr Val Val
 65      70      75
Gly Glu Ala Asp Ala Glu Pro Glu Arg Pro Ser Met Gln Thr Arg Ala
 85      90      95
Thr Ala Lys Ser Ile Ala Ala Val Cys Thr Ala Ala Asp Phe Ala Gln
100      105      110
Ala Ser Gly Glu Ala Leu Val Thr Leu Ile Lys Gly Ser Thr Thr Asp
115      120      125
Cys Val Asn Thr Leu Phe Ser Val Lys Gly Ser Gln Ala Ala Ser Ile
130      135      140
Phe Thr Glu Ala Lys Met Val Thr Ala Ala Asn Gly Leu Arg Ala Val
145      150      155
Ala Gln Ser Tyr Thr Gly Asp Asn Ser Gly Ser Ala Ala Gln Leu Val
165      170      175
Leu Phe Leu Arg Ala Gly Tyr Tyr Val Gln Trp Tyr Asp Ser Val
180      185      190
Pro Ala Phe Gly Thr Ala Leu Arg Ser Ala Val Ser Ala Ala Leu Asp
195      200      205
Glu Phe Phe Asn Ser Pro Arg Ser Lys Asp Val Thr Asp Ala Asn Gly
210      215      220
Glu Thr Leu Ser Glu Ala Val Thr Leu Ile Asp Ser Ala Glu Leu Asn
225      230      235
Asp Arg Tyr Ile His Val Val Lys Arg Leu Thr Asp Tyr Asn Ala
245      250      255
Gly Tyr Asn Ser Ser Trp Trp Met Met Asn Ala Val Asn Gly Thr Phe
260      265      270
Thr Val Leu Phe Arg Gly His Gln Val Pro Ala Phe Val Gln Lys Val
275      280      285
Ala Ser Asp Thr Ser Leu Leu Thr Thr Leu Arg Asp Phe Ala Leu Gly
290      295      300
His Thr Asp Leu Leu Ala Gly Glu Asn Ala Tyr Leu Val Thr Asn Ala
305      310      315
Gly Arg Glu Leu Gly Arg Phe Leu Gly Asp Ala Pro Ile Lys Ala Ala
325      330      335
Val Lys Pro Met Val Lys Ala Val Leu Asp Gln Thr Ser Leu Asp Gly
340      345      350
Pro Thr Ser Gly Leu Trp Val Ala Leu Ala Glu Met Ala Asp Trp Tyr
355      360      365
Asp Lys Thr Asp Cys Ser Tyr Tyr Gly Thr Cys Asn Leu Gln Glu Arg
370      375      380
Ile Glu Ala Lys Val Leu Pro Thr Thr His Val Cys Ser Pro Ser Ile
385      390      395
Thr Ile Arg Ala Gln Asp Met Asn Ala Glu Gln Leu Thr Ala Ser Cys
405      410      415
Ala Ser Leu Asn Ala Gln Asp Ala Tyr Phe His Ala Val Ala Lys Asp
420      425      430
Pro Gly Pro Val Pro Gly Asp Val Asn Thr Lys Ile Glu Val Val Val
435      440      445
Phe Asp Ser Ser Thr Glu Tyr Gln Ala Tyr Ala Gly Thr Leu Phe Gly
450      455      460
Ile Asp Thr Asn Asn Gly Gly Met Tyr Leu Glu Gly Asp Pro Thr Lys
465      470      475      480

```

## 10336256.txt

Thr Asn Asn Lys Ala Arg Phe Ile Ala Tyr Glu Ala Glu Trp Leu Arg  
 485 490 495  
 Pro Glu Phe Ala Ile Trp Asn Leu Asn His Glu Tyr Thr His Tyr Leu  
 500 505 510  
 Asp Gly Arg Phe Asn Met His Gly Asp Phe Thr Glu Asn Ile Ser Thr  
 515 520 525  
 Pro Thr Ile Trp Trp Val Glu Gly Phe Ala Glu Tyr Ile Ser Tyr His  
 530 535 540  
 Tyr Arg Gln Met Pro Tyr Thr Ala Ala Gln Gln Leu Ala Ala Thr Gly  
 545 550 555 560  
 Gln Tyr Lys Leu Ser Gln Leu Phe Asp Thr Thr Tyr Asp His Asp Thr  
 565 570 575  
 Asp Arg Ile Tyr Arg Trp Gly Tyr Leu Ala Val Ser Phe Met Leu Asn  
 580 585 590  
 Lys His Pro Ile Glu Met Gln Ala Val Leu Gly Asn Tyr Arg Ser Gly  
 595 600 605  
 Asn Trp Asn Ala Ala Arg Ser Tyr Leu Lys Asn Ser Ile Gly Thr Thr  
 610 615 620  
 Tyr Asp Ala Glu Phe Thr Ala Phe Leu Ala Glu Cys Ala Gln Gly Asn  
 625 630 635 640  
 Cys Ser Ala Asp Leu Gly Gly Gly Gly Glu Pro Pro Arg Asn Gln Ala  
 645 650 655  
 Pro Thr Ala Ala Phe Thr Val Ala Thr Asn Gly Leu Thr Ala Thr Phe  
 660 665 670  
 Thr Asp Gly Ser Ser Asp Pro Asp Gly Gln Ile Ala Ser Arg Ala Trp  
 675 680 685  
 Asp Phe Gly Asn Gly Arg Thr Ser Thr Glu Lys Asn Pro Ser Val Thr  
 690 695 700  
 Tyr Ala Gln Ala Gly Ser Phe Thr Val Ala Leu Thr Val Lys Asp Asp  
 705 710 715 720  
 Lys Gly Ala Thr Ala Thr Thr Arg Thr Val Thr Val Lys Met Pro  
 725 730 735  
 Asp Thr Gly Asn Pro Asp Pro Gly Gly Asp Thr Trp Ser Val Pro Val  
 740 745 750  
 Cys Ala Asp Ala Asp Thr Arg Leu Leu Gly Gln Ala Cys Gly Arg Met  
 755 760 765  
 Gly Leu Thr Ala Lys Lys Gly Glu Ser Arg Tyr Leu Met Val Trp Val  
 770 775 780  
 Pro Ala Gly Thr Pro Arg Leu Thr Val Thr Ser Gly Gly Gly Ser Gly  
 785 790 795 800  
 Asp Ala Asn Leu Tyr Val Ser His Tyr Gly Trp Pro Ser Pro Gln Asn  
 805 810 815  
 His Val Ala Arg Ser Thr Asn Ser Gly Asn Gly Glu Gln Val Val Val  
 820 825 830  
 Glu Trp Pro Ala Ser Gly Trp Asn Tyr Val Ala Leu His Gly Val Lys  
 835 840 845  
 Asp Phe Ala Asn Val Ser Ala Val Ala His Tyr  
 850 855

&lt;210&gt; 55

&lt;211&gt; 2022

&lt;212&gt; DNA

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; obtained from an environmental sample.

&lt;400&gt; 55

atg	cg	caaat	cca	acc	gcac	cct	gcg	gctg	cag	tcg	cttg	cgg	ccg	ctac	act	gtt	cg	cg	60	
ttt	tc	cgcca	tcg	gtt	tcgc	ggg	cg	agg	cgc	aac	atcc	atc	tcg	atg	cgc	cac	cg	agg	ggc	120
atc	ccg	tacg	acc	gctt	cat	cg	tca	agtt	cgc	gat	ggca	gcc	ctg	agca	tgt	gaat	gcc			180
ggc	gc	acgcg	agc	agg	cgct	ggt	cg	cgcc	gct	cg	cggt	c	agg	gcct	gca	gct	cg	gcc	at	240
ctg	cg	tcggc	tgg	ccat	cg	tg	ccg	ac	ctg	gtc	ga	agt	gt	cg	acca	agct	gcc	gg	caa	300
gcg	gc	cgagg	cct	tgat	gcg	cg	cg	ctgg	ca	cg	aat	ccga	ac	gtc	gaata	cg	tcg	ag	ccg	360
gac	gc	gatca	tg	cg	ctcg	gct	ca	cgcc	g	aac	gata	ccc	g	ctac	cccc	ga	ccag	tgg	cat	420
tact	tc	cgagg	cc	acc	ggtg	cg	cca	atct	t	ccc	cg	gctt	ggg	aca	agg	c	cac	cg	gag	480
ggc	gt	ggtcg	tc	gc	ggtg	ct	cg	ac	ccgg	c	agc	acg	att	ac	agc	gat	ct	cg	ac	540
acc	gt	cgccg	gct	ac	gactt	cat	cag	cag	c	tcg	ac	gac	g	cg	cg	acg	g	ca	acg	600

## 10336256.txt

gatgccaaacc	ctcgcgacga	aggcgattgg	gtcagcgcca	acgagtgcgg	ctacacccat	660
ccggcacaga	actcgagctg	gcatggcacc	cacgtcgccg	gcaccatcgg	cgcggtcacc	720
aacaacgcca	agggcggtgg	cggcgtggcc	ttcggcgcca	aggtgcagca	tgtgcgcgtg	780
ctcggccggg	gtggcggtgc	gttggtccgac	atcgccgatg	cgatcggtg	ggcctcgggt	840
ggcagtgtca	gcggtgtgcc	cgccaatgcc	acgcccggcg	aggtgatcaa	catgagcctg	900
gggggagcgg	gcagctgcgg	ttcgacctat	caggccgcga	tcgattcggc	agtgaaccgc	960
ggcagcgtgg	tcgtgggtcgc	tgccggcaac	gacaacgtca	acgtgtccaa	cgcgctccg	1020
gccaactgca	acaacgtgat	cgcggtggcg	gccaccgatc	gcaacggcgc	acgtgccagt	1080
ttctccaact	acggcagcct	gatcgacgtc	tcggcgccag	gtgtgggtat	ctggtcgacg	1140
ctcaattcgg	gtaccaccac	gccgggcagc	gagagctacg	ccgcctacaa	cggcacctcg	1200
atggcgacac	cgcacgtggc	cggcacgtg	gcgctgatgc	aaagcgtatc	ggccaagacc	1260
ccggcccagg	tggagcagat	tctcaaggac	acggcgcgctc	cgctgccggg	tgcctgctcc	1320
ggcggttgcg	gggcccggcat	cgtcgacgcg	ctggcgccgg	tgaatgccgc	gatcggcggg	1380
ggcggcggca	acgtgctgca	gaacgggtgtc	accgtgaccg	gcctggctgc	cagcaccggc	1440
aacgcgctca	actacacgat	ggaggtgccc	gccggtgcca	ccaacctgca	gttcgcgatc	1500
agcggtgga	ccggcgatgc	tgatctctac	gtcaagttcg	gcagcgacac	gaccgacagc	1560
agctacgact	ggcgctcccta	caagtcgggc	aatgccgaga	gctgcagctt	cgccacgccc	1620
gccgcccggga	cctggcacgt	gcgctggaag	gcctattcga	ccttttccgg	ggtcagcctg	1680
accggcagtt	acactccgcc	gagcagcgcg	ccgtgcagcg	actgcaccaa	gtacagcggc	1740
tcgctttccg	gcagcggcag	cgcacagatc	cagcccagcg	gcagctacta	ccagtcgacc	1800
atctccggca	cgcaccaggg	ctggctcaag	gggtccggctg	gtaccgactt	cgatctggag	1860
ttgtaccgct	ggaacggcag	cagctggagt	cggtcgcgcg	gtgcccgcgac	cagcggctcg	1920
gaggaaacgc	tcagctacag	cggcgcggcc	ggctattact	actggcggat	cggtgtctat	1980
acgggcagcg	gcagctacga	cttctggctc	aagcggccct	ga		2022

&lt;210&gt; 56

&lt;211&gt; 673

&lt;212&gt; PRT

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; Obtained from an environmental sample.

&lt;221&gt; SIGNAL

&lt;222&gt; (1)...(27)

&lt;400&gt; 56

Met	Arg	Lys	Ser	Asn	Arg	Thr	Leu	Arg	Leu	Gln	Ser	Leu	Ala	Ala	Ala
1				5					10					15	
Thr	Leu	Phe	Ala	Phe	Ser	Ala	Ile	Gly	Phe	Ala	Gly	Glu	Ala	Asn	Ile
			20					25					30		
His	Leu	Asp	Ala	Leu	Thr	Glu	Gly	Ile	Pro	Tyr	Asp	Arg	Phe	Ile	Val
		35					40					45			
Lys	Phe	Arg	Asp	Gly	Ser	Pro	Glu	His	Val	Asn	Ala	Gly	Ala	Arg	Glu
	50					55				60					
Gln	Ala	Leu	Val	Ala	Ala	Ala	Arg	Gly	Gln	Gly	Leu	Gln	Leu	Gly	His
65				70					75					80	
Leu	Arg	Arg	Leu	Ala	Ile	Gly	Ala	Asp	Leu	Val	Glu	Val	Ser	Thr	Lys
			85						90					95	
Leu	Pro	Ala	Lys	Ala	Ala	Glu	Ala	Leu	Met	Arg	Ala	Leu	Ala	Arg	Asn
			100					105					110		
Pro	Asn	Val	Glu	Tyr	Val	Glu	Pro	Asp	Ala	Ile	Met	Arg	Ser	Leu	Leu
		115					120					125			
Thr	Pro	Asn	Asp	Thr	Arg	Tyr	Pro	Asp	Gln	Trp	His	Tyr	Phe	Glu	Ala
	130					135					140				
Thr	Gly	Gly	Ala	Asn	Leu	Pro	Ala	Ala	Trp	Asp	Lys	Ala	Thr	Gly	Ser
145				150						155					160
Gly	Val	Val	Val	Ala	Val	Leu	Asp	Thr	Gly	Ser	Thr	Ile	His	Ser	Asp
			165						170					175	
Leu	Asp	Ala	Asn	Thr	Val	Ala	Gly	Tyr	Asp	Phe	Ile	Ser	Ser	Ser	Thr
			180					185					190		
Thr	Ala	Arg	Asp	Gly	Asn	Gly	Arg	Asp	Ala	Asn	Pro	Arg	Asp	Glu	Gly
	195						200					205			
Asp	Trp	Val	Ser	Ala	Asn	Glu	Cys	Gly	Tyr	Thr	His	Pro	Ala	Gln	Asn
	210					215					220				
Ser	Ser	Trp	His	Gly	Thr	His	Val	Ala	Gly	Thr	Ile	Gly	Ala	Val	Thr
225					230						235				240
Asn	Asn	Ala	Lys	Gly	Val	Ala	Gly	Val	Ala	Phe	Gly	Ala	Lys	Val	Gln

10336256.txt

His Val Arg Val 245 Leu Gly Arg Cys Gly 250 Gly Ala Leu Ser Asp 255 Ile Ala  
 Asp Ala Ile Val 260 Trp Ala Ser Gly 265 Gly Ser Val Ser Gly 270 Val Pro Ala  
 Asn Ala 275 Thr Pro Ala Glu Val 280 Ile Asn Met Ser Leu 285 Gly Gly Ser Gly  
 Ser 290 Cys Gly Ser Thr Tyr 295 Gln Ala Ala Ile Asp 300 Ser Ala Val Asn Arg  
 305 Gly Ser Val Val 310 Val Ala Ala Gly Asn 315 Asp Asn Val Asn Val Ser  
 Asn Ala Arg Pro 325 Ala Asn Cys Asn 330 Val Ile Ala Val Ala Thr  
 Asp Arg Asn 340 Gly Ala Arg Ala Ser 345 Phe Ser Asn Tyr Gly 350 Ser Leu Ile  
 Asp Val 355 Ser Ala Pro Gly Val 360 Gly Ile Trp Ser Thr 365 Leu Asn Ser Gly  
 Thr 370 Thr Thr Pro Gly Ser 375 Glu Ser Tyr Ala Ala 380 Tyr Asn Gly Thr Ser  
 385 Met Ala Thr Pro His 390 Val Ala Gly Ile Val 395 Ala Leu Met Gln Ser Val  
 Ser Ala Lys Thr 405 Pro Ala Gln Val Glu 410 Gln Ile Leu Lys Asp 415 Thr Ala  
 Arg Pro Leu 420 Pro Gly Ala Cys Ser 425 Gly Gly Cys Gly Ala 430 Gly Ile Val  
 Asp Ala 435 Leu Ala Ala Val Asn 440 Ala Ala Ile Gly Gly 445 Gly Gly Asn  
 Val 450 Leu Gln Asn Gly Val 455 Thr Val Thr Gly Leu Ala Ala Ser Thr Gly  
 465 Asn Ala Leu Asn Tyr 470 Thr Met Glu Val Pro 475 Ala Gly Ala Thr Asn Leu  
 Gln Phe Ala Ile 485 Ser Gly Gly Thr Gly 490 Asp Ala Asp Leu Tyr Val Lys  
 Phe Gly Ser 500 Ala Pro Thr Asp 505 Ser Tyr Asp Cys Arg 510 Pro Tyr Lys  
 Ser Gly Asn Ala Glu Ser 515 Cys Ser Phe Ala Thr Pro 525 Ala Ala Gly Thr  
 Trp 530 His Val Arg Val Lys 535 Ala Tyr Ser Thr Phe 540 Ser Gly Val Ser Leu  
 545 Thr Gly Ser Tyr Thr 550 Pro Pro Ser Ser Ala 555 Pro Cys Ser Asp Cys Thr  
 Lys Tyr Ser Gly 560 Ser Leu Ser Gly Ser 565 Gly Ser Ala Gln Ile Gln Pro  
 Asp Gly Ser 570 Tyr Tyr Gln Ser Thr 575 Ile Ser Gly Thr His 580 Gln Gly Trp  
 Leu Lys 585 Gly Pro Ala Gly Thr 590 Asp Phe Asp Leu Glu 595 Leu Tyr Arg Trp  
 Asn 600 Gly Ser Ser Trp Ser 605 Arg Val Ala Arg Ala 610 Thr Ser Gly Ser  
 625 Glu Glu Thr Leu Ser 630 Tyr Ser Gly Ala Ala 635 Gly Tyr Tyr Tyr Trp Arg  
 Ile Val Ser 645 Thr Gly Ser Gly Ser 650 Tyr Asp Phe Trp Leu 655 Lys Arg  
 Pro 660

<210> 57  
 <211> 1293  
 <212> DNA  
 <213> Unknown

<220>  
 <223> Obtained from an environmental sample.

<400> 57

gtggcaccgg	tgacgacgac	ctaccgtacg	gccgccctgc	tcgccgcggg	caccctcacc	60
gccctcctcg	cggcccccgg	ccaggcctcc	gccgccggcc	ccacgagcgg	cccggccggc	120
gtgccccgcc	ccgcgggacc	cgctcctggac	ggcagcggcg	agtgcacctt	cccgatgaag	180

## 10336256.txt

aagcagatcg	agggcacccc	ctggccgctc	cagcgggtcc	tcctcgacga	gctgtggcag	240
gacaccaagg	gcaagggcgt	ccgggtcgcg	gtcatcgaca	cgggcgtcga	cgacgtcaac	300
ccgcagctga	agcaggccgt	cgacgccaag	gcgggcaagg	actacctcaa	gcccgcacaag	360
aagaacccgg	gcttcggcga	cgagctgcgc	ggcaagaccg	acggcaccgt	cgacgaggtc	420
ggccacggca	ccaaggtcgc	cgggatcatc	gccgcccggc	cccgccccgg	caccggcttc	480
gtcggcctcg	cgcccagggc	gacgatcatc	ccgatccggc	agaacgacga	gaagaacagc	540
ggcaagtccg	acacgatggc	cgaggccatc	aagtggggcg	tcgccaaggg	cgcccacgtc	600
atcaacatct	cgcaggacac	caccagccg	ctggacgccg	actcgccgat	ggccaaggcg	660
atcgccctcg	cgctgtccaa	gcagatcgtc	gtggtcgctt	ccgccggcaa	cgacggcatg	720
gacggctccc	tgaagaagac	ctatccggcc	gcgttccccg	gcgtcctcgc	cgtcgcctcc	780
tccgaccgga	acaacgagcg	ggccgcgttc	tcccagtcgg	gcaccttcgt	gggcgtcgcc	840
gccccggcg	tcgacgtcgt	ctccaccgtg	cccggcgggc	gccagtgctg	cgacaacggc	900
accagcttct	cgcgcccgta	cgtcgcccgc	gtcgcggccc	tgctgcgcgc	caagtaccgg	960
gagtggaccg	cggcgagat	cgtcacccgg	atcgagcaga	ccgccgtccg	ccccgtcaag	1020
gggcggggaca	accacgtggg	ctggggcggtg	gtcgacccgg	tgccggcgct	cgccgacacc	1080
cccggcagcg	cgccctcctc	gcccacgccc	gaccggggcc	cgcccaagcc	gccgggtccc	1140
gagccggccc	gactggcgct	gtcggagacg	cctcaggagc	gctccgaacg	gctcgccacc	1200
tacacgttgg	ggatcgggtg	cgtcctgggtg	gccgtggctg	ccggaaccgc	catcggtgatc	1260
cgcgacagcc	gccgcccggag	ggaggcccgt	tga			1293

<210> 58  
 <211> 430  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Obtained from an environmental sample.

<221> SIGNAL  
 <222> (1)...(31)

<400> 58

Met	Ala	Pro	Val	Thr	Thr	Thr	Tyr	Arg	Thr	Ala	Ala	Leu	Leu	Ala	Ala
1				5					10					15	
Gly	Thr	Leu	Thr	Ala	Leu	Leu	Ala	Ala	Pro	Gly	Gln	Ala	Ser	Ala	Ala
			20					25					30		
Gly	Pro	Thr	Ser	Gly	Pro	Ala	Gly	Val	Pro	Arg	Pro	Ala	Gly	Pro	Val
		35					40					45			
Leu	Asp	Gly	Ser	Gly	Glu	Cys	Thr	Phe	Pro	Met	Lys	Lys	Gln	Ile	Glu
	50					55					60				
Gly	Thr	Pro	Trp	Pro	Leu	Gln	Arg	Val	Leu	Leu	Asp	Glu	Leu	Trp	Gln
	65				70					75					80
Asp	Thr	Lys	Gly	Lys	Gly	Val	Arg	Val	Ala	Val	Ile	Asp	Thr	Gly	Val
				85					90					95	
Asp	Asp	Val	Asn	Pro	Gln	Leu	Lys	Gln	Ala	Val	Asp	Ala	Lys	Ala	Gly
			100					105					110		
Lys	Asp	Tyr	Leu	Lys	Pro	Asp	Lys	Lys	Asn	Pro	Gly	Phe	Gly	Asp	Glu
		115					120					125			
Leu	Arg	Gly	Lys	Thr	Asp	Gly	Thr	Val	Asp	Glu	Val	Gly	His	Gly	Thr
	130					135					140				
Lys	Val	Ala	Gly	Ile	Ile	Ala	Ala	Arg	Pro	Arg	Pro	Gly	Thr	Gly	Phe
	145				150					155					160
Val	Gly	Leu	Ala	Pro	Glu	Ala	Thr	Ile	Ile	Pro	Ile	Arg	Gln	Asn	Asp
				165					170					175	
Glu	Lys	Asn	Ser	Gly	Lys	Ser	Asp	Thr	Met	Ala	Glu	Ala	Ile	Lys	Trp
			180					185						190	
Ala	Val	Ala	Lys	Gly	Ala	His	Val	Ile	Asn	Ile	Ser	Gln	Asp	Thr	Thr
		195					200								
Gln	Pro	Leu	Asp	Ala	Asp	Ser	Pro	Met	Ala	Lys	Ala	Ile	Ala	Leu	Ala
	210					215					220				
Leu	Ser	Lys	Gln	Ile	Val	Val	Val	Ala	Ser	Ala	Gly	Asn	Asp	Gly	Met
	225				230					235					240
Asp	Gly	Ser	Leu	Lys	Lys	Thr	Tyr	Pro	Ala	Ala	Phe	Pro	Gly	Val	Leu
				245					250					255	
Ala	Val	Ala	Ser	Ser	Asp	Arg	Asn	Asn	Glu	Arg	Ala	Ala	Phe	Ser	Gln
			260					265					270		
ser	Gly	Thr	Phe	Val	Gly	Val	Ala	Ala	Pro	Gly	Val	Asp	Val	Val	Ser
	275						280					285			

10336256.txt

Thr	Val	Pro	Gly	Gly	Gly	Gln	Cys	Val	Asp	Asn	Gly	Thr	Ser	Phe	Ser
290						295					300				
Ala	Pro	Tyr	Val	Ala	Gly	Val	Ala	Ala	Leu	Leu	Arg	Ala	Lys	Tyr	Pro
305					310					315					320
Glu	Trp	Thr	Ala	Ala	Gln	Ile	Val	Thr	Arg	Ile	Glu	Gln	Thr	Ala	Val
				325					330					335	
Arg	Pro	Val	Lys	Gly	Arg	Asp	Asn	His	Val	Gly	Trp	Gly	Val	Val	Asp
			340					345					350		
Pro	Val	Arg	Ala	Leu	Ala	Asp	Thr	Pro	Gly	Thr	Pro	Pro	Ser	Ser	Pro
			355				360					365			
Thr	Pro	Asp	Pro	Gly	Pro	Pro	Lys	Pro	Pro	Ala	Pro	Glu	Pro	Ala	Arg
			370				375				380				
Leu	Ala	Leu	Ser	Glu	Thr	Pro	Gln	Glu	Arg	Ser	Glu	Arg	Leu	Ala	Thr
385					390					395					400
Tyr	Thr	Leu	Gly	Ile	Gly	Val	Val	Leu	Val	Ala	Val	Val	Ala	Gly	Thr
				405					410					415	
Ala	Ile	Val	Ile	Arg	Asp	Ser	Arg	Arg	Arg	Arg	Glu	Ala	Arg		
			420					425					430		

<210> 59  
 <211> 1203  
 <212> DNA  
 <213> Unknown

<220>  
 <223> obtained from an environmental sample.

<400> 59

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accaccgagg	acatctcccg	cgatgggagg	gcggtggcct	cgggcgagaa	cctcgaaatg	180
gtcgggtacg	acgtcaacca	gtacgaggcg	ccgatcctga	tggccgcct	cactaacgag	240
gagatcgccg	agctgaagaa	gaacaaggac	gtcggccggg	tggaggacga	cggcgagatg	300
tacgcccctt	agcttagccg	cgaggggagc	ccgtcgggtg	tttcgcagac	cattcccacc	360
ggcatctccc	agatcaaggc	gcccgaaggc	tggggctcca	gccaggggct	cggcattccag	420
gtctacatcc	tcgataccgg	gatccagtcg	gaccatcccg	atctcgtcca	gaacctgaaa	480
gcgggcaaga	gcttcgtgac	caacgagagc	tcgaccgagg	acttccacgg	ccacggcacc	540
cactgcgccc	gcaccgtcgc	cgccgccttc	aacaacttcg	gcgtcgtcgg	cgtcgccccg	600
tctgcctatc	tctaccgggt	gaaggttctc	tcggcgaccg	gcagcgggcca	gtggagctgg	660
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ctcggcgagg	ggggcgcgcc	gcaggcgctc	gccgacatgt	gcgaggcggt	ctacaacaag	780
ggcgtcctgc	tcgtcgccgc	cgccggcaac	aacggccctg	gcaacaacac	ggtcggcttc	840
ccggcggaagt	acccccacgt	catggccgtg	tcggcggtcg	acagcaacga	ccagatcgcc	900
agcttctcga	gccgtggggc	ggaggtcgag	atccgcggcg	ccggcgtgca	ggtgctctcg	960
accatccgca	actccggcta	cggccggatg	agcggcacct	cgatggcctg	cccgcacgct	1020
gccggcgccg	ccgcgctcgc	ctggggctcg	caccgcggcc	acaacaacaa	gcagatccgc	1080
tggctgtcca	acgtctttgc	ggacaaggct	ggcgaccagg	acccgcagca	ctacggcaac	1140
ggccgcgtca	acgccaacaa	ctcggcgctt	tttatcgga	acgccgccga	gcaccagctc	1200
tga						1203

<210> 60  
 <211> 400  
 <212> PRT  
 <213> Unknown

<220>  
 <223> obtained from an environmental sample.

<400> 60

Met	Ser	Asn	Asn	Ser	Arg	Lys	Pro	Val	Ile	Ile	Thr	Phe	Lys	Arg	Lys
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Asp	Lys	Arg	Gln	Ser	Lys	Gln	Asp	Lys	Gln	Glu	Ala	Val	Arg	Ser	Ala
			20				25					30			
Ile	Ser	Ser	Arg	Leu	Arg	Phe	Leu	Thr	Thr	Glu	Asp	Ile	Ser	Arg	Asp
			35				40				45				
Gly	Arg	Ala	Val	Ala	Ser	Gly	Glu	Asn	Leu	Glu	Met	Val	Gly	Tyr	Asp
	50					55				60					
Val	Asn	Gln	Tyr	Glu	Ala	Pro	Ile	Leu	Met	Ala	Arg	Leu	Thr	Asn	Glu

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65	Glu	Ile	Ala	Glu	Leu	70	Lys	Lys	Asn	Lys	Asp	Val	Ala	Arg	Val	80	Glu	Asp
	Asp	Gly	Glu	Met	Tyr	85	Ala	Leu	Glu	Leu	90	Ser	Arg	Glu	Gly	95	Pro	Ser
	Val	Leu	Ser	Gln	Thr	100	Ile	Pro	Thr	105	Gly	Ile	Ser	Gln	Ile	110	Lys	Ala
	Glu	Ala	Trp	Gly	Ser	115	Ser	Gln	Gly	120	Leu	Gly	Ile	Gln	Val	125	Tyr	Ile
	Asp	Thr	Gly	Ile	Gln	130	Ser	Asp	His	135	Pro	Asp	Leu	Val	Gln	140	Asn	Leu
	Ala	Gly	Lys	Ser	Phe	145	Val	Thr	Asn	150	Glu	Ser	Ser	Thr	Glu	155	Asp	Phe
	Gly	His	Gly	Thr	His	165	Cys	Ala	Gly	170	Thr	Val	Ala	Ala	Ala	175	Phe	Asn
	Phe	Gly	Val	Val	Gly	180	Val	Ala	Pro	185	Phe	Ala	Tyr	Leu	Tyr	190	Pro	Val
	Val	Leu	Ser	Ala	Thr	195	Gly	Ser	Gly	200	Gln	Trp	Ser	Trp	Leu	205	Ile	Ala
	Leu	Asp	Trp	Val	Ala	210	Ser	Lys	Lys	215	Gly	His	Arg	Ile	Ala	220	Ser	Met
	Leu	Gly	Gly	Gly	Gly	225	Ala	Pro	Gln	230	Ala	Leu	Ala	Asp	Met	235	Cys	Glu
	Val	Tyr	Asn	Lys	Gly	245	Val	Leu	Leu	250	Val	Ala	Ala	Ala	Gly	255	Asn	Asn
	Pro	Gly	Asn	Thr	Val	260	Gly	Phe	Pro	265	Ala	Lys	Tyr	Pro	His	270	Val	Met
	Ala	Val	Ser	Ala	Val	275	Asp	Ser	Asn	280	Asp	Gln	Ile	Ala	Ser	285	Phe	Ser
	Arg	Gly	Pro	Glu	Val	290	Glu	Ile	Ala	295	Pro	Gly	Val	Gln	Val	300	Leu	Ser
	Thr	Ile	Arg	Asn	Ser	305	Gly	Tyr	Gly	310	Arg	Met	Ser	Gly	Thr	315	Ser	Met
	Cys	Pro	His	Val	Ala	325	Gly	Ala	Ala	330	Ala	Leu	Ala	Trp	Gly	335	Ser	His
	Gly	His	Asn	Asn	Lys	340	Gln	Ile	Arg	345	Trp	Leu	Leu	Asn	Val	350	Phe	Ala
	Lys	Val	Gly	Asp	Gln	355	Asp	Pro	Gln	360	His	Tyr	Gly	Asn	Gly	365	Arg	Val
	Ala	Asn	Asn	Ser	Ala	370	Phe	Phe	Ile	375	Gly	Asn	Ala	Ala	Glu	380	His	Gln
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<210> 61  
 <211> 1824  
 <212> DNA  
 <213> Unknown

<220>  
 <223> obtained from an environmental sample.

<400> 61

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gcgcaaggcg	cgggcatgct	cgaccagacc	gatcgccctga	tcgtcaagta	caagggcgaa	180
tccgcaccga	gcgccaaggg	cctgacccgc	gccgcccgcct	acgtgccgat	ggccgcatcg	240
cgcaaggccg	tggtcgacca	ggtcggccgc	aagcacagcc	tgacgggtcca	ggaactgcac	300
gcgatcggta	ccggcgcccc	cgctgctcaag	ctgaaccgca	aggtctcggg	ggccgaggcc	360
gccaaagctcg	ccgccgaact	ggcagccagc	gatgtctcga	tcgagtacgc	cgagccggac	420
cgcatcatga	agccgatgtt	cacgccgaac	gacacctact	acaaccagca	gtgggattat	480
ttcgacgccg	tcggcgggcat	gaacatgccc	gcagcctggg	acaaatcgac	cggcaccggc	540
atccgcgtgg	ccgtgatcga	caccggctac	cgcccgcacg	tcgacctgca	gggcccagatc	600
ctggccggct	atgacttcat	catcgatacc	gccatctcga	acgacggcaa	cggccgcgac	660
agcgacgcca	gcgatccggg	cgactggacc	gtcgccggcc	agtgcggcac	cggtcggcca	720
gcctcgaact	cgagctggca	cggcacccac	gtggccggca	ccatcgccgc	cctgaccaac	780
aacggcatgg	gcgtggccgg	cgctgcctac	aacgccaagg	tcgtgcccgg	gcgcgtgctg	840
ggccagtcgg	gcggctacac	ttccgacatc	cgcgacggca	ttatctgggc	ctcgggcccgc	900
actgtctcgg	gcgtgaccaa	catcgcgccc	cgcgcacagg	tgatcaacat	gtccctgggc	960
ggcggcgggc	cttgcgacac	caccacccag	accgcaatca	acggcgcccc	ctcgcgcccgc	1020

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accgtggtcgc	tggtcgcggc	cggcaacgag	aaccagaacg	ccagcaacag	cagccccggcc	1080
aactgctcgg	gcgtgatcac	ggtggcggcc	accaacaagt	cgggcggcaa	ggcctcgtac	1140
tcgaactacg	gcaccatcgt	cgacgtggcg	gcaccgggcg	gcgacagcgg	cgcgggccatc	1200
ctgtcgaccc	tgaacgccgg	caccaccacc	ccgggcggcg	acaactacgt	cggctacatg	1260
ggcacctcga	tggtccacccc	gcacgtggcc	ggcgtggtcg	cgctgatgct	ggcgaagaac	1320
ccgaacctga	ccccggacga	agtcgaagcc	aagctgaagt	cgagcgcccc	tgcccttcccc	1380
gcagcgtgca	gcggctgcgg	cgccggcatc	gtcgacgcct	cggcggcaat	cgatgcccg	1440
gtcgggcaccg	gcaccggcac	gacgatgtcc	gaaaccgagt	cgaacaacac	gatcagcacc	1500
gcgaacgctg	tctcgacttc	cggcaccacg	gtcaacggca	acatgggcag	caccacggat	1560
tccggactact	tctcgggtcca	gctcccggcc	ggcaagaccc	tgacctcgac	cctgacgccc	1620
aacgcgcacct	ccgactacga	cctgtacatc	tacaacagcg	ccggcaccca	gatcacgtcg	1680
agcaccacg	gtacgggttc	ggtggattcg	gcaagcgtga	tcaacaacgg	cacgaccacc	1740
acgaccgctt	acgtgcgcgt	gaagtactac	agcggcggca	ccggttcgac	cagcggtacg	1800
tacacgctga	agctgagctg	gtaa				1824

<210> 62  
 <211> 607  
 <212> PRT  
 <213> Unknown

<220>  
 <223> obtained from an environmental sample.

<221> SIGNAL  
 <222> (1)...(40)

<400> 62

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			20					25					30		
Ala	Gly	Ala	Ala	Thr	Ala	Ser	Ala	Ala	Gln	Gly	Ala	Gly	Met	Leu	Asp
			35					40					45		
Gln	Thr	Asp	Arg	Leu	Ile	Val	Lys	Tyr	Lys	Gly	Glu	Ser	Ala	Pro	Ser
			50					55				60			
Ala	Lys	Gly	Leu	Thr	Arg	Ala	Ala	Ala	Tyr	Val	Pro	Met	Ala	Ala	Ser
			65					70				75			80
Arg	Lys	Ala	Val	Val	Asp	Gln	Val	Gly	Arg	Lys	His	Ser	Leu	Thr	Val
				85				90						95	
Gln	Glu	Leu	His	Ala	Ile	Gly	Thr	Gly	Ala	Arg	Val	Leu	Lys	Leu	Asn
			100					105					110		
Arg	Lys	Val	Ser	Val	Ala	Glu	Ala	Ala	Lys	Leu	Ala	Ala	Glu	Leu	Ala
			115					120					125		
Ala	Ser	Asp	Ala	Ser	Val	Glu	Tyr	Ala	Glu	Pro	Asp	Arg	Ile	Met	Lys
			130					135				140			
Pro	Met	Phe	Thr	Pro	Asn	Asp	Thr	Tyr	Tyr	Asn	Gln	Gln	Trp	Asp	Tyr
			145					150				155			160
Phe	Asp	Ala	Val	Gly	Gly	Met	Asn	Met	Pro	Ala	Ala	Trp	Asp	Lys	Ser
				165				170						175	
Thr	Gly	Thr	Gly	Ile	Arg	Val	Ala	Val	Ile	Asp	Thr	Gly	Tyr	Arg	Pro
			180					185						190	
His	Val	Asp	Leu	Gln	Gly	Gln	Ile	Leu	Ala	Gly	Tyr	Asp	Phe	Ile	Ile
			195					200					205		
Asp	Thr	Ala	Ile	Ser	Asn	Asp	Gly	Asn	Gly	Arg	Asp	Ser	Asp	Ala	Ser
			210					215				220			
Asp	Pro	Gly	Asp	Trp	Thr	Val	Ala	Gly	Gln	Cys	Gly	Thr	Gly	Ser	Ala
			225					230							240
Ala	Ser	Asn	Ser	Ser	Trp	His	Gly	Thr	His	Val	Ala	Gly	Thr	Ile	Ala
				245				250						255	
Ala	Leu	Thr	Asn	Asn	Gly	Met	Gly	Val	Ala	Gly	Val	Ala	Tyr	Asn	Ala
			260					265						270	
Lys	Val	Val	Pro	Val	Arg	Val	Leu	Gly	Gln	Cys	Gly	Gly	Tyr	Thr	Ser
			275					280						285	
Asp	Ile	Ala	Asp	Gly	Ile	Ile	Trp	Ala	Ser	Gly	Gly	Thr	Val	Ser	Gly
			290					295						300	
Val	Thr	Asn	Ile	Ala	Ala	Arg	Ala	Gln	Val	Ile	Asn	Met	Ser	Leu	Gly
			305					310						315	
Gly	Gly	Gly	Ala	Cys	Asp	Thr	Thr	Thr	Gln	Thr	Ala	Ile	Asn	Gly	Ala
														320	

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Arg	Ser	Arg	Gly	325	Thr	Val	Val	Val	Val	330	Ala	Ala	Gly	Asn	Glu	335	Asn	Gln
Asn	Ala	Ser	340	Asn	Ser	Ser	Pro	Ala	345	Asn	Cys	Ser	Gly	Val	350	Ile	Thr	Val
Ala	Ala	355	Thr	Asn	Lys	Ser	Gly	360	Gly	Lys	Ala	Ser	Tyr	365	Ser	Asn	Tyr	Gly
Thr	370	Ile	Val	Asp	Val	Ala	375	Ala	Pro	Gly	Gly	Asp	380	Ser	Gly	Ala	Ala	Ile
385	Leu	Ser	Thr	Leu	Asn	Ala	390	Gly	Thr	Thr	Thr	Pro	395	Gly	Ala	Asp	Asn	Tyr
Val	Gly	Tyr	Met	405	Gly	Thr	Ser	Met	410	Ala	Thr	Pro	415	His	Val	Ala	Gly	Val
Val	Ala	Leu	Met	420	Leu	Ala	Lys	Asn	425	Pro	Asn	Leu	430	Thr	Pro	Asp	Glu	Val
Glu	Ala	Lys	Leu	435	Lys	Ser	Ser	Ala	440	Arg	Ala	Phe	445	Pro	Ala	Ala	Cys	Ser
Gly	450	Cys	Gly	Ala	Gly	Ile	Val	Asp	455	Ala	Ser	Ala	460	Ala	Ile	Asp	Ala	Ala
465	Val	Gly	Thr	Gly	470	Gly	Thr	Thr	475	Met	Ser	Glu	480	Thr	Glu	Ser	Asn	Asn
Thr	Ile	Ser	Thr	485	Ala	Asn	Ala	Val	490	Ser	Thr	Ser	495	Gly	Thr	Thr	Val	Asn
Gly	Asn	Met	Gly	500	Ser	Thr	Thr	Asp	505	Ser	Asp	Tyr	510	Phe	Ser	Val	Gln	Leu
Pro	Ala	Gly	Lys	515	Thr	Leu	Thr	520	Ser	Thr	Leu	Thr	525	Pro	Asn	Ala	Thr	Ser
Asp	530	Tyr	Asp	Leu	Tyr	Ile	Tyr	535	Asn	Ser	Ala	Gly	540	Thr	Gln	Ile	Thr	Ser
545	Ser	Thr	Asn	Gly	550	Gly	Ser	Val	555	Asp	Ser	Ala	560	Ser	Val	Ile	Asn	Asn
Gly	Thr	Thr	Thr	565	Thr	Thr	Ala	Tyr	570	Val	Arg	Val	575	Lys	Tyr	Tyr	Ser	Gly
Gly	Thr	Gly	580	Ser	Thr	Ser	Gly	Thr	585	Tyr	Thr	Leu	590	Lys	Leu	Ser	Trp	
			595					600					605					

&lt;210&gt; 63

&lt;211&gt; 1869

&lt;212&gt; DNA

&lt;213&gt; Archea

&lt;400&gt; 63

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tacgagagca	cggttgttgt	tgaagacctt	gaaacgggct	caaggcgctt	catcgagaac	180
gcctcaatgc	cgaggatttc	gccagacggc	agaaagctcg	ccttcacctg	ctttaacgag	240
gagaagaagg	agaccgagat	atgggtggcc	gatatccaga	ccctgagcgc	caagaaagtc	300
ctctcaacta	aaaacgtccg	ctcgtatgag	tggaacgacg	attcaaggag	actcttagtt	360
gtcggcttca	agaggaggga	cgatgaggac	ttcgtctttg	acgacgacgt	ccgggtctgg	420
ttcgacaata	tgggattctt	tgatggagag	aagacgacgt	tctgggttct	tgacactgag	480
gccgaggaga	taatcgagca	gttcgagaag	ccgaggtttt	cgagtggcct	ctggcacggc	540
gatgcgatag	ttgtgaacgt	cccgcaccgc	gaggggagca	agcctgccct	gttcaagttc	600
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gaggcgggtg	actccgacgg	aaagagaata	ctcctgaggg	gcaagaaaaa	aaagcggttc	720
atcagcgagc	acgactggct	gtacctctgg	gacggcgagc	ttaaaccgat	ctacgagggc	780
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cactggattt	acgggcttga	cgctacggat	ggcaaacgat	tgctcctcat	catgaccggc	960
acgaggatag	gcgagctcta	cctctacgac	ggcgagctga	aacagggtcac	cgaatacaac	1020
gggccgatat	tcaggaagct	caagaccttc	gagccgaggg	acttccgctt	caagagcaaa	1080
gacctcgaga	taccagggctg	gtacctcagg	ccggagggtta	aagaggagaa	ggccccgggtg	1140
atagtcttcg	ttcacggcgg	gccgaagggc	atgtacggac	accgcttcgt	ctacgagatg	1200
cagctgatgg	cgagcaaggg	ctactacgtc	gtcttcgtga	acccgcgcgg	cagcgacggc	1260
tatagcgaag	acttcgcgct	ccgcgtcctg	gagaggactg	gcttgaggga	ctttgaggac	1320
ataatgaacg	gcatacgagga	gttcttcaag	ctcgaaccgc	aggccgacag	ggagcgcggt	1380
ggaataacgg	gcataagcta	cggcggcttc	atgaccaact	gggccttgac	tcagagcgac	1440
ctcttcaagg	caggaataag	cgagaacggc	ataagctact	ggctcaccag	ctacgccttc	1500
tcggacatag	ggctctggta	cgacgtcgag	gtcatcgggc	caaattccgtt	agagaacgag	1560

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aacttcagga	agctcagccc	gctgttctac	gctcagaacg	tgaaggcgcc	gatactccta	1620
atccactcgc	ttgaggacta	ccgctgtccg	ctcgaccaga	gccttatgtt	ctacaacgtg	1680
ctcaaggaca	tgggcaagga	agcctacata	gcgatattca	agcgcgccgc	ccacggccac	1740
agcgtccgcg	gaagcccag	gcacaggccg	aagcgctaca	ggctcttcat	agagttcttc	1800
gagcgcaagc	tcaagaagta	cgaggagggc	tttgaggtag	agaagatact	caaggggaat	1860
gggaactga						1869

<210> 64  
 <211> 622  
 <212> PRT  
 <213> Archea

<400> 64

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Leu	Gly	Asp	Pro	Arg	Ile	Arg	Gly	Asn	Leu	Ile	Ala	Tyr	Thr	Leu	Thr
			20					25					30		
Lys	Ala	Asn	Met	Lys	Asp	Asn	Lys	Tyr	Glu	Ser	Thr	Val	Val	Val	Glu
		35				40					45				
Asp	Leu	Glu	Thr	Gly	Ser	Arg	Arg	Phe	Ile	Glu	Asn	Ala	Ser	Met	Pro
	50				55					60					
Arg	Ile	Ser	Pro	Asp	Gly	Arg	Lys	Leu	Ala	Phe	Thr	Cys	Phe	Asn	Glu
65					70					75					80
Glu	Lys	Lys	Glu	Thr	Glu	Ile	Trp	Val	Ala	Asp	Ile	Gln	Thr	Leu	Ser
			85						90					95	
Ala	Lys	Lys	Val	Leu	Ser	Thr	Lys	Asn	Val	Arg	Ser	Met	Gln	Trp	Asn
			100					105					110		
Asp	Asp	Ser	Arg	Arg	Leu	Leu	Val	Val	Gly	Phe	Lys	Arg	Arg	Asp	Asp
		115					120					125			
Glu	Asp	Phe	Val	Phe	Asp	Asp	Val	Pro	Val	Trp	Val	Phe	Asp	Asn	Met
	130					135				140					
Gly	Phe	Phe	Asp	Gly	Glu	Lys	Thr	Thr	Phe	Trp	Val	Leu	Asp	Thr	Glu
145					150					155					160
Ala	Glu	Glu	Ile	Ile	Glu	Gln	Phe	Glu	Lys	Pro	Arg	Phe	Ser	Ser	Gly
			165						170					175	
Leu	Trp	His	Gly	Asp	Ala	Ile	Val	Val	Asn	Val	Pro	His	Arg	Glu	Gly
		180						185					190		
Ser	Lys	Pro	Ala	Leu	Phe	Lys	Phe	Tyr	Asp	Ile	Val	Leu	Trp	Lys	Asp
		195					200					205			
Gly	Glu	Glu	Glu	Lys	Leu	Phe	Glu	Arg	Val	Ser	Phe	Glu	Ala	Val	Asp
	210					215					220				
Ser	Asp	Gly	Lys	Arg	Ile	Leu	Leu	Arg	Gly	Lys	Lys	Lys	Lys	Arg	Phe
	225				230					235					240
Ile	Ser	Glu	His	Asp	Trp	Leu	Tyr	Leu	Trp	Asp	Gly	Glu	Leu	Lys	Pro
			245						250					255	
Ile	Tyr	Glu	Gly	Pro	Leu	Asp	Val	Trp	Glu	Ala	Lys	Leu	Thr	Glu	Gly
		260						265					270		
Lys	Val	Tyr	Phe	Leu	Thr	Pro	Asp	Ala	Gly	Arg	Val	Asn	Leu	Trp	Leu
		275					280					285			
Trp	Asp	Gly	Lys	Ala	Glu	Arg	Val	Val	Thr	Gly	Asp	His	Trp	Ile	Tyr
	290					295					300				
Gly	Leu	Asp	Val	Ser	Asp	Gly	Lys	Ala	Leu	Leu	Leu	Ile	Met	Thr	Ala
	305				310					315					320
Thr	Arg	Ile	Gly	Glu	Leu	Tyr	Leu	Tyr	Asp	Gly	Glu	Leu	Lys	Gln	Val
			325						330					335	
Thr	Glu	Tyr	Asn	Gly	Pro	Ile	Phe	Arg	Lys	Leu	Lys	Thr	Phe	Glu	Pro
		340						345					350		
Arg	His	Phe	Arg	Phe	Lys	Ser	Lys	Asp	Leu	Glu	Ile	Asp	Gly	Trp	Tyr
	355						360					365			
Leu	Arg	Pro	Glu	Val	Lys	Glu	Glu	Lys	Ala	Pro	Val	Ile	Val	Phe	Val
	370					375					380				
His	Gly	Gly	Pro	Lys	Gly	Met	Tyr	Gly	His	Arg	Phe	Val	Tyr	Glu	Met
385					390					395					400
Gln	Leu	Met	Ala	Ser	Lys	Gly	Tyr	Tyr	Val	Val	Phe	Val	Asn	Pro	Arg
			405						410				415		
Gly	Ser	Asp	Gly	Tyr	Ser	Glu	Asp	Phe	Ala	Leu	Arg	Val	Leu	Glu	Arg
		420						425					430		
Thr	Gly	Leu	Glu	Asp	Phe	Glu	Asp	Ile	Met	Asn	Gly	Ile	Glu	Glu	Phe

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435 440 445  
 Phe Lys Leu Glu Pro Gln Ala Asp Arg Glu Arg Val Gly Ile Thr Gly  
 450 455 460  
 Ile Ser Tyr Gly Gly Phe Met Thr Asn Trp Ala Leu Thr Gln Ser Asp  
 465 470 475 480  
 Leu Phe Lys Ala Gly Ile Ser Glu Asn Gly Ile Ser Tyr Trp Leu Thr  
 485 490 495  
 Ser Tyr Ala Phe Ser Asp Ile Gly Leu Trp Tyr Asp Val Glu Val Ile  
 500 505 510  
 Gly Pro Asn Pro Leu Glu Asn Glu Asn Phe Arg Lys Leu Ser Pro Leu  
 515 520 525  
 Phe Tyr Ala Gln Asn Val Lys Ala Pro Ile Leu Leu Ile His Ser Leu  
 530 535 540  
 Glu Asp Tyr Arg Cys Pro Leu Asp Gln Ser Leu Met Phe Tyr Asn Val  
 545 550 555 560  
 Leu Lys Asp Met Gly Lys Glu Ala Tyr Ile Ala Ile Phe Lys Arg Gly  
 565 570 575  
 Ala His Gly His Ser Val Arg Gly Ser Pro Arg His Arg Pro Lys Arg  
 580 585 590  
 Tyr Arg Leu Phe Ile Glu Phe Phe Glu Arg Lys Leu Lys Lys Tyr Glu  
 595 600 605  
 Glu Gly Phe Glu Val Glu Lys Ile Leu Lys Gly Asn Gly Asn  
 610 615 620

&lt;210&gt; 65

&lt;211&gt; 1740

&lt;212&gt; DNA

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; Obtained from an environmental sample.

&lt;400&gt; 65

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cagtccgcac	agaccaccca	gcgtttcatc	gtgaagtacc	gcgacggcag	cgcgccgggtg	180
gccaacacca	ccgcactggc	ctcttcgctg	aagagcgccg	ccgcccggcct	ggccagcagc	240
cagggccgcg	cgctgggcct	gcagcaggtc	cgcaagctgg	ccgtcggccc	caccctgggtc	300
aagaccgatc	gtccgctcga	ccaggccgaa	tccgagcagc	tgatgcgcaa	gctggccggc	360
gacccgaacg	tggaatacgt	tgaagtgcac	cagatcatgc	gtgccacgct	gaccccgaa	420
gacacccgct	tcagcgagca	atggggcttc	ggtacctcca	atgccggcat	caacatccgg	480
ccggcctggg	acaaggccac	cggcaccggc	gtggctcggtg	cggtgatcga	caccggcatc	540
accaaccacg	ccgacctcaa	tgccaacatc	ctggcccgtt	acgacttcat	cagtgatgcg	600
gcgatggcgc	gcgacggcaa	cgcccgcgac	aacaacccga	acgatgaggg	tgactgggtac	660
ggcgacaacg	agtgccaggc	aggctacccg	ggttccaact	ccagctggca	cggtaccac	720
gtggccggca	cggtggcggc	ggtgaccaac	aacagcaccg	gcgtggcagg	tactgcgttc	780
aacgccaagg	tcgtgcccgt	gcgcgtactc	ggcaagtgcg	gcgggttacac	ctccgacatt	840
gccgacgcga	tcgtgtgggc	gtccggcggc	agcgtcagcg	gcgtgccggc	caatgccaat	900
ccggccgagg	tcataaatct	ctcgctcggc	ggtggcgcca	gctgctcgag	cacctaccag	960
aacgcgatca	atggcgctgt	cgggcggtgg	accaccgtgg	tggtcgctgc	cggcaacagc	1020
aacaccaacg	tgctctcgtc	ggttcccggc	aactgcccga	acgtgatcgc	agtggcggcc	1080
accacctcgg	ccggtgcgcg	tgccagcttc	tccaactatg	gcaacggcat	cgacatctcg	1140
gcaccggggc	agggcatcct	gtccaccctc	aacagcgcca	ccaccacccc	gggcagcgcc	1200
agctacgctt	cgtacaacgg	cacctcgatg	gcggcaccgc	acgtggccgg	cgtagtcgcg	1260
ctgatgcagt	ccgtagcccc	gagcccgtg	agcccggcgc	aggtggagag	catcatcaag	1320
agcactgcac	gtccgctgcc	gggcgcctgc	tcgggcccgt	gcggcgccgg	catcatcgac	1380
gccgacgcgg	ccgtggccgc	ggcgatcaac	ggcggtggcc	cgaatccggg	cggcaacgtg	1440
ctgcagaaca	acgttccggg	gaccggcctc	ggcgctgcca	gcggcgcttc	gttgagctac	1500
acggtcaacg	ttccggccgg	cagcaccag	ctgcgcgtgg	cgatcagttg	cggcagcggt	1560
gatgccgatc	tgtacgttcg	ccagggcagt	gctccgactg	ataccgccta	cacctgccgc	1620
ccgtacctga	gcggcaacag	cgagacctgc	accatcaaca	gtccggccgc	cggcacctgg	1680
tatgtgcggg	tgaaggccta	cagcaccttc	tcgggcctga	ccctcaacgc	ccagtactga	1740

&lt;210&gt; 66

&lt;211&gt; 579

&lt;212&gt; PRT

&lt;213&gt; Unknown

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&lt;220&gt;

&lt;223&gt; Obtained from an environmental sample.

&lt;400&gt; 66

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Met Ser Gln Val Thr Gln Pro Arg Val Arg Arg Val Trp Val Val Leu
1      5      10      15
Gly Ala Ser Val Leu Ser Ser Leu Leu Ala Thr Pro Ala Leu Ala
20      25      30
Gly Asp Val Gln Leu Ser Gly Leu Gln Ser Ala Gln Thr His Gln Arg
35      40      45
Phe Ile Val Lys Tyr Arg Asp Gly Ser Ala Pro Val Ala Asn Thr Thr
50      55      60
Ala Leu Ala Ser Ser Leu Lys Ser Ala Ala Ala Gly Leu Ala Ser Ser
65      70      75      80
Gln Gly Arg Ala Leu Gly Leu Gln Gln Val Arg Lys Leu Ala Val Gly
85      90      95
Pro Thr Leu Val Lys Thr Asp Arg Pro Leu Asp Gln Ala Glu Ser Glu
100      105      110
Gln Leu Met Arg Lys Leu Ala Ala Asp Pro Asn Val Glu Tyr Val Glu
115      120      125
Val Asp Gln Ile Met Arg Ala Thr Leu Thr Pro Asn Asp Thr Arg Phe
130      135      140
Ser Glu Gln Trp Gly Phe Gly Thr Ser Asn Ala Gly Ile Asn Ile Arg
145      150      155      160
Pro Ala Trp Asp Lys Ala Thr Gly Thr Gly Val Val Val Ala Val Ile
165      170      175
Asp Thr Gly Ile Thr Asn His Ala Asp Leu Asn Ala Asn Ile Leu Pro
180      185      190
Gly Tyr Asp Phe Ile Ser Asp Ala Ala Met Ala Arg Asp Gly Asn Gly
195      200      205
Arg Asp Asn Asn Pro Asn Asp Glu Gly Asp Trp Tyr Gly Asp Asn Glu
210      215      220
Cys Gln Ala Gly Tyr Pro Gly Ser Asn Ser Ser Trp His Gly Thr His
225      230      235      240
Val Ala Gly Thr Val Ala Ala Val Thr Asn Asn Ser Thr Gly Val Ala
245      250      255
Gly Thr Ala Phe Asn Ala Lys Val Val Pro Val Arg Val Leu Gly Lys
260      265      270
Cys Gly Gly Tyr Thr Ser Asp Ile Ala Asp Ala Ile Val Trp Ala Ser
275      280      285
Gly Gly Ser Val Ser Gly Val Pro Ala Asn Ala Asn Pro Ala Glu Val
290      295      300
Ile Asn Leu Ser Leu Gly Gly Gly Ser Cys Ser Ser Thr Tyr Gln
305      310      315      320
Asn Ala Ile Asn Gly Ala Val Gly Arg Gly Thr Thr Val Val Ala
325      330      335
Ala Gly Asn Ser Asn Thr Asn Val Ser Ser Ser Val Pro Ala Asn Cys
340      345      350
Pro Asn Val Ile Ala Val Ala Ala Thr Thr Ser Ala Gly Ala Arg Ala
355      360      365
Ser Phe Ser Asn Tyr Gly Asn Gly Ile Asp Ile Ser Ala Pro Gly Gln
370      375      380
Gly Ile Leu Ser Thr Leu Asn Ser Gly Thr Thr Thr Pro Gly Ser Ala
385      390      395      400
Ser Tyr Ala Ser Tyr Asn Gly Thr Ser Met Ala Ala Pro His Val Ala
405      410      415
Gly Val Val Ala Leu Met Gln Ser Val Ala Pro Ser Pro Leu Ser Pro
420      425      430
Ala Gln Val Glu Ser Ile Ile Lys Ser Thr Ala Arg Pro Leu Pro Gly
435      440      445
Ala Cys Ser Gly Gly Cys Gly Ala Gly Ile Ile Asp Ala Asp Ala Ala
450      455      460
Val Ala Ala Ala Ile Asn Gly Gly Gly Pro Asn Pro Gly Gly Asn Val
465      470      475      480
Leu Gln Asn Asn Val Pro Val Thr Gly Leu Gly Ala Ala Ser Gly Ala
485      490      495
Ser Leu Ser Tyr Thr Val Asn Val Pro Ala Gly Ser Thr Gln Leu Arg
500      505      510

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Val	Ala	Ile	Ser	Gly	Gly	Ser	Gly	Asp	Ala	Asp	Leu	Tyr	Val	Arg	Gln
		515					520					525			
Gly	Ser	Ala	Pro	Thr	Asp	Thr	Ala	Tyr	Thr	Cys	Arg	Pro	Tyr	Leu	Ser
	530					535					540				
Gly	Asn	Ser	Glu	Thr	Cys	Thr	Ile	Asn	Ser	Pro	Ala	Ala	Gly	Thr	Trp
545					550					555					560
Tyr	Val	Arg	Val	Lys	Ala	Tyr	Ser	Thr	Phe	Ser	Gly	Leu	Thr	Leu	Asn
			565						570					575	
Ala	Gln	Tyr													

<210> 67  
 <211> 1854  
 <212> DNA  
 <213> Unknown

<220>  
 <223> Obtained from an environmental sample.

<400> 67

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gctgtcggtg	ccgtccacgc	cgccggccctg	ccgacccgtg	agccgggtgcg	ccaggccagc	120
accgccccac	cgggcgccga	gcgcatcatc	gtcaagtacc	gggctggcgc	tgctgccgcc	180
accgaccgct	cggcgaagct	gtctaccgtg	caatcggcgc	tgacccgggc	cagcctgtcc	240
ggcgggtacct	cacgtgccag	taccctcggc	ccgcaggtgg	tacgcaagct	cgctaccggt	300
gcggacctga	tccgcgtgca	gggcccgcctg	gccccggccg	aactgcagcg	tgtgctgaag	360
gaactgcagg	ccgacccgtc	ggtgcagtac	gccgaagccg	acgtgaagct	gcgccgcacc	420
gagctgcgtg	ccggcgatgt	gcagccggca	ctggtgccga	acgatccctt	ctaccagcag	480
aaccagtggc	acctgcacaa	tgcggtcggc	ggcatcaacg	caccggcggc	atgggatgtc	540
tcgcaggggc	aaggcatcgt	ggtggcgggtg	atcgataccg	gcacccctgc	gcagcatccg	600
gacctggttg	gcaacctgtt	ggaggggttac	gatttcatca	gcgacgccga	gacctcgcgc	660
cgccccacca	atgatcgtgt	gccaggcgcg	cttgaccagg	gcgactgggt	ggagaacgac	720
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ggtaccgtcg	ccgagcagac	caacaatggc	gtcggcatgg	ccggtgtcgc	ctacaaggcc	840
aagggtgctg	cggtgcgcgt	gctggggcaag	tgccggcgct	acctgtccga	catcgccgac	900
gcgggtggtct	gggcatcggg	tggcacgggtg	accggcatcc	cggcccaacac	caaccgggcc	960
gagatcatca	acatgagcct	gggcccgcagc	ggcgccctgc	gcagcaccta	ccaggacgcc	1020
atcaacggcg	ccatctcgcg	cggtaccacg	gtggtggtgg	cgcccgccaa	tgagaccgac	1080
aacgcgtcca	agtaccgtcc	ggccagctgc	gaaggcgtgg	tgaccgtggg	tgcgaccgct	1140
atcaccggcg	gcatcaccta	ctactccaac	tacggcaccc	gcgtggatct	gtccggcccc	1200
ggcggcggtg	gcagcgtcga	cggaatccc	ggtggctaca	tctggcagac	cggtccaat	1260
gcggcgacca	cgccggattc	gggtacgccc	ggctacatgg	gcattggcgg	cacctcgatg	1320
gcctcgccgc	atgtggccgc	cggtgtcga	ctggtgcaga	gcgcgctgat	cgccaagggc	1380
aaggatccgc	tgaccccggc	ggccatgcgc	accctgctga	aggaaccgcg	gcgtccgttc	1440
ccggtcgcca	tcccggcggc	caccccgatc	ggtaccggca	tcctcgacgc	caaggccgcg	1500
ctggccaagg	cactggaaga	gccgtgcacc	gagaactgcg	gaccgggtgg	cacgccgctg	1560
accaacaagg	cgccatcggg	cggtctgtcc	ggtgcggctg	gcagcagcaa	gctttacagc	1620
ttcgaagcgg	ccgccggcaa	gcagttcagc	gtgatcacct	acggcggcac	cggaatgtt	1680
tcggtctacg	tggtgaagg	ccgtgagccc	agtgccagcg	acaacgacgc	caagtcgacc	1740
cgtccgggca	cctccgagac	agtgcgggtg	accaagccgg	tgccggccac	ctactacatc	1800
aagggtggtg	gtgaagcgcc	ctacaacggg	gtgagcattc	tcgccacgca	gtaa	1854

<210> 68  
 <211> 617  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Obtained from an environmental sample.

<221> SIGNAL  
 <222> (1)...(27)

<400> 68

Met	Ile	Lys	Lys	Gln	Asn	Leu	Arg	Ile	Asn	Val	Leu	Ala	Ala	Ala	Val
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Leu	Ser	Met	Thr	Ala	Val	Gly	Ala	Val	His	Ala	Ala	Gly	Leu	Pro	Thr
			20					25					30		

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Arg	Glu	Pro	Val	Arg	Gln	Ala	Ser	Thr	Ala	Gln	Pro	Gly	Ala	Glu	Arg
Ile	Ile	35	Val	Lys	Tyr	Arg	Ala	40	Gly	Ala	Ala	Ala	45	Thr	Asp
Ala	Lys	50	Leu	Ser	Thr	Val	55	Gln	Ser	Ala	Leu	Thr	60	Arg	Ala
65	Gly	Gly	Thr	Ser	Arg	Ala	70	Ser	Thr	Leu	Gly	Pro	75	Gln	Val
85	Leu	Ala	Thr	Gly	Ala	Asp	Leu	Ile	Arg	Val	Gln	Gly	Arg	Leu	Ala
100	Ala	Glu	Leu	Gln	Arg	Val	Leu	Lys	105	Glu	Leu	Gln	Ala	Asp	Pro
115	Gln	Tyr	Ala	Glu	Ala	Asp	Val	Lys	120	Leu	Arg	Arg	Thr	Glu	Leu
130	Gly	Asp	Val	Gln	Pro	Ala	Leu	Val	Pro	Asn	Asp	Pro	Phe	Tyr	Gln
145	Asn	Gln	Trp	His	Leu	His	Asn	Ala	Val	Gly	155	Ile	Asn	Ala	Pro
165	Ala	Trp	Asp	Val	Ser	Gln	Gly	Glu	Gly	Ile	Val	Val	Ala	Val	Ile
180	Thr	Gly	Ile	Leu	Pro	Gln	His	Pro	Asp	Leu	Val	Gly	Asn	Leu	Leu
195	Gly	Tyr	Asp	Phe	Ile	Ser	Asp	Ala	Glu	Thr	Ser	Arg	Arg	Pro	Thr
210	Asp	Arg	Val	Pro	Gly	Ala	Leu	Asp	Gln	Gly	Asp	Trp	Val	Glu	Asn
225	Asn	Glu	Cys	Tyr	Asp	Gly	Ser	Leu	Ala	Glu	Asp	Ser	Ser	Trp	His
245	Thr	His	Val	Ala	Gly	Thr	Val	Ala	Glu	Gln	Thr	Asn	Asn	Gly	Val
260	Met	Ala	Gly	Val	Ala	Tyr	Lys	Ala	Lys	Val	Leu	Pro	Val	Arg	Val
275	Gly	Lys	Cys	Gly	Gly	Tyr	Leu	Ser	Asp	Ile	Ala	Asp	Ala	Val	Val
290	Ala	Ser	Gly	Gly	Thr	Val	Thr	Gly	Ile	Pro	Ala	Asn	Thr	Asn	Pro
305	Glu	Ile	Ile	Asn	Met	Ser	Leu	Gly	Gly	Ser	Gly	Ala	Cys	Gly	Ser
325	Tyr	Gln	Asp	Ala	Ile	Asn	Gly	Ala	Ile	Ser	Arg	Gly	Thr	Thr	Val
340	Val	Ala	Ala	Gly	Asn	Glu	Thr	Asp	Asn	Ala	Ser	Lys	Tyr	Arg	Pro
355	Ser	Cys	Glu	Gly	Val	Val	Thr	Val	Gly	Ala	Thr	Arg	Ile	Thr	Gly
370	Ile	Thr	Tyr	Tyr	Ser	Asn	Tyr	Gly	Thr	Arg	Val	Asp	Leu	Ser	Gly
385	Gly	Gly	Gly	Gly	Ser	Val	Asp	Gly	Asn	Pro	Gly	Gly	Tyr	Ile	Trp
405	Thr	Gly	Ser	Asn	Ala	Ala	Thr	Thr	Pro	Asp	Ser	Gly	Thr	Pro	Gly
420	Met	Gly	Met	Gly	Gly	Thr	Ser	Met	Ala	Ser	Pro	His	Val	Ala	Ala
435	Ala	Ala	Leu	Val	Gln	Ser	Ala	Leu	Ile	Ala	Lys	Gly	Lys	Asp	Pro
450	Thr	Pro	Ala	Ala	Met	Arg	Thr	Leu	Leu	Lys	Glu	Thr	Ala	Arg	Pro
465	Pro	Val	Ala	Ile	Pro	Ala	Ala	Thr	Pro	Ile	Gly	Thr	Gly	Ile	Leu
485	Ala	Lys	Ala	Ala	Leu	Ala	Lys	Ala	Leu	Glu	Glu	Pro	Cys	Thr	Glu
500	Cys	Gly	Pro	Val	Ala	Thr	Pro	Leu	Thr	Asn	Lys	Ala	Ala	Ile	Gly
515	Leu	Ser	Gly	Ala	Ala	Gly	Ser	Ser	Lys	Leu	Tyr	Ser	Phe	Glu	Ala
530	Ala	Gly	Lys	Gln	Phe	Ser	Val	Ile	Thr	Tyr	Gly	Gly	Thr	Gly	Asn
545	Ser	Val	Tyr	Val	Ala	Glu	Gly	Arg	Glu	Pro	Ser	Ala	Ser	Asp	Asn
565										570					575

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Ala Lys Ser Thr Arg Pro Gly Thr Ser Glu Thr Val Arg Val Thr Lys  
 580 585 590  
 Pro Val Ala Thr Tyr Tyr Ile Lys Val Val Gly Glu Ala Ala Tyr  
 595 600 605  
 Asn Gly Val Ser Ile Leu Ala Thr Gln  
 610 615

<210> 69  
 <211> 1740  
 <212> DNA  
 <213> Unknown

<220>  
 <223> Obtained from an environmental sample.

<400> 69  
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 cagtccgcgc cgacgcatca gcgcttcacg gtgaagtacc gcgacggcag tgcgcccgtg 180  
 gccagcacca ccgcactggc ttcttcgctg aagagtgccg ccgccggcct ggccagcagc 240  
 cagggccgcg cgctgggcct gcaggaggtc cgcaagctgg ccgtcggccc gacctgggtc 300  
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 gacacccgct tcagcgaaca atggggcttc ggtacctcca acgcgtcgat caacgtgcag 480  
 ccggcctggg acaaggccac cggcaccggc gtggtggtgg ccgtgatcga taccggcatc 540  
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 gtcgcccggc ccgtggcggc ggtgaccaac aacagcaccg gcgtggccgg tactgcgttc 780  
 aatgccaagg tcgtcccggg gcgcgtgctc ggcaagtgcg gcggttacac ctccgacatc 840  
 gccgacgcga tcgtgtgggc ttctggcggc acggtcagtg gcgtgcccgc caatgccaac 900  
 ccggccgaag tcatcaacat gtcgctgggc ggcggcggca cctgctcggc cactaccag 960  
 aatgcatca acggcgcggt cagccgtggt accaccgtgg tgggtgccgc cggcaacagc 1020  
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 ccgtacctga gcggcaacag cgagacctgc accatcaaca gccctgccgc cggcacctgg 1680  
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<210> 70  
 <211> 579  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Obtained from an environmental sample.

<221> SIGNAL  
 <222> (1)...(32)

<400> 70  
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 Gly Ala Ser Val Leu Ser Ser Leu Leu Ala Thr Pro Ala Leu Ala  
 20 25 30  
 Gly Asp Val Gln Leu Ser Gly Leu Gln Ser Ala Pro Thr His Gln Arg  
 35 40 45  
 Phe Ile Val Lys Tyr Arg Asp Gly Ser Ala Pro Val Ala Ser Thr Thr  
 50 55 60  
 Ala Leu Ala Ser Ser Leu Lys Ser Ala Ala Ala Gly Leu Ala Ser Ser  
 65 70 75 80

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Gln	Gly	Arg	Ala	Leu	Gly	Leu	Gln	Glu	Val	Arg	Lys	Leu	Ala	Val	Gly
Pro	Thr	Leu	Val	85	Thr	Asp	Arg	Pro	90	Leu	Asp	Gln	Ala	95	Glu
Leu	Leu	Met	Arg	100	Lys	Leu	Ala	105	Asp	Pro	Asn	Val	110	Tyr	Glu
Val	Asp	115	Gln	Ile	Met	Arg	Ala	120	Thr	Leu	Thr	Pro	125	Asp	Phe
Ser	130	Gln	Trp	Gly	Phe	135	Thr	Ser	Asn	Ala	140	Ile	Asn	Val	Gln
145	Glu	Gln	Trp	Asp	Lys	150	Ala	Thr	Gly	Thr	Gly	Val	Val	Ala	Ile
Pro	Ala	Trp	Asp	165	Thr	Asn	His	Pro	170	Leu	Asn	Ala	Asn	175	Pro
Asp	Thr	Gly	Ile	180	Thr	Asn	His	Pro	185	Leu	Asn	Ala	Asn	190	Gly
Gly	Tyr	Asp	Phe	195	Ile	Ser	Asp	Ala	200	Met	Ala	Arg	Asp	205	Gly
Arg	Asp	210	Ser	Asn	Pro	Asn	Asp	215	Glu	Gly	Asp	Trp	Tyr	220	Gly
Cys	Gly	Ser	Gly	Ile	Pro	Ala	Ser	Asn	Ser	Ser	Trp	His	Gly	Thr	His
225	Val	Ala	Gly	Thr	Val	Ala	Ala	Val	Thr	Asn	Asn	Ser	Thr	Gly	Val
Val	Ala	Gly	Thr	245	Ala	Ala	Val	Thr	250	Asn	Asn	Ser	Thr	Gly	255
Gly	Thr	Ala	Phe	260	Asn	Ala	Lys	Val	265	Pro	Val	Arg	Val	Leu	Lys
Cys	Gly	Gly	Tyr	275	Thr	Ser	Asp	Ile	280	Ala	Asp	Ala	Ile	Val	Ser
Gly	Gly	Thr	Val	Ser	Gly	Val	295	Pro	Ala	Asn	Ala	Asn	Pro	Ala	Val
Ile	Asn	Met	Ser	Leu	Gly	Gly	Gly	Gly	Thr	Cys	Ser	Ala	Thr	Tyr	Gln
305	Asn	Ala	Ile	Asn	Gly	Ala	Val	Ser	Arg	Gly	Thr	Thr	Val	Val	Ala
Ala	Gly	Asn	Ser	325	Asn	Thr	Asn	Val	Ser	Ser	Ser	Val	Pro	Ala	Cys
Ala	Asn	Val	Ile	Ala	Val	Ala	Ala	Ala	Thr	Thr	Ser	Ala	Gly	Ala	Ala
Ser	Phe	Ser	Asn	Tyr	Gly	Ala	Gly	Ile	Asp	Ile	Ser	Gly	Pro	Gly	Gln
Ser	Ile	Leu	Ser	Thr	Leu	Asn	Thr	Gly	Thr	Thr	Thr	Pro	Gly	Ser	Ala
385	Ser	Tyr	Ala	Ser	Tyr	Asn	Gly	Thr	Ser	Met	Ala	Ala	Pro	His	Val
Ser	Val	Val	Ala	Leu	Met	Gln	Ser	Val	Ala	Pro	Ser	Ala	Leu	Ser	Pro
Gly	Val	Val	Ala	420	Ser	Ile	Ile	Lys	Ser	Thr	Ala	Arg	Pro	Leu	Gly
Ala	Gln	Val	Glu	435	Ser	Ile	Ile	Lys	440	Ser	Thr	Ala	Arg	Pro	Gly
Ala	Cys	Ser	Gly	Gly	Cys	Gly	Ala	Gly	Ile	Val	Asp	Ala	Asn	Ala	Ala
Val	Ala	Ala	Ala	Ile	Asn	Gly	Gly	Gly	Pro	Asn	Pro	Gly	Gly	Asn	Val
465	Leu	Gln	Asn	Asn	Val	Pro	Val	Thr	Gly	Leu	Gly	Ala	Ala	Thr	Gly
Glu	Leu	Asn	Tyr	485	Thr	Val	Ala	Val	Pro	Ala	Gly	Ser	Ser	Gln	Arg
Val	Ala	Ile	Ser	Gly	Gly	Ser	Gly	Asp	Ala	Asp	Leu	Tyr	Val	Arg	Gln
Gly	Ser	Ala	Pro	Thr	Asp	Thr	Thr	Tyr	Thr	Cys	Arg	Pro	Tyr	Leu	Ser
Gly	Asn	Ser	Glu	Thr	Cys	Thr	Ile	Asn	Ser	Pro	Ala	Ala	Gly	Thr	Trp
545	Tyr	Val	Arg	Val	Lys	Ala	Tyr	Ser	Thr	Phe	Ser	Gly	Leu	Thr	Asn
Ala	Gln	Tyr		565						570				575	

<210> 71  
 <211> 1620  
 <212> DNA

10336256.txt

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; obtained from an environmental sample.

&lt;400&gt; 71

atgcaacgat	cacgacgcct	cgctcgtcacg	gtgttgacgc	tggcactctg	cctgatggcg	60
gtaccggccg	gcgctgccgc	tcctgaccag	cctgcggccc	ccgaaggggt	gcccggcgcc	120
cccgatcggg	tacccgccgc	gaccgagacg	ccggacacgc	ctctgcccgg	agccgatcgt	180
gccgctggcg	agcccccccc	cgctcgtggc	tccgaccatc	ccgaggcgat	cgagggggcg	240
tacatcgctc	tggtccgcga	ggatgccgca	caggggtgagg	tagccccggg	ggccgagcgg	300
gccaccgctc	gcggcgcgac	ggtgcacgcc	acgtaccgcc	acgcccctga	cgggttcgcg	360
gccaccctcc	ccgagcaggc	gctggggggc	ctcacgcgca	acccgaacgt	cgcgttcatc	420
gacgcggacc	ttgccgtctc	gatcgagcag	gtgcagagcc	ccgcgacctg	gggcctggac	480
cgcacgcacc	agcggcgcc	gccgctggac	aaccaatacc	actacacca	caccggcgcg	540
ggcgtgcacg	cctacatcat	cgacaccggg	atccacgaca	cccacgccga	gttcggcggt	600
cgcgcgcacc	tcgcgttcac	ggcgatccac	gacggcctcg	gcgcccgcga	ctgcagcggc	660
cacggtaccc	acgtcgcggg	caccgtcggg	ggccagacct	acggcgtcgc	gaaggccgtg	720
cagctgtact	ccgtccgggt	gctcgactgc	ctgggcggcg	gcacgatggc	tggcgtcac	780
aacggcgctc	actgggtcac	ggccaaccac	gtcaagccag	ccgtggccaa	catgagcctc	840
ggcgccctgg	ccagctcggc	gctcgacacg	gccgtgaaca	actcgatcaa	cgccgggggtc	900
cactacgtcg	tgcccgctgc	caacagcagc	gccgacgcgt	gcggcttctc	ccccgctcgg	960
gtgagccggg	cgctgacggt	cggcgccagc	accagttcgg	acgcgcgcgc	ggcattcagc	1020
aactacggaa	cctgcgtcga	cctgttcgcc	cccggccaga	gcacacgcgc	ggcatggcac	1080
acgagcaaca	cggcgacgaa	tacgagcagc	ggcacgtcga	tggccgcgcc	gcacgtcgct	1140
gggtgctcgt	ccctgtatct	gcagcagggc	aaccagacgc	ccgatgggt	ccacggcggt	1200
gtcacgagcc	agtcgacgca	tgggctgctg	agcgggatcg	ggccggggtc	gccgaaccgc	1260
ctgctgtact	ccctgatccc	cgcgcgcatc	accaccgcgg	ccccctgcag	ctaccccgag	1320
cggttccgcg	ggttgctggc	gcggacgggt	gactggcatt	tcctgcccgt	gattccggag	1380
tacgggtaca	actcgcaggc	aggggtccat	cgcgccctgc	tgaccggccc	cgccggcgcg	1440
accctaggcc	tgacactgtt	ctgggtggaac	ggctcccagt	ggcaactcgt	ccgcagcgcc	1500
cagtcggtga	acggttcagt	cgccagcatc	acgcacagtg	gcgcccgcgg	gtggtacacc	1560
tggcgagtgg	attcgacgtc	cggctcgggc	acctacacct	tcctgatgca	gcgaccgtag	1620

&lt;210&gt; 72

&lt;211&gt; 539

&lt;212&gt; PRT

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; obtained from an environmental sample.

&lt;221&gt; SIGNAL

&lt;222&gt; (1)...(25)

&lt;400&gt; 72

Met	Gln	Arg	Ser	Arg	Arg	Leu	Val	Val	Thr	Val	Leu	Thr	Leu	Ala	Leu
1				5					10					15	
Cys	Leu	Met	Ala	Val	Pro	Ala	Gly	Ala	Ala	Ala	Pro	Asp	Gln	Pro	Ala
			20					25					30		
Ala	Pro	Glu	Gly	Val	Pro	Gly	Ala	Pro	Asp	Arg	Ile	Pro	Ala	Ala	Thr
			35				40					45			
Glu	Thr	Pro	Asp	Thr	Pro	Leu	Pro	Gly	Ala	Asp	Arg	Ala	Ala	Gly	Glu
			50			55					60				
Pro	Ala	Pro	Val	Leu	Gly	Ser	Asp	His	Pro	Glu	Ala	Ile	Glu	Gly	Arg
65					70				75						80
Tyr	Ile	Val	Val	Phe	Arg	Glu	Asp	Ala	Ala	Gln	Gly	Glu	Val	Ala	Arg
				85					90					95	
Ala	Ala	Glu	Arg	Ala	Thr	Ala	Arg	Gly	Ala	Thr	Val	His	Ala	Thr	Tyr
			100					105					110		
Arg	His	Ala	Leu	His	Gly	Phe	Ala	Ala	Thr	Leu	Pro	Glu	Gln	Ala	Leu
			115				120					125			
Gly	Ala	Leu	Thr	Arg	Asn	Pro	Asn	Val	Ala	Phe	Ile	Asp	Ala	Asp	Leu
			130			135					140				
Ala	Val	Ser	Ile	Glu	Gln	Val	Gln	Ser	Pro	Ala	Thr	Trp	Gly	Leu	Asp
145					150				155						160
Arg	Ile	Asp	Gln	Arg	Arg	Leu	Pro	Leu	Asp	Asn	Gln	Tyr	His	Tyr	Thr
				165					170					175	

10336256.txt

His	Thr	Gly	Ala	Gly	Val	His	Ala	Tyr	Ile	Ile	Asp	Thr	Gly	Ile	His
Asp	Thr	His	180	Glu	Phe	Gly	Gly	185	Arg	Ala	His	Leu	Ala	190	Thr
Ile	His	Asp	195	Gly	Leu	Gly	Ala	Arg	Asp	Cys	Ser	Gly	His	205	Thr
Val	Ala	Gly	210	Thr	Val	Gly	Ala	Arg	Asp	Cys	Ser	Gly	His	220	Thr
225	Ala	Gly	230	Thr	Val	Gly	Gln	Thr	Tyr	Gly	Val	Ala	Lys	Ala	Val
Gln	Leu	Tyr	245	Ser	Val	Arg	Val	Leu	Asp	Cys	Leu	Gly	Gly	Gly	255
Ala	Gly	Val	260	Ile	Asn	Gly	Val	Asp	Trp	Val	Thr	Ala	Asn	His	270
Pro	Ala	Val	275	Ala	Asn	Met	Ser	Leu	Gly	Gly	Leu	Ala	Ser	Ser	Ala
Asp	Thr	Ala	290	Val	Asn	Asn	Ser	Ile	Asn	Ala	Gly	Val	His	Tyr	Val
Ala	Ala	Ala	305	Asn	Ser	Ser	Ala	Asp	Ala	Cys	Gly	Phe	Ser	Pro	Ala
Val	Ser	Arg	325	Ala	Leu	Thr	Val	Gly	Ala	Ser	Thr	Ser	Ser	Asp	Ala
Ala	Ala	Phe	340	Ser	Asn	Tyr	Gly	Thr	Cys	Val	Asp	Leu	Phe	Ala	Pro
Gln	Ser	Ile	355	Thr	Ser	Ala	Trp	His	Thr	Ser	Asn	Thr	Ala	Thr	Asn
Ser	Ser	Gly	370	Thr	Ser	Met	Ala	Ala	Pro	His	Val	Ala	Gly	Val	Val
Leu	Tyr	Leu	385	Gln	Gln	Gly	Asn	Gln	Thr	Pro	Ala	Trp	Val	His	Gly
Val	Thr	Ser	405	Gln	Ser	Thr	His	Gly	Leu	Leu	Ser	Gly	Ile	Gly	Pro
Ser	Pro	Asn	420	Arg	Leu	Leu	Tyr	Ser	Leu	Ile	Pro	Ala	Arg	Ile	Thr
Ala	Ala	Pro	435	Cys	Ser	Tyr	Pro	Glu	Arg	Phe	Arg	Gly	Leu	Leu	Ala
Thr	Gly	Asp	450	Trp	His	Phe	Leu	Pro	Val	Ile	Pro	Glu	Tyr	Gly	Tyr
Ser	Gln	Ala	465	Gly	Val	His	Arg	Ala	Cys	Val	Thr	Gly	Pro	Ala	Gly
Thr	Leu	Gly	485	Leu	His	Leu	Phe	Trp	Trp	Asn	Gly	Ser	Gln	Trp	Gln
Val	Arg	Ser	500	Ala	Gln	Ser	Val	Asn	Gly	Ser	Val	Ala	Ser	Ile	Thr
Ser	Gly	Ala	515	Ala	Gly	Trp	Tyr	Thr	Trp	Arg	Val	Asp	Ser	Thr	Ser
Ser	Gly	Thr	530	Tyr	Thr	Phe	Ser	Met	Gln	Arg	Pro				
							535								

&lt;210&gt; 73

&lt;211&gt; 1836

&lt;212&gt; DNA

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; Obtained from an environmental sample.

&lt;400&gt; 73

atgcaacagc	acagcaagat	ggcccccg	ttgaagtttt	gcgcggcg	cctgatcgcc	60
ctgggggtcga	cggcagccca	cgccggtccg	cacgacgcgg	catcaccgcc	cttcatcacc	120
cagaccgacc	gcctgatcat	ccgctacaag	gatgcggtcg	acacctcgaa	gtcccagacg	180
ccggtggccc	cgctcccat	tccccaggca	cgcaaggccc	agctcgaccg	cgccggccag	240
ggcttcggcg	cgaccctgcg	cgcactgcgc	gcgaccgcca	acggcgccca	cgctcctgcag	300
ctcagccgca	ccatgtcgct	ggacgaagcg	aagcagctgg	cggccgacct	gaaggcgcg	360
gacgccaacg	tcgagtacgc	cgagccggac	cgcacatga	ccgcgctggc	cacgcccagc	420
gacccagct	acagccagca	gtgggacctg	tatgaagcca	agggcgccat	caacgtgcag	480
gccgcctggg	acaagtcgac	cggcagcggc	atcaacgtgg	ccgtgatcga	caccggctac	540
cgctccgcatg	ccgacctggc	cggccagatc	ctgcaaggct	acgatttcac	caccaacacc	600
accatggcca	acgacggggg	cggccgcgac	agcgacgcca	gcgatccggg	cgactggacc	660
ccggccggca	gctgctcggc	aggtacgcgc	gcccaggacc	aggcctcggg	ctggcacggc	720

## 10336256.txt

accacgtgg	ccggcaccat	cgccgcgcgc	gccacaacg	gcgcccgcgcat	cgcgggcatc	780
gcctacaacg	ccaagatcgt	cccggcgcgc	gtgctgggccc	gctgcggcgg	ctacacctcg	840
gacatcgccg	acgccatcgt	ctgggcttcg	ggcggcagcg	tgaacggcgt	gccggcgaat	900
gccaacaagg	cgcgctgct	gaacctgtcg	ctgggcggca	gcggcggtg	cgacagcacg	960
accagaacg	ccatcaacag	tgcgcgctcg	cgcggcgcgg	tggtcgtggt	cgccgccggc	1020
aattcgaacg	tcgatgccgc	gggctccagc	ccggccaact	gcgcccggcgt	gatcgcggtg	1080
gcggcggtcg	gccgcagcgg	cggcaaggcc	tcgtactcga	actacggcaa	cacggtcgac	1140
gtggcggcgc	cgggcggcga	cagcggcgcc	ggcatcctgt	cgacgctgaa	cagcggcacc	1200
accaccccgg	cgggcgacag	ctacgcctac	tacatgggca	cctcgatggc	cgccccgcac	1260
gtggcggcgc	tgggcgcgct	gatgctgtcg	gcgaaccgga	acctgacccc	ggacgaggtc	1320
gaggccaagc	tgaagtcgac	cgcgcgcgcc	ttcccggcca	cctgcaacgg	ctgcggcagc	1380
ggcatcatcg	acgccgcagc	cgccgtcaac	gcgtcgctgc	ctgccggcag	cacgcccacg	1440
ccgccggcat	cgggctggac	cgaatgcgcg	cccgaacacg	gcacctgtc	gttcagcggc	1500
acccgtgaag	tacgctacgg	cgccggtacc	agcttcgtct	cgaagatcgt	gaccggttcc	1560
gtcgctgtct	cgaacgccgt	gttcggcgat	ccgctgccga	acgtgggtcaa	gtcgtgcagc	1620
tattcgaacg	ccacggtgag	cgtgccgacc	tggaaccaact	gcgcccggcga	ggcgggcacc	1680
tgctcgttca	gcggcaccgg	cgaagtgcgc	tacggcgcca	acaacaactt	cgtgtcgcgc	1740
gtcttcaccg	gcggcgccgt	gtgctcgaat	gccaccttcg	gcgatccggg	gccgaacgtg	1800
gtcaaggcct	gcagctattc	cagcgtcacg	caataa			1836

<210> 74  
 <211> 611  
 <212> PRT  
 <213> Unknown

<220>  
 <223> obtained from an environmental sample.

<221> SIGNAL  
 <222> (1)...(28)

<400> 74

Met	Gln	Gln	His	Ser	Lys	Met	Ala	Pro	Val	Leu	Lys	Phe	Cys	Ala	Ala
1				5					10					15	
Ala	Leu	Ile	Ala	Leu	Gly	Ser	Thr	Ala	Ala	His	Ala	Gly	Pro	His	Asp
			20					25					30		
Ala	Ala	Ser	Pro	Arg	Phe	Ile	Thr	Gln	Thr	Asp	Arg	Leu	Ile	Ile	Arg
		35					40					45			
Tyr	Lys	Asp	Ala	Val	Asp	Thr	Ser	Lys	Ser	Gln	Thr	Pro	Val	Ala	Pro
	50					55					60				
Arg	Pro	Ile	Pro	Glu	Ala	Arg	Lys	Ala	Gln	Leu	Asp	Arg	Ala	Gly	Gln
65					70					75					80
Gly	Phe	Gly	Ala	Thr	Leu	Arg	Ala	Leu	Arg	Ala	Thr	Ala	Asn	Gly	Ala
				85					90					95	
His	Val	Leu	Gln	Leu	Ser	Arg	Thr	Met	Ser	Leu	Asp	Glu	Ala	Lys	Gln
		100						105							
Leu	Ala	Ala	Asp	Leu	Lys	Ala	Arg	Asp	Ala	Asn	Val	Glu	Tyr	Ala	Glu
		115					120					125			
Pro	Asp	Arg	Ile	Met	Thr	Ala	Leu	Ala	Thr	Pro	Ser	Asp	Pro	Ser	Tyr
	130					135					140				
Ser	Gln	Gln	Trp	Asp	Leu	Tyr	Glu	Ala	Lys	Gly	Gly	Ile	Asn	Val	Gln
145					150					155					160
Ala	Ala	Trp	Asp	Lys	Ser	Thr	Gly	Ser	Gly	Ile	Asn	Val	Ala	Val	Ile
				165					170						175
Asp	Thr	Gly	Tyr	Arg	Pro	His	Ala	Asp	Leu	Ala	Gly	Gln	Ile	Leu	Gln
		180						185							
Gly	Tyr	Asp	Phe	Ile	Thr	Asn	Thr	Thr	Met	Ala	Asn	Asp	Gly	Gly	Gly
	195						200					205			
Arg	Asp	Ser	Asp	Ala	Ser	Asp	Pro	Gly	Asp	Trp	Thr	Pro	Ala	Gly	Ser
	210					215					220				
Cys	Ser	Ala	Gly	Thr	Pro	Ala	Gln	Asp	Gln	Ala	Ser	Gly	Trp	His	Gly
225					230					235					240
Thr	His	Val	Ala	Gly	Thr	Ile	Ala	Ala	Arg	Ala	Asn	Asn	Gly	Ala	Gly
			245						250					255	
Ile	Ala	Gly	Ile	Ala	Tyr	Asn	Ala	Lys	Ile	Val	Pro	Ala	Arg	Val	Leu
		260						265							
Gly	Arg	Cys	Gly	Gly	Tyr	Thr	Ser	Asp	Ile	Ala	Asp	Ala	Ile	Val	Trp
	275						280					285			

10336256.txt

Ala	Ser	Gly	Gly	Ser	Val	Asn	Gly	Val	Pro	Ala	Asn	Ala	Asn	Lys	Ala
290						295					300				
Arg	Val	Leu	Asn	Leu	Ser	Leu	Gly	Gly	Ser	Gly	Gly	Cys	Asp	Ser	Thr
305					310					315					320
Thr	Gln	Asn	Ala	Ile	Asn	Ser	Ala	Arg	Ser	Arg	Gly	Ala	Val	Val	Val
				325					330					335	
Val	Ala	Ala	Gly	Asn	Ser	Asn	Val	Asp	Ala	Ala	Gly	Ser	Ser	Pro	Ala
			340					345					350		
Asn	Cys	Ala	Gly	Val	Ile	Ala	Val	Ala	Ala	Val	Gly	Arg	Ser	Gly	Gly
		355					360					365			
Lys	Ala	Ser	Tyr	Ser	Asn	Tyr	Gly	Asn	Thr	Val	Asp	Val	Ala	Ala	Pro
	370					375					380				
Gly	Gly	Asp	Ser	Gly	Ala	Gly	Ile	Leu	Ser	Thr	Leu	Asn	Ser	Gly	Thr
385					390					395					400
Thr	Thr	Pro	Ala	Gly	Asp	Ser	Tyr	Ala	Tyr	Tyr	Met	Gly	Thr	Ser	Met
				405					410					415	
Ala	Ala	Pro	His	Val	Ala	Gly	Val	Ala	Ala	Leu	Met	Leu	Ser	Ala	Asn
			420					425						430	
Pro	Asn	Leu	Thr	Pro	Asp	Glu	Val	Glu	Ala	Lys	Leu	Lys	Ser	Thr	Ala
		435					440					445			
Arg	Ala	Phe	Pro	Ala	Thr	Cys	Asn	Gly	Cys	Gly	Ser	Gly	Ile	Ile	Asp
	450					455					460				
Ala	Ala	Ala	Ala	Val	Asn	Ala	Ser	Leu	Pro	Ala	Gly	Ser	Thr	Pro	Thr
465					470				475						480
Pro	Pro	Ala	Ser	Gly	Trp	Thr	Glu	Cys	Ala	Pro	Glu	Asn	Gly	Thr	Cys
				485					490					495	
Ser	Phe	Ser	Gly	Thr	Arg	Glu	Val	Arg	Tyr	Gly	Ala	Gly	Thr	Ser	Phe
			500					505					510		
Val	Ser	Lys	Ile	Val	Thr	Gly	Ser	Val	Ala	Cys	Ser	Asn	Ala	Val	Phe
		515					520					525			
Gly	Asp	Pro	Leu	Pro	Asn	Val	Val	Lys	Ser	Cys	Ser	Tyr	Ser	Asn	Ala
	530					535					540				
Thr	Val	Ser	Val	Pro	Thr	Trp	Thr	Asn	Cys	Ala	Gly	Glu	Gly	Gly	Thr
545					550				555						560
Cys	Ser	Phe	Ser	Gly	Thr	Arg	Glu	Val	Arg	Tyr	Gly	Ala	Asn	Asn	Asn
				565					570					575	
Phe	Val	Ser	Arg	Val	Phe	Thr	Gly	Ala	Ala	Val	Cys	Ser	Asn	Ala	Thr
			580					585					590		
Phe	Gly	Asp	Pro	Val	Pro	Asn	Val	Val	Lys	Ala	Cys	Ser	Tyr	Ser	Ser
		595					600					605			
Val	Thr	Gln													
		610													

<210> 75  
 <211> 2262  
 <212> DNA  
 <213> Unknown

<220>  
 <223> Obtained from an environmental sample.

<400> 75

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tcaaatgcta	tggccgcatac	aacagactca	ttgcccagg	cagcagaaca	agccagcagc	120
gatcgctata	tcgtaaaata	taaagacaac	agtctgagta	aagatccact	tctcaaccgc	180
agtaaagctg	caaaagatag	tgcgctatca	gcattaacct	ctaacagcga	acgtttaagc	240
cggaaggtg	cacgtgttca	ccatgtttctg	gccaaacgta	acgccatagc	agccgagcta	300
agccctgcc	cggttaaagc	gttaaaagca	gatacctaag	tggaatatgt	cgagcgcgat	360
ttaccgcgtt	ttcctatgtc	gcagcaagtg	ccttacgggtt	ataccatggt	gcaggccgat	420
ctggtcagtg	atcagtttgc	ctctaaccag	acggatatgtg	ttatcgactc	tggcctgggc	480
ttaccacatg	aagacttta	cgatgccaat	atcaccggca	ccaatgatata	aggtaccggg	540
aactggttcg	acgccgggtg	cccacacggg	acacatgtag	ccggtaccat	tgctgcgctg	600
aataataatg	ttgggtattgt	tggcgtattg	cccaacggca	atgtgaaact	gcatatcatt	660
aaagtattta	acgccgggtg	ctgggggttac	tcttccactc	tggcacatgc	ggtagataacc	720
tgtgtgcaaa	acggctctac	cgtaattaat	atgagcttag	gcgggtgccg	ctcaaacgta	780
acagagcgta	acgccatgca	ggccgcctat	gacgccgggtg	tggtacttgt	tgcagcagcg	840
ggtaattggcg	gcaatactgc	catgtcgtat	ccggcttctt	atgattctgt	cgtatcagtt	900
gcagcgggtg	acgacaccaa	agccacagct	gacttttcgc	agcgtaatac	ccaggtagaa	960

## 10336256.txt

ctggcaggcc	cgggtgtagc	ggtaatgagt	acttatccaa	ccggtacagg	cctggaaacc	1020
agcctgacgg	ttaacggtag	aacctacagt	accaaccggt	tcgaaggctc	tgccatggcc	1080
agtttgaatg	cggaactggc	cagctgcggc	cttgcggtaa	atacctgtac	cggcgttacc	1140
gataaaatct	gtctgatcca	gcgcggcgaa	gtatctttcg	cacaaaaagt	ggaatcctgt	1200
caggctggcg	gtgggtattg	cgcggttatt	tataacaacg	aaccaggcaa	tttcagcggc	1260
accttaggtg	acgccccac	tactaatata	gtagcggttaa	gcgtatcgca	ggaagatggc	1320
cagttgttgg	ttgcagaagt	aggtaacgat	gccagcttat	ttgccggccc	gtctaactat	1380
ggcctgtagg	acggtacctc	tatggcgctc	ccgcatgtag	ccggtgtagc	agcattggta	1440
tggagccatt	acccggattg	tagcaatgca	caaattccgca	gtgcttttagc	agcaacagca	1500
gaagatttag	gcgcccgtgg	gcgtgataca	tcttatggct	atggcttggg	acaagccaaa	1560
gccgcggtag	attatctggc	cgagtttggc	tgtgacggcg	acggtgacga	taacgagcca	1620
ccaccaccaa	ccggcacaga	actgagtaac	ggtgtaacag	tatcaggcat	cagtgcctgt	1680
gccgggtgaag	aactgctgta	cacgctggcc	gtacctgcag	gtgccagcaa	cctgtcgttt	1740
gttatgaatg	gcgggtaccg	cgatgccgat	ctgtatgtca	agtttggcag	cgagccaacc	1800
gcatcaaaact	gggactgccg	gccttacctg	tttggttaaca	acgaaagctg	tgctatcgac	1860
ccggcacaaa	ccggtactta	ctttgttaag	ttagtagcat	acagcgcctt	taccggtgta	1920
aaccttaccg	gtagctttac	cgcaccggat	ttaccggatg	caggcggcga	aaccattacc	1980
aacatcaaca	tagcgcggcg	ggcctggcag	cactacacgc	tggacgtacc	ggaaggatg	2040
gcacagctaa	ctgttgaaat	cagtgggtggc	agcgggtgatg	ctgatctgta	cgtgaagcat	2100
ggcagccagc	ctaccagcgg	tagctatgat	tgccggccaa	ataaaaaacg	caatagcgaa	2160
acctgtgtta	ttaacaaccc	gcaagccggg	gtatggcatc	tgtcagttaa	tgccctccgg	2220
gcggtaagcg	gcttaacact	ggtaagtga	taccaaccgt	aa		2262

<210> 76  
 <211> 753  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Obtained from an environmental sample.

<221> SIGNAL  
 <222> (1)...(25)

<400> 76

Met	Ser	Arg	Ser	His	His	Thr	Val	Leu	Leu	Ile	Gly	Val	Ser	Leu	Leu
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Ala	Ser	Ala	Val	Ser	Asn	Ala	Met	Ala	Ala	Ser	Thr	Asp	Ser	Leu	Arg
			20					25					30		
Gln	Ala	Ala	Glu	Gln	Ala	Ser	Ser	Asp	Arg	Tyr	Ile	Val	Lys	Tyr	Lys
		35					40					45			
Asp	Asn	Ser	Leu	Ser	Lys	Asp	Pro	Leu	Leu	Asn	Arg	Ser	Lys	Ala	Ala
	50				55					60					
Lys	Asp	Ser	Ala	Leu	Ser	Ala	Leu	Thr	Ser	Asn	Ser	Glu	Arg	Leu	Ser
65				70				75						80	
Arg	Gln	Gly	Ala	Arg	Val	His	His	Val	Leu	Ala	Lys	Arg	Asn	Ala	Ile
			85					90						95	
Ala	Ala	Glu	Leu	Ser	Pro	Ala	Thr	Val	Lys	Ala	Leu	Lys	Ala	Asp	Pro
		100						105					110		
Asn	Val	Glu	Tyr	Val	Glu	Arg	Asp	Leu	Pro	Arg	Phe	Pro	Met	Ser	Gln
	115						120					125			
Gln	Val	Pro	Tyr	Gly	Tyr	Thr	Met	Val	Gln	Ala	Asp	Leu	Val	Ser	Asp
	130					135					140				
Gln	Phe	Ala	Ser	Asn	Gln	Thr	Val	Cys	Val	Ile	Asp	Ser	Gly	Leu	Gly
145				150				155						160	
Leu	Pro	His	Glu	Asp	Phe	Asn	Asp	Ala	Asn	Ile	Thr	Gly	Thr	Asn	Asp
			165					170						175	
Ile	Gly	Thr	Gly	Asn	Trp	Phe	Asp	Ala	Gly	Gly	Pro	His	Gly	Thr	His
		180					185						190		
Val	Ala	Gly	Thr	Ile	Ala	Ala	Leu	Asn	Asn	Asn	Val	Gly	Ile	Val	Gly
	195						200					205			
Val	Leu	Pro	Asn	Gly	Asn	Val	Lys	Leu	His	Ile	Ile	Lys	Val	Phe	Asn
	210				215						220				
Ala	Gly	Gly	Trp	Gly	Tyr	Ser	Ser	Thr	Leu	Ala	His	Ala	Val	Asp	Thr
225					230					235				240	
Cys	Val	Gln	Asn	Gly	Ser	Thr	Val	Ile	Asn	Met	Ser	Leu	Gly	Gly	Ala
			245					250						255	
Gly	Ser	Asn	Val	Thr	Glu	Arg	Asn	Ala	Met	Gln	Ala	Ala	Tyr	Asp	Ala

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Gly Val Leu 260 Leu Val Ala Ala Ala 265 Gly Asn Gly Gly Asn 270 Thr Ala Met  
 Ser Tyr 275 Pro Ala Ser Tyr Asp 280 Ser Val Val Ser Val 285 Ala Ala Val Asp  
 Asp Thr 290 Lys Ala His Ala 295 Phe Ser Gln Arg Asn 300 Thr Gln Val Glu  
 305 Leu Ala Gly Pro Gly 310 Val Ala Val Met Ser Thr Tyr Pro Thr Gly Thr  
 Gly Leu Glu Thr 325 Ser Leu Thr Val Asn Gly Thr Thr Tyr Ser Thr Asn  
 Pro Phe 340 Gly Ser Ala Met Ala 345 Ser Leu Asn Ala Glu 350 Leu Ala Ser  
 Cys Gly 355 Leu Ala Val Asn Thr 360 Cys Thr Gly Val Thr Asp 365 Lys Ile Cys  
 370 Leu Ile Gln Arg Gly Glu 375 Val Ser Phe Ala Gln Lys Val Glu Ser Cys  
 385 Gln Ala Gly Gly Gly 390 Ile Gly Ala Val Ile Tyr Asn Asn Glu Pro Gly  
 405 Asn Phe Ser Gly Thr Leu Gly Asp Ala Pro Thr Thr Asn Ile Val Ala  
 420 Leu Ser Val Ser Gln Glu Asp Gly 425 Gln Leu Leu Val Ala Glu Val Gly  
 435 Asn Asp Ala Ser Leu Phe Ala Gly Pro Ser Asn Tyr Gly Leu Met Asp  
 450 Gly Thr Ser Met Ala Ser 455 His Val Ala Gly Val Ala Ala Leu Val  
 465 Trp Ser His Tyr Pro 470 Asp Cys Ser Asn Ala Gln Ile Arg Ser Ala Leu  
 485 Ala Ala Thr Ala Glu Asp Leu Gly Ala Ala Gly Arg Asp Thr Ser Tyr  
 500 Gly Tyr Gly Leu Val Gln Ala Lys Ala Ala Val Asp Tyr Leu Ala Glu  
 515 Phe Gly Cys Asp Gly Asp Gly 520 Asp Asp Asn Glu Pro Pro Pro Thr  
 530 Gly Thr Glu Leu Ser Asn Gly Val Thr Val Ser 540 Gly Ile Ser Ala Ala  
 545 Ala Gly Glu Glu Leu 550 Leu Tyr Thr Leu Ala Val Pro Ala Gly Ala Ser  
 565 Asn Leu Ser Phe Val Met Asn Gly Gly Thr Gly Asp Ala Asp 575 Leu Tyr  
 580 Val Lys Phe Gly Ser Glu Pro Thr Ala Ser Asn Trp Asp 590 Cys Arg Pro  
 595 Tyr Leu Phe Gly Asn Asn Glu 600 Ser Cys Ala Ile Asp 605 Pro Ala Gln Thr  
 610 Gly Thr Tyr Phe Val Lys Leu Val Ala Tyr Ser Ala Phe Thr Gly Val  
 625 Asn Leu Thr Gly Ser Phe Thr Ala Pro Asp 635 Leu Pro Asp Ala Gly Gly  
 645 Glu Thr Ile Thr Asn Ile Asn Ile Ala Arg Arg Ala Trp Gln His Tyr  
 660 Thr Leu Asp Val Pro Glu Gly Met Ala Gln Leu Thr Val Glu Ile Ser  
 675 Gly Gly Ser Gly Asp Ala Asp 680 Leu Tyr Val Lys His 685 Gly Ser Gln Pro  
 690 Thr Ser Gly Ser Tyr Asp 695 Cys Arg Pro Asn Lys Asn Gly Asn Ser Glu  
 705 Thr Cys Val Ile Asn Asn Pro Gln Ala Gly 715 Val Trp His Leu Ser Val  
 725 Tyr Ala Phe Arg Ala Val Ser Gly Leu 730 Thr Leu Val Ser Glu Tyr Gln  
 740 Pro

<210> 77  
 <211> 2136  
 <212> DNA  
 <213> Unknown

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&lt;220&gt;

&lt;223&gt; obtained from an environmental sample.

&lt;400&gt; 77

atgcctcacg	tcaaatttgg	aaccagtgat	gaaccgggat	tcgagttgga	agagagtggc	60
gacctgatcg	cggtgctgac	ccacagccgg	cgttcgggtcg	tgggtgcggg	tccggtgatg	120
ccgcccacgg	ctgccgaagt	cagtgatggc	gaactcgtgg	ccagttttcc	cgaggctggg	180
gtcgaggtgt	accgagtgcc	cgccgctgat	cgctcactcg	accaacggaa	gctggaacta	240
cgggaggccc	ctgacgtgca	gttcgcccgt	tcggtgctgg	tccgcccagg	ttcggacgaa	300
cctgtgctgt	atacggagaa	cctgtatatc	cgcttcgggg	aggatctcga	tccggatgac	360
tgcgaagcga	tcattcgtca	ggctggcctg	acggtgaagc	aacgtctgga	tttcgccacc	420
aacgcctact	tcctggccgc	tcccaggggg	acgggacagc	gcgtcttcga	catcgcggtg	480
gagctggtga	agcgcgaacg	cgtgatctat	tgccatccgg	aactgatcga	gcgacgcgta	540
cacaagcaac	gcattctttcc	tgaacaatgg	cacctgaagg	cgaccagcat	caatggcacg	600
gcggtgaatg	cccatgcgaa	tgtcggggcg	gctcacgcca	tcacgctggg	cgccgggggtc	660
acgatcgcg	tcattcgacg	cgggggtggc	atcgatcacc	cggagttcag	cgcaacggggc	720
aagattattg	cccctcgcg	cgccacgttg	caaacgaatg	atccccgtcc	aaaggacacg	780
gtcccagagtc	ggcgcgggga	aaaccatggc	acggcgtgcg	cgggctggg	atgcgcccgt	840
ggaaccgatg	gtgcggccgg	cgttgctccg	ctggcccggc	tgatgcccac	tcggttgcca	900
agtggcctgg	ggtcggttcg	cgaggccgag	gccttccaat	gggcagccga	caatggagcg	960
gacatcatct	cgtgcatttg	gggaccgcgc	gacggggact	ggtggaatcc	gaacgaccca	1020
ctgcacaacc	atgtcttcca	actgcccggc	agcaccgcgc	acgcaatcga	ctacgccgta	1080
agtgaaggcc	gcggagggaa	aggctgcgtc	atcctgtttg	ccgccggcaa	cggaacacgag	1140
tcggtggata	acgatggcta	tgcgagctac	cacaaggcca	ttgcggtggc	ggcgtgcaac	1200
gaccgaaata	cgcgacgcgt	ctacagcgac	tttggcaagg	ccatctggtg	ctcgttcccc	1260
agcagtgact	tcggccacgc	cccgttcaat	catccccagc	cgctgactcc	cggaatctgg	1320
acgaccgacc	ggatggggcg	ctttggatac	aaacccggaa	acgtccggtt	cggcgacgcc	1380
gccggcaact	atacgaacga	ctttggaggt	acctccagtt	cctgcccggg	tgcggctggc	1440
gtcgccgctt	tagtgctgtc	ggtcaatccg	gccctgctgt	ggaacgaggt	gaaggatctc	1500
ttacgcccgc	cctgcgactc	gacgcacttg	gcgaatggcc	aatacgacgc	cgagggggcac	1560
agccacttct	atgggtacgg	ccggctaacc	cccgagacgg	ccgtgaagct	cgccaagcag	1620
tccgtgggga	aactggtgat	tatcaacaag	ttgctcaacg	aaccaattcc	ggatttgggc	1680
agcgtgcaga	caaccatcga	cgttacggaa	acggaccccg	tggagaagtt	ggctgtctcg	1740
gtccgcctgg	agcacacctg	gatcggggac	ttggttatca	cggcgattgc	tccgtccaac	1800
accggacaag	gaaaaatcgt	cctgcacaat	cgggcgggtg	gcagccgcaa	gaacattgac	1860
atgctgtacg	atccttccaa	tactcccaag	ctgggtgctc	ttgccggaaa	gaagtgtagc	1920
ggcacctgga	cgatcaaagt	cgaggatcag	gccgcccagg	actcgggcac	cttgatccag	1980
gtcggcttgc	acttgtttct	gccagccgct	cagtcggacg	gtgccgggga	cggggcccgc	2040
gccgcgggtg	cctcacaaagc	cgcgacagga	aaaacgaaac	gagcggctgc	gaagaaaaaca	2100
gccgctcgcc	gaacccgcgc	gaagaaaaaa	cgataa			2136

&lt;210&gt; 78

&lt;211&gt; 711

&lt;212&gt; PRT

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; obtained from an environmental sample.

&lt;400&gt; 78

Met	Pro	His	Val	Lys	Phe	Gly	Thr	Ser	Asp	Glu	Pro	Gly	Phe	Glu	Leu
1				5					10					15	
Glu	Glu	Ser	Gly	Asp	Leu	Ile	Ala	Val	Arg	Thr	His	Ser	Arg	Arg	Ser
			20					25					30		
Val	Val	Gly	Ala	Gly	Pro	Val	Met	Pro	Pro	Thr	Ala	Ala	Glu	Val	Ser
			35				40					45			
Asp	Gly	Glu	Leu	Val	Ala	Ser	Phe	Pro	Glu	Ala	Gly	Val	Glu	Val	Tyr
	50					55					60				
Arg	Val	Pro	Ala	Ala	Asp	Arg	Ser	Leu	Asp	Gln	Arg	Lys	Leu	Glu	Leu
	65				70					75				80	
Arg	Ala	Ala	Pro	Asp	Val	Gln	Phe	Ala	Gly	Ser	Val	Leu	Val	Arg	Pro
				85					90					95	
Gly	Ser	Asp	Glu	Pro	Val	Leu	Tyr	Thr	Glu	Asn	Leu	Tyr	Ile	Arg	Phe
			100					105					110		
Arg	Glu	Asp	Leu	Asp	Pro	Asp	Asp	Cys	Glu	Ala	Ile	Ile	Arg	Gln	Ala
		115				120						125			
Gly	Leu	Thr	Val	Lys	Gln	Arg	Leu	Asp	Phe	Ala	Thr	Asn	Ala	Tyr	Phe

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130	Leu	Ala	Ala	Pro	Glu	Gly	Thr	Gly	Gln	Arg	Val	Phe	Asp	Ile	Ala	Leu
145	Glu	Leu	Leu	Lys	Arg	Asn	Asp	Val	Ile	Tyr	Cys	His	Pro	Glu	Leu	Ile
				165	His	Lys	Gln	Arg	Ile	170	Phe	Pro	Glu	Gln	Trp	His
				180	Ile	Asn	Gly	Thr	Ala	185	Val	Asn	Ala	His	Ala	Asn
				195	Ser	Ile	Asn	Gly	Thr	200	Ala	Val	Asn	Ala	His	Ala
				210	Ala	His	Ala	Ile	Thr	215	Leu	Gly	Ala	Gly	Val	Thr
				225	Asp	Asp	Gly	Val	Asp	230	Ile	Asp	His	Pro	Glu	Phe
										235	Leu	Gln	Thr	Asn	Asp	Pro
										245	Pro	Ser	Arg	Arg	Gly	Thr
										250	Gln	Thr	Asn	His	Gly	Thr
										260	Val	Pro	Ser	Arg	Arg	Gly
										265	Gly	Glu	Asn	His	Gly	Thr
										270	Ala	Val	Pro	Ser	Arg	Arg
										275	Val	Ala	Cys	Ala	Gly	Thr
										280	Gly	Thr	Asp	Gly	Ala	Gly
										285	Ala	Val	Pro	Ser	Gly	Leu
										290	Pro	Leu	Ala	Arg	Leu	Met
										295	Met	Pro	Ile	Arg	Leu	Arg
										300	Arg	Leu	Arg	Ser	Gly	Leu
										305	Val	Arg	Glu	Ala	Glu	Ala
										310	Ala	Phe	Gln	Trp	Ala	Ala
										315	Ala	Ala	Asp	Asn	Gly	Ala
										320	Ala	Ala	Asp	Asn	Gly	Ala
										325	Cys	Ser	Trp	Gly	Pro	Arg
										330	Arg	Asp	Gly	Asp	Trp	Trp
										335	Trp	Gly	Asp	Trp	Trp	Asn
										340	Leu	His	Asn	His	Val	Phe
										345	Val	Ser	Glu	Gly	Arg	Gly
										350	Ala	Val	Ser	Glu	Gly	Arg
										355	Ala	Ile	Asp	Tyr	Ala	Val
										360	Ala	Ala	Gly	Asn	Gly	Asn
										365	Gly	Asn	Gly	Asn	Glu	Ser
										370	Ile	Leu	Phe	Ala	Ala	Ala
										375	His	Lys	Val	Ile	Ala	Val
										380	Val	Ile	Ala	Val	Ala	Ala
										385	Gly	Tyr	Ala	Ser	Tyr	His
										390	Tyr	Ser	Val	Tyr	Ser	Asp
										395	Val	Tyr	Ser	Asp	Phe	Gly
										400	Ser	Val	Tyr	Ser	Asp	Phe
										405	Ser	Val	Tyr	Ser	Asp	Phe
										410	Ser	Val	Tyr	Ser	Asp	Phe
										415	Ser	Val	Tyr	Ser	Asp	Phe
										420	Ser	Val	Tyr	Ser	Asp	Phe
										425	Ser	Val	Tyr	Ser	Asp	Phe
										430	Ser	Val	Tyr	Ser	Asp	Phe
										435	Ser	Val	Tyr	Ser	Asp	Phe
										440	Ser	Val	Tyr	Ser	Asp	Phe
										445	Ser	Val	Tyr	Ser	Asp	Phe
										450	Ser	Val	Tyr	Ser	Asp	Phe
										455	Ser	Val	Tyr	Ser	Asp	Phe
										460	Ser	Val	Tyr	Ser	Asp	Phe
										465	Ser	Val	Tyr	Ser	Asp	Phe
										470	Ser	Val	Tyr	Ser	Asp	Phe
										475	Ser	Val	Tyr	Ser	Asp	Phe
										480	Ser	Val	Tyr	Ser	Asp	Phe
										485	Ser	Val	Tyr	Ser	Asp	Phe
										490	Ser	Val	Tyr	Ser	Asp	Phe
										495	Ser	Val	Tyr	Ser	Asp	Phe
										500	Ser	Val	Tyr	Ser	Asp	Phe
										505	Ser	Val	Tyr	Ser	Asp	Phe
										510	Ser	Val	Tyr	Ser	Asp	Phe
										515	Ser	Val	Tyr	Ser	Asp	Phe
										520	Ser	Val	Tyr	Ser	Asp	Phe
										525	Ser	Val	Tyr	Ser	Asp	Phe
										530	Ser	Val	Tyr	Ser	Asp	Phe
										535	Ser	Val	Tyr	Ser	Asp	Phe
										540	Ser	Val	Tyr	Ser	Asp	Phe
										545	Ser	Val	Tyr	Ser	Asp	Phe
										550	Ser	Val	Tyr	Ser	Asp	Phe
										555	Ser	Val	Tyr	Ser	Asp	Phe
										560	Ser	Val	Tyr	Ser	Asp	Phe
										565	Ser	Val	Tyr	Ser	Asp	Phe
										570	Ser	Val	Tyr	Ser	Asp	Phe
										575	Ser	Val	Tyr	Ser	Asp	Phe
										580	Ser	Val	Tyr	Ser	Asp	Phe
										585	Ser	Val	Tyr	Ser	Asp	Phe
										590	Ser	Val	Tyr	Ser	Asp	Phe
										595	Ser	Val	Tyr	Ser	Asp	Phe
										600	Ser	Val	Tyr	Ser	Asp	Phe
										605	Ser	Val	Tyr	Ser	Asp	Phe
										610	Ser	Val	Tyr	Ser	Asp	Phe
										615	Ser	Val	Tyr	Ser	Asp	Phe
										620	Ser	Val	Tyr	Ser	Asp	Phe
										625	Ser	Val	Tyr	Ser	Asp	Phe
										630	Ser	Val	Tyr	Ser	Asp	Phe
										635	Ser	Val	Tyr	Ser	Asp	Phe
										640	Ser	Val	Tyr	Ser	Asp	Phe
										645	Ser	Val	Tyr	Ser	Asp	Phe
										650	Ser	Val	Tyr	Ser	Asp	Phe
										655	Ser	Val	Tyr	Ser	Asp	Phe
										660	Ser	Val	Tyr	Ser	Asp	Phe
										665	Ser	Val	Tyr	Ser	Asp	Phe
										670	Ser	Val	Tyr	Ser	Asp	Phe

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675 680 685  
 Thr Gly Lys Thr Lys Arg Ala Ala Ala Lys Lys Thr Ala Ala Arg Arg  
 690 695 700  
 Thr Arg Ala Lys Lys Lys Arg  
 705 710

<210> 79  
 <211> 1407  
 <212> DNA  
 <213> Unknown

<220>  
 <223> obtained from an environmental sample.

<400> 79  
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 ctgtacgacc gcggcgacgg tcaggtcaac ggcaaaccgt cgttcaccgc cgaccaggcc 120  
 gccgcccaga tcctgcgcaa gggcatgtcc tggcaggaca agaacggcga cggcaagatc 180  
 gacctcagct ataccttctt gaccgacaag cctgccaaact acaaccgaa actgggcaac 240  
 ttccggcgagt tcagcgccct gcagaaagcc caggccgtgc tcgccatgca atcctggggc 300  
 gacgtggcca acgtcacctt caccgaaggc aacggcgggc acggccacat gacgttcggc 360  
 aactacgacg tcagcaccgg cggcgcggcg ttccgctacc tgccccaggg cagcagctac 420  
 gacggccagt cgtggtacct gatcaacgac cagtaccagg tcaacaagac tcccggcacc 480  
 aacaactacg ggcgccagac cctgaccac gaaatcggcc acaccctcg cctgtcgcac 540  
 cccggcgccct acaacgcccg caacggcaac ccgacctacg gtgacgcca gtacgccga 600  
 gacacccgcg gctacagcct catgagctac tggagcgaaa gcaacaccgc ccagaacttc 660  
 agcaaggacg gcagcgggcg ctacgcgtcg gcgccgttgc tggacgacat cgtggcggtg 720  
 cagaaactct acggcgccaa cctgcagacc cgtgccgacg acaccgtcta cggcttcaac 780  
 tccaacgccg agcgcgactt ctacagcgcc acctccaaca gctccaaggg ggtgttctcg 840  
 gtgtgggacg gcggcgggca cgacaccctg gacttctccg gcttcagcca caaccagaag 900  
 atcaacctca atgaagggtt gttctccgac gtcggcgggc tgggtgggcaa cgtgtccatc 960  
 gcctatggcg tgaccctgga gaacgccatc ggcgggttcg gcaacgacct gctgatcggc 1020  
 aacgcggcgcg ccaacgaact ggtgggcgga gccggcaacg acctgatcta cggcggtggc 1080  
 ggcggcgaca cgctgtgggg cggggaaggg gccgacacct tcgtgttcgg cgcggccagc 1140  
 gactcgacca tgaccgcgcc ggactggatc atggatttca ccagcggcct ggacaagatc 1200  
 gacctgtcgg gcatcgccgg cttcgccagc ggcgcggcca cgtgaactt cgtcagcggc 1260  
 ttaccgggcc atgcgggcga tgcgatcctc acctacttcg cgcagaccaa ccagaccagc 1320  
 ctgatgatcg acctgaccgg ccaagggttcg gtggacttcg ccgtgggcgt ggtggggcag 1380  
 gcgctggcaa gcgacatcgt cgcgtga 1407

<210> 80  
 <211> 468  
 <212> PRT  
 <213> Unknown

<220>  
 <223> obtained from an environmental sample.

<400> 80  
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 Thr Phe Arg His Leu Tyr Asp Arg Gly Asp Gly Gln Val Asn Gly Lys  
 20 25 30  
 Pro Ser Phe Thr Ala Asp Gln Ala Ala Ala Glu Ile Leu Arg Lys Gly  
 35 40 45  
 Met Ser Trp Gln Asp Lys Asn Gly Asp Gly Lys Ile Asp Leu Ser Tyr  
 50 55 60  
 Thr Phe Leu Thr Asp Lys Pro Ala Asn Tyr Asn Pro Lys Leu Gly Asn  
 65 70 75 80  
 Phe Gly Glu Phe Ser Ala Leu Gln Lys Ala Gln Ala Val Leu Ala Met  
 85 90 95  
 Gln Ser Trp Ala Asp Val Ala Asn Val Thr Phe Thr Glu Gly Asn Gly  
 100 105 110  
 Gly Asp Gly His Met Thr Phe Gly Asn Tyr Asp Val Ser Thr Gly Gly  
 115 120 125  
 Ala Ala Phe Ala Tyr Leu Pro Gln Gly Ser Ser Tyr Asp Gly Gln Ser  
 130 135 140  
 Trp Tyr Leu Ile Asn Asp Gln Tyr Gln Val Asn Lys Thr Pro Gly Thr

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145 Asn Asn Tyr Gly Arg 150 Gln Thr Leu Thr His 155 Glu Ile Gly His Thr 160 Leu  
 Gly Leu Ser His 165 Pro Gly Ala Tyr Asn 170 Ala Gly Asn Gly Asn 175 Pro Thr  
 Tyr Gly Asp 180 Ala Lys Tyr Ala Glu 185 Asp Thr Arg Gly Tyr Ser Leu Met  
 Ser Tyr 195 Trp Ser Glu Ser Asn 200 Thr Ala Gln Asn Phe 205 Ser Lys Asp Gly  
 Ser Gly Ala Tyr Ala Ser 215 Ala Pro Leu Leu Asp 220 Ile Val Ala Val  
 225 Gln Lys Leu Tyr Gly 230 Ala Asn Leu Gln Thr 235 Arg Ala Asp Asp Thr Val  
 Tyr Gly Phe Asn Ser Asn Ala Glu Arg 250 Asp Phe Tyr Ser Ala 255 Thr Ser  
 Asn Ser Ser 260 Lys Val Val Phe Ser 265 Val Trp Asp Gly Gly 270 Gly Asn Asp  
 Thr Leu Asp Phe Ser Gly Phe 280 Ser His Asn Gln Lys 285 Ile Asn Leu Asn  
 Glu Gly Ser Phe Ser Asp 295 Val Gly Gly Leu Val Gly Asn Val Ser Ile  
 305 Ala Tyr Gly Val Thr 310 Leu Glu Asn Ala Ile 315 Gly Gly Ser Gly Asn Asp  
 Leu Leu Ile Gly Asn Ala Ala Ala Asn 330 Glu Leu Val Gly Gly Ala Gly  
 Asn Asp Leu 340 Ile Tyr Gly Gly Gly 345 Gly Gly Asp Thr Leu Trp Gly Gly  
 Glu Gly Ala Asp Thr Phe Val Phe Gly Ala Ala Ser 365 Asp Ser Thr Met  
 Thr Ala Pro Asp Trp Ile Met Asp Phe Thr Ser 380 Gly Leu Asp Lys Ile  
 385 Asp Leu Ser Gly Ile Ala Gly Phe Ala Ser 395 Gly Ala Ala Thr Leu Asn  
 Phe Val Ser Gly 405 Phe Thr Gly His Ala Gly Asp Ala Ile Leu Thr Tyr  
 Phe Ala Gln Thr Asn Gln Thr Ser 425 Leu Met Ile Asp Leu Thr Gly Gln  
 Gly Ser Val Asp Phe Ala Val 440 Gly Val Val Gly Gln Ala Leu Ala Ser  
 Asp Ile Val Ala 455  
 465

<210> 81  
 <211> 1629  
 <212> DNA  
 <213> Unknown

<220>  
 <223> Obtained from an environmental sample.

<400> 81  
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 gagcgtgtga tcgtgattat gaaagacaag caagctttca aaatggctga ccaagtgtat 120  
 aagatgaagg ggtcttacac attaaaagg ttccatggac aagagtggag cggattgcct 180  
 caagttgaag gccaaagtga ggacagccta gagcacctga acacgcttat catcgatgca 240  
 aaagacgatg cagcgatctc caatctagt tcaaattccag ctgttgctta tgttgaaaga 300  
 gaaatcttcc acgaaggctc tcttcaaaa acaaccttg ggcatctctg ctgtaaaagc tcctgaagca 360  
 tcaaaagccg tttctcaaaa ttcacaggt tcaggggtgct cgcgttctag tacttgatac tgggatcgat 420  
 tggcctctat ctaatgaagg gaaaaatttc gaagcgggca tggacttcac tggcaagtct 480  
 caagctcacg ctcttttgac ctctgtaggt cacggaactc acgttgctgg tactattgctg 540  
 gacggttctg acttcacaga tttcacaggt ttgtctccta aagcaaaagt tttggcaggt 600  
 ggtgtgaaag caagatctgg tttcacaggt atcgctatcg ctcaagggtat caactggggt 660  
 cgtgtttgtt ctgaaaacgg ttgctctaac tctttgggtg gtatgtgggtc gactcctgca 720  
 attactcaaa acgtagacgt tatctctatg tctttgggtg gtatgtgggtc gactcctgca 780  
 gagcgtgacg ccgtttctaa agcagacgct gcgggcatca ctgtttgtggc ggcttctggt 840  
 aacagcggaa ctccgctgtt ttctttccg gcggcattgc caacagttat cgcagtcggc 900  
 gcgatcgaca atacattgaa aaaagctgat ttcttcaat ggggtcctga attggctgtt 960  
 gttgctccgg gtgtggcggg tgtttcttct gttccaacgg gaacgggtcg tgaagcggct 1020

## 10336256.txt

gttgaaatcg	ctttctctgc	taaattctggc	aaagtaaacg	cgacaacttt	ccagggtgct	1080
aaagagatcc	tgaatgcaga	aactaatgag	ttgggttgctg	taggtcttgg	taaaactgaa	1140
gatttcgcaa	aagcaaacgt	aactggtaaa	tacgctttga	tcagccgtgg	tgagatcact	1200
ttcgggtgata	aagttaaaaa	cgcatcgcg	gcgggtgctg	cgggtgtggt	tatctacaat	1260
aacgctccag	gcttgatcca	aggttctttg	actaacgatg	gatctacatt	gtcagttcca	1320
gttttcatgg	tggaacaaac	tactggtaac	gatatcgtag	cgtctttgga	aaaaggcgaa	1380
actgtgaaag	ccactttgca	aactcttgca	actgactact	ctgctttcga	cggtacttct	1440
atggcaactc	cacacgtatc	tggtgtagtg	gctcttatga	aagcggcaaa	caaggctttg	1500
acgggcgctc	aagtaaaaga	catcttgaag	caaacagctc	aagctttggg	accaaacgat	1560
gaaaaccaat	acgggtgcggg	tttggtaaat	gcggaagcgg	cagtcaatgc	tgcgatccag	1620
gcaaaataa						1629

<210> 82  
 <211> 542  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Obtained from an environmental sample.

<221> SIGNAL  
 <222> (1)...(20)

<400> 82

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			20					25					30		
Phe	Lys	Met	Ala	Asp	Gln	Val	Tyr	Lys	Met	Lys	Gly	Ser	Tyr	Thr	Leu
		35					40					45			
Lys	Gly	Phe	His	Gly	Gln	Glu	Trp	Ser	Gly	Leu	Pro	Gln	Val	Glu	Gly
	50					55					60				
Gln	Val	Glu	Asp	Ser	Leu	Glu	His	Leu	Asn	Thr	Leu	Ile	Ile	Asp	Ala
	65				70				75					80	
Lys	Asp	Asp	Ala	Ala	Ile	Ser	Asn	Leu	Val	Ser	Asn	Pro	Ala	Val	Ala
			85					90					95		
Tyr	Val	Glu	Arg	Glu	Ile	Phe	His	Glu	Gly	Pro	Arg	Pro	Val	Arg	Gly
			100					105					110		
Phe	Val	Ala	Ala	Pro	Leu	Ala	Lys	Ser	Lys	Ala	Val	Ser	Gln	Lys	Gln
		115					120					125			
Pro	Trp	Gly	Ile	Ser	Ala	Val	Lys	Ala	Pro	Glu	Ala	Trp	Pro	Leu	Ser
	130				135					140					
Asn	Glu	Gly	Gln	Gly	Ala	Arg	Val	Leu	Val	Leu	Asp	Thr	Gly	Ile	Asp
	145				150					155				160	
Gln	Ala	His	Ala	Ser	Leu	Thr	Lys	Asn	Phe	Glu	Ala	Gly	Met	Asp	Phe
			165					170					175		
Thr	Gly	Lys	Ser	Asp	Gly	Ser	Asp	Phe	Thr	Asp	Ser	Val	Gly	His	Gly
		180						185					190		
Thr	His	Val	Ala	Gly	Thr	Ile	Ala	Gly	Val	Lys	Ala	Arg	Ser	Gly	Phe
	195						200					205			
Thr	Gly	Val	Ala	Pro	Lys	Ala	Lys	Val	Leu	Ala	Gly	Arg	Val	Cys	Ser
	210				215						220				
Glu	Asn	Gly	Cys	Ser	Asn	Ile	Ala	Ile	Ala	Gln	Gly	Ile	Asn	Trp	Gly
	225				230				235					240	
Ile	Thr	Gln	Asn	Val	Asp	Val	Ile	Ser	Met	Ser	Leu	Gly	Gly	Met	Trp
			245					250					255		
Ser	Thr	Pro	Ala	Glu	Arg	Asp	Ala	Val	Ser	Lys	Ala	Asp	Ala	Ala	Gly
			260					265					270		
Ile	Thr	Val	Val	Ala	Ala	Ser	Gly	Asn	Ser	Gly	Thr	Pro	Arg	Val	Ser
		275					280					285			
Phe	Pro	Ala	Ala	Leu	Pro	Thr	Val	Ile	Ala	Val	Gly	Ala	Ile	Asp	Asn
	290				295						300				
Thr	Leu	Lys	Lys	Ala	Asp	Phe	Ser	Gln	Trp	Gly	Pro	Glu	Leu	Ala	Val
	305				310					315				320	
Val	Ala	Pro	Gly	Val	Ala	Val	Val	Ser	Ser	Val	Pro	Thr	Gly	Thr	Gly
			325					330					335		
Arg	Glu	Ala	Ala	Val	Glu	Ile	Ala	Phe	Ser	Ala	Lys	Ser	Gly	Lys	Val
			340				345						350		

10336256.txt

Asn Ala Thr Thr Phe Gln Gly Ala Lys Glu Ile Leu Asn Ala Glu Thr  
 355 360 365  
 Asn Glu Leu Val Ala Val Gly Leu Gly Lys Thr Glu Asp Phe Ala Lys  
 370 375 380  
 Ala Asn Val Thr Gly Lys Tyr Ala Leu Ile Ser Arg Gly Glu Ile Thr  
 385 390 395 400  
 Phe Gly Asp Lys Val Lys Asn Ala Ile Ala Ala Gly Ala Ala Gly Val  
 405 410 415  
 Val Ile Tyr Asn Asn Ala Pro Gly Leu Ile Gln Gly Ser Leu Thr Asn  
 420 425 430  
 Asp Gly Ser Thr Leu Ser Val Pro Val Phe Met Val Glu Gln Thr Thr  
 435 440 445  
 Gly Asn Asp Ile Val Ala Ser Leu Glu Lys Gly Glu Thr Val Lys Ala  
 450 455 460  
 Thr Leu Gln Thr Leu Ala Thr Asp Tyr Ser Ala Phe Asp Gly Thr Ser  
 465 470 475 480  
 Met Ala Thr Pro His Val Ser Gly Val Val Ala Leu Met Lys Ala Ala  
 485 490 495  
 Asn Lys Ala Leu Thr Gly Ala Gln Val Lys Asp Ile Leu Lys Gln Thr  
 500 505 510  
 Ala Gln Ala Leu Gly Pro Asn Asp Glu Asn Gln Tyr Gly Ala Gly Leu  
 515 520 525  
 Val Asn Ala Glu Ala Ala Val Asn Ala Ala Ile Gln Ala Lys  
 530 535 540

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 <211> 3048  
 <212> DNA  
 <213> Unknown

<220>  
 <223> obtained from an environmental sample.

<400> 83  
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 cacgcggcgc cttacgtgga aaacggtaga gcaggcgatc ccaacagttg gcgcagcact 120  
 gaattcaatg ccgattgggg gctgggagcg gtcaacgcac aggaggccta cgctgccggt 180  
 tacaccggca aaggcgtgaa gctggggatc ttgaccaaac cggctctacgc cgcgcattccg 240  
 gagttttccg gccccaaaca agtgatcacg ctgggtacca gcggcatccg cgaatacacc 300  
 gatccgtaca tcccgggtcaa agcgggagac gcctttcgct acgacgggtt gccctcgata 360  
 gggtccgacg gcaagctggg ggcccacggc acccacgttg gcgggattgc tgccggcagt 420  
 cgcgatggcg gtccgatgca tgggtgtggcg tttggcgcgc agatcatcag tgcggacaac 480  
 ggagatccgg gcccgaaga cggcatcatt cgcggaatg acggtgcggt ctacaaggcc 540  
 gggtgggatg cttgatcgc cagcggcgcg cggatcatca acaacagttg gggcatcggg 600  
 atcaccgatc gcttcgacct cggcggacgc aatcccgcct acccgattt caccgtgcag 660  
 gacgcgcaat tgcagttcaa cgagatccgt ccgttgctcg ggaccaaacc gggcggagcc 720  
 tacgacggcg ccatcgcggc ggcccgcagc ggtatcgtga cgatcttcgc ggccggcaac 780  
 gactacaacc tcaacaaccc ggacgccatc gccggcctgg gctatttcgt cccggacatc 840  
 gcgcccgaact ggggtaccgt ggcggcgttg cagaaaaacc cggacctcaa cagcccggat 900  
 ctctacaaca tcagcacctt ctcatcgcg cagctcgatc atcagcggta ccaacgccgg cgacctgacc 1020  
 gcaccgggca gcaagatcta cggcacctcg atggcgggcg cgcatgtcgc cggttccatg 1080  
 gccgtgttga tggaaacgctt cccgtacatg accggcgccc aggtcgccag cgtgttgccg 1140  
 accacggcca ccgacctcgg tgcgccaggt gtcgattcgc tgtacggctg gggcatgatc 1200  
 aacctgcgca aaggcatcga tggcccggcg atgtttgtca ccgagcaaga cattcccag 1260  
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 ctggcaatca acggctcgcg attgaccgcg aaaagcgggtg gcaccgtagc gccaggcaat 1560  
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 tccatcgcca cgccgaccag cagcgatcgg cctggaaaac agcccgcact tgctgaccac cagtgaagt 1680  
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 ggcattcaac tggcggtaga gcgtaacgca gcgtcttcg ccagcgtcgg ccaaaccgcc 1980  
 aaccaacgcg ctgtcgcagc ggccgcccag caactggcgg ccggcaatcc tctctatgaa 2040

## 10336256.txt

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agcaacgcct	gggtcaaagt	cctcggcgcc	tggggcaaga	gcgatggcgg	gcatgacaac	2280
gccagttcca	acagctccat	cggcggttg	ctggccggtg	tcgacggtct	gatcactgaa	2340
aatacgcggc	tgggtttcgt	gactgggttac	agcgacagtt	cgttgagcat	gggcgatggc	2400
acgcattcct	cagcctccgt	cgatagctac	cacttgggcg	cctatctggg	ccatgaaatc	2460
gatgcgctgc	gtctgagcgt	cggcggtgca	tacagctggc	atcgcatcga	cgtgaagcgt	2520
gacctgcaat	tgggcgacgt	cagcggcaaa	cagaaatcca	aacgcgatgc	gacaaccgca	2580
caactgttta	ccgaagcggc	gtatcgctg	gacctgcagc	cgctggcgct	ggaaccgttc	2640
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cagcacaacc	tgagcaacac	ccgttccgaa	gatcacctgg	ccttcgccaa	cggcaacacc	2880
gcgttcagcg	tgcagagcgt	ttccctggac	cgtaacgctg	ccgtcatcgg	tgcgcgggcc	2940
ggtttggtcg	tggcgcagga	cgttcgttg	agcctggatt	acaacggact	gctcggctcc	3000
cgcgagaaag	accacggtgt	gggtctgacg	ctcgactggc	agttctga		3048

&lt;210&gt; 84

&lt;211&gt; 1015

&lt;212&gt; PRT

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; Obtained from an environmental sample.

&lt;221&gt; SIGNAL

&lt;222&gt; (1)...(22)

&lt;400&gt; 84

Met	Asn	Asn	Lys	His	Asn	Asn	Leu	Ala	Met	Leu	Cys	Ala	Leu	Ala	Thr
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Leu	Gly	Thr	Ala	His	Ala	Ala	Pro	Tyr	Val	Glu	Asn	Gly	Arg	Ala	Gly
			20					25					30		
Asp	Pro	Asn	Ser	Trp	Arg	Ser	Thr	Glu	Phe	Asn	Ala	Asp	Trp	Gly	Leu
		35					40					45			
Gly	Ala	Val	Asn	Ala	Gln	Glu	Ala	Tyr	Ala	Ala	Gly	Tyr	Thr	Gly	Lys
	50					55					60				
Gly	Val	Lys	Leu	Gly	Ile	Phe	Asp	Gln	Pro	Val	Tyr	Ala	Ala	His	Pro
65				70					75					80	
Glu	Phe	Ser	Gly	Pro	Asn	Lys	Val	Ile	Thr	Leu	Val	Thr	Ser	Gly	Ile
			85					90					95		
Arg	Glu	Tyr	Thr	Asp	Pro	Tyr	Ile	Pro	Val	Lys	Ala	Gly	Asp	Ala	Phe
			100					105					110		
Arg	Tyr	Asp	Gly	Ser	Pro	Ser	Ile	Gly	Ser	Asp	Gly	Lys	Leu	Gly	Ala
		115					120					125			
His	Gly	Thr	His	Val	Gly	Gly	Ile	Ala	Ala	Gly	Ser	Arg	Asp	Gly	Gly
	130					135					140				
Pro	Met	His	Gly	Val	Ala	Phe	Gly	Ala	Gln	Ile	Ile	Ser	Ala	Asp	Asn
145					150					155				160	
Gly	Asp	Pro	Gly	Pro	Glu	Asp	Gly	Ile	Ile	Arg	Gly	Asn	Asp	Gly	Ala
			165						170					175	
Val	Tyr	Lys	Ala	Gly	Trp	Asp	Ala	Leu	Ile	Ala	Ser	Gly	Ala	Arg	Ile
			180					185					190		
Ile	Asn	Asn	Ser	Trp	Gly	Ile	Gly	Ile	Thr	Asp	Arg	Phe	Asp	Leu	Gly
		195					200					205			
Gly	Arg	Asn	Pro	Ala	Tyr	Pro	His	Phe	Thr	Val	Gln	Asp	Ala	Gln	Leu
	210					215					220				
Gln	Phe	Asn	Glu	Ile	Arg	Pro	Leu	Leu	Gly	Thr	Lys	Pro	Gly	Gly	Ala
225					230					235				240	
Tyr	Asp	Gly	Ala	Ile	Ala	Ala	Ala	Arg	Ser	Gly	Ile	Val	Thr	Ile	Phe
			245						250					255	
Ala	Ala	Gly	Asn	Asp	Tyr	Asn	Leu	Asn	Asn	Pro	Asp	Ala	Ile	Ala	Gly
			260					265					270		
Leu	Gly	Tyr	Phe	Val	Pro	Asp	Ile	Ala	Pro	Asn	Trp	Val	Thr	Val	Ala
		275					280						285		
Ala	Leu	Gln	Lys	Asn	Pro	Asp	Leu	Asn	Ser	Pro	Asp	Leu	Tyr	Asn	Ile
	290					295					300				

10336256.txt

Ser Thr Phe Ser Ser Arg Cys Gly Tyr Thr Ala Ser Phe Cys Val Ser  
 305 310 315 320  
 Ala Pro Gly Ser Lys Ile Tyr Ser Ser Ile Ile Ser Gly Thr Asn Ala  
 325 330 335  
 Gly Asp Leu Thr Thr Gly Tyr Lys Asn Tyr Asn Gly Thr Ser Met Ala  
 340 345 350  
 Ala Pro His Val Ala Gly Ser Met Ala Val Leu Met Glu Arg Phe Pro  
 355 360 365  
 Tyr Met Thr Gly Ala Gln Val Ala Ser Val Leu Arg Thr Thr Ala Thr  
 370 375 380  
 Asp Leu Gly Ala Pro Gly Val Asp Ser Leu Tyr Gly Trp Gly Met Ile  
 385 390 395  
 Asn Leu Arg Lys Gly Ile Asp Gly Pro Ala Met Phe Val Thr Glu Gln  
 400 405 410  
 Asp Ile Pro Glu Gly Phe Arg Ile Gln Gly Ala Tyr Gly Ser Ser Gln  
 420 425 430  
 Phe Val Ala Asp Leu Pro Gly Ile Gly Ala Ile Ile Asp Ala Gly Lys  
 435 440 445  
 Pro Thr Glu Arg Val Cys Asn Asp Val His Cys Gly Leu Asp Thr Trp  
 450 455 460  
 Arg Asn Asp Ile Ser Gly His Gly Gly Leu Thr Lys Gln Gly Ile Gly  
 465 470 475  
 Thr Leu Val Leu Thr Gly Ala Asn Thr Tyr Ala Gly Pro Thr Leu Val  
 480 485 490  
 Asn Gln Gly Arg Leu Ala Ile Asn Gly Ser Leu Leu Ser Ala Val Thr  
 500 505 510  
 Val Asn Asp Ser Gly Ile Leu Gly Gly Asn Gly Arg Ile Gly Ala Leu  
 515 520 525  
 Thr Ala Lys Ser Gly Gly Thr Val Ala Pro Gly Asn Ser Ile Gly Thr  
 530 535 540  
 Leu Gln Val Ala Gly Asp Val Thr Phe Glu Pro Gly Ser Thr Tyr Ala  
 545 550 555  
 Val Glu Leu Ser Pro Thr Ser Ser Asp Arg Ile Val Ala Gly Gly Lys  
 560 565 570  
 Ala Val Ile Asp Gly Ala Thr Val Ser Leu Ser Leu Glu Asn Ser Pro  
 580 585 590  
 Thr Leu Leu Thr Thr Ser Glu Val Lys Ser Leu Leu Gly Asn Gln Tyr  
 595 600 605  
 Thr Ile Leu Gln Ala Ala Gly Ile Glu Gly Arg Phe Gly Ala Val  
 610 615 620  
 Ile Pro Asp Tyr Leu Phe Ile Gly Gly Thr Leu Gly Tyr Ser Ala Asn  
 625 630 635  
 Gly Ile Gln Leu Ala Val Glu Arg Asn Ala Ala Ser Phe Ala Ser Val  
 640 645 650  
 Gly Gln Thr Pro Asn Gln Arg Ala Val Ala Ala Ala Ala Glu Gln Leu  
 655 660 665  
 Gly Ala Gly Asn Pro Leu Tyr Glu Thr Leu Leu Leu Ser Pro Thr Ala  
 670 675 680  
 Ala Val Ala Gln Gln Ala Phe Gln Gln Leu Ser Gly Ile His Pro  
 685 690 695  
 Ala Ile Gly Thr Leu Leu Ile Asn Asp Ser Arg Tyr Leu Arg Asp Ala  
 700 705 710  
 Val Gly Glu Arg Leu Arg Glu Arg Asp Leu Phe Asn Ala Ala Ala Pro  
 715 720 725  
 Thr Asp Asp Arg Ser Asn Ala Trp Val Lys Val Leu Gly Ala Trp Gly  
 730 735 740  
 Lys Ser Asp Gly Gly His Asp Asn Ala Ser Ser Asn Ser Ile Gly  
 745 750 755  
 Gly Leu Leu Ala Gly Val Asp Gly Leu Ile Thr Glu Asn Thr Arg Leu  
 760 765 770  
 Gly Phe Val Thr Gly Tyr Ser Asp Ser Ser Leu Ser Met Gly Asp Gly  
 775 780 785  
 Thr His Ser Ser Ala Ser Val Asp Ser Tyr His Leu Gly Ala Tyr Gln  
 790 795 800  
 Gly His Glu Ile Asp Ala Leu Arg Leu Ser Val Gly Gly Ala Tyr Ser  
 805 810 815  
 Trp His Arg Ile Asp Val Lys Arg Asp Leu Gln Leu Gly Asp Val Ser  
 820 825 830  
 835 840 845

10336256.txt

Gly	Lys	Gln	Lys	Ser	Lys	Arg	Asp	Ala	Thr	Thr	Ala	Gln	Leu	Phe	Thr
850	850					855					860				
Glu	Ala	Ala	Tyr	Arg	Leu	Asp	Leu	Gln	Pro	Leu	Ala	Leu	Glu	Pro	Phe
865					870					875					880
Ala	Asn	Leu	Ala	Tyr	Val	His	Leu	Asn	Ser	Asp	Ser	Phe	Thr	Glu	Lys
				885						890				895	
Gly	Asp	Ala	Ala	Ala	Leu	Lys	Gly	Gly	Glu	Asp	Asn	Arg	Asp	Ala	Val
			900					905					910		
Leu	Ser	Thr	Leu	Gly	Leu	Arg	Ala	Ser	Lys	Ala	Ile	Ala	Leu	Ser	Asp
		915					920					925			
Gln	Gln	Gln	Leu	Glu	Leu	Ser	Gly	Thr	Leu	Gly	Trp	Gln	His	Asn	Leu
		930				935					940				
Ser	Asn	Thr	Arg	Ser	Glu	Asp	His	Leu	Ala	Phe	Ala	Asn	Gly	Asn	Thr
945					950					955					960
Ala	Phe	Ser	Val	Gln	Ser	Val	Ser	Leu	Asp	Arg	Asn	Ala	Ala	Val	Ile
				965					970					975	
Gly	Ala	Arg	Ala	Gly	Leu	Ala	Val	Ala	Gln	Asp	Val	Arg	Leu	Ser	Leu
			980					985					990		
Asp	Tyr	Asn	Gly	Leu	Leu	Gly	Ser	Arg	Glu	Lys	Asp	His	Gly	Val	Gly
		995					1000					1005			
Leu	Thr	Leu	Asp	Trp	Gln	Phe									
1010						1015									

&lt;210&gt; 85

&lt;211&gt; 2166

&lt;212&gt; DNA

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; Obtained from an environmental sample.

&lt;400&gt; 85

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gcac	caac	ccatt	caat	tcgt	acaa	120
aatt	cat	cgc	atga	tggt	acga	180
caag	gat	gag	atga	atct	acac	240
tttg	gag	aaa	atga	atga	aga	300
agtt	gag	gag	atga	atga	aga	360
aaag	gag	gag	atga	atga	aga	420
catg	gag	gag	atga	atga	aga	480
ggtg	gag	gag	atga	atga	aga	540
gaat	gag	gag	atga	atga	aga	600
caag	gag	gag	atga	atga	aga	660
catg	gag	gag	atga	atga	aga	720
tact	gag	gag	atga	atga	aga	780
acag	gag	gag	atga	atga	aga	840
ttct	gag	gag	atga	atga	aga	900
gtct	gag	gag	atga	atga	aga	960
catg	gag	gag	atga	atga	aga	1020
ttcg	gag	gag	atga	atga	aga	1080
aagg	gag	gag	atga	atga	aga	1140
gcgg	gag	gag	atga	atga	aga	1200
agc	gag	gag	atga	atga	aga	1260
atga	gag	gag	atga	atga	aga	1320
atgt	gag	gag	atga	atga	aga	1380
ttta	gag	gag	atga	atga	aga	1440
attg	gag	gag	atga	atga	aga	1500
atcg	gag	gag	atga	atga	aga	1560
ctga	gag	gag	atga	atga	aga	1620
ggct	gag	gag	atga	atga	aga	1680
ggtg	gag	gag	atga	atga	aga	1740
gtcg	gag	gag	atga	atga	aga	1800
gaat	gag	gag	atga	atga	aga	1860
gata	gag	gag	atga	atga	aga	1920
cagg	gag	gag	atga	atga	aga	1980
gata	gag	gag	atga	atga	aga	2040
ttca	gag	gag	atga	atga	aga	2100
						2160

10336256.txt

aaataa

2166

<210> 86  
 <211> 721  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Obtained from an environmental sample.

<221> SIGNAL  
 <222> (1)...(20)

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 Gly Cys Ser Asn Gln Gly Leu Pro Thr Met Asn His Tyr Ser Gln Ser  
 20 25 30  
 Gln Leu Val Ala Gln Gln Thr Gln Ala Pro Val Ala Lys Lys Val Arg  
 35 40 45  
 His Ala Met Asn Ile His Gly Asp Thr Arg Ile Asp Asn Tyr Tyr Trp  
 50 55 60  
 Met Arg Asp Asp Glu Arg Gln Asp Pro Glu Ile Leu Gln His Leu Glu  
 65 70 75 80  
 Gln Glu Asn Gln Tyr Ala Glu Thr Val Leu Lys His Thr Glu Ala Leu  
 85 90 95  
 Gln Glu Gln Leu Phe Glu Glu Ile Lys Gly Arg Ile Ala Lys Asp Asp  
 100 105 110  
 Asn Ser Val Pro Val Arg Lys Gly Ser Tyr Tyr Tyr Ser Asn Glu Val  
 115 120 125  
 Thr Gly Asp Asn Glu Tyr Glu Val His Leu Arg Ala Lys Asp Phe Ala  
 130 135 140  
 Gly Thr Asp Lys Gln Val Ile Leu Asp Val Asn Glu Leu Ala Lys Glu  
 145 150 155 160  
 His Glu Phe Phe Ser Ile Gly Gly Leu Tyr Val Ser Pro Asn Glu Asn  
 165 170 175  
 Met Leu Ala Tyr Gly Glu Asp Thr Leu Ser Arg Arg Ile Tyr Thr Ile  
 180 185 190  
 Lys Ile Lys Asp Leu Thr Thr Gly Glu Tyr Leu Lys Asp Glu Ile Glu  
 195 200 205  
 Gly Ala Ser Ser Ala Ile Ala Trp Gln Asn Asp Asn Gln Ala Phe Tyr  
 210 215 220  
 Tyr Ile Lys Lys Asp Pro Gln Thr Leu Leu Gly Tyr Gln Val Tyr Arg  
 225 230 235 240  
 His Val Leu Gly Thr Pro Gln Thr Ser Asp Glu Leu Ile Tyr Glu Glu  
 245 250 255  
 Thr Asp Ser Ala Tyr Tyr Thr Phe Leu Ser Lys Ser Lys Asp Gly Glu  
 260 265 270  
 Gln Val Tyr Ile Trp His Ser Ser Thr Glu Thr Ser Gly Val Ser Val  
 275 280 285  
 Ile Asp Ala Asn Asn Pro Asn Ala Lys Ala Glu Ala Phe Tyr Pro Arg  
 290 295 300  
 Glu Thr Gly Ile Glu Tyr Ser Ile Ala Lys Leu Gly Asp Trp Tyr Tyr  
 305 310 315 320  
 Val Tyr Thr Asn Tyr Gln Ala Val Asn Phe Arg Leu Met Lys Val Lys  
 325 330 335  
 Ala Glu Glu Met His Asp Arg Ser Lys Trp Val Asp Val Ile Pro Ala  
 340 345 350  
 Asp Asp Asn Thr Gln Leu Val Asp Phe Asp Leu Phe Asp Asp His Leu  
 355 360 365  
 Val Tyr Glu Gln Arg Thr Asn Gly Leu Ser Thr Val Lys Val Arg Gln  
 370 375 380  
 Leu Ser Thr Gly Lys Glu Phe Pro Leu Glu Phe Asn Asp Thr Ala Phe  
 385 390 395 400  
 Ala Ala Tyr Leu Thr Gly Asn Tyr Glu Leu Asp Asn Ser Lys Val Arg  
 405 410 415  
 Ile Tyr Tyr Ser Ser Leu Thr Thr Pro Gly Thr Tyr Tyr Asp Phe Asp  
 420 425 430

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Leu Asn Thr Gly Glu Ser Glu Ile Met Lys Gln Thr Pro Leu Leu Gly  
 435 440 445  
 Asp Leu Asp Ala Asp Asn Tyr His Ser Lys Gln Ile Met Val Thr Ala  
 450 455 460  
 Arg Asp Gly Asn Gln Leu Pro Val Ser Leu Val Tyr Arg Lys Asp Leu  
 465 470 475 480  
 Phe Lys Lys Asn Gly Thr Asn Pro Ile Tyr Gln Tyr Gly Tyr Gly Ser  
 485 490 495  
 Tyr Gly Ser Thr Ile Glu Pro Thr Phe Arg Ser Thr Arg Leu Ser Leu  
 500 505 510  
 Leu Asp Arg Gly Phe Val Tyr Ala Ile Ala His Ile Arg Gly Ser Glu  
 515 520 525  
 Met Leu Gly Arg Pro Trp Tyr Glu Asp Gly Lys Lys Leu Thr Lys Gln  
 530 535 540  
 Asn Thr Phe Asn Asp Phe Ile Asp Val Thr Lys Gly Leu Val Glu Glu  
 545 550 555 560  
 Gly Tyr Gly Ala Lys Asp Lys Val Phe Ala Val Gly Gly Ser Ala Gly  
 565 570 575  
 Gly Leu Leu Met Gly Ala Ile Ile Asn Gln Ala Pro Glu Leu Tyr Arg  
 580 585 590  
 Gly Ile Gly Ala His Val Pro Phe Val Asp Val Val Thr Thr Met Leu  
 595 600 605  
 Asp Glu Ser Ile Pro Leu Thr Thr Asn Glu Tyr Asp Glu Trp Gly Asn  
 610 615 620  
 Pro Asn Asp Lys Thr Tyr Tyr Asp Tyr Met Val Ser Tyr Ser Pro Tyr  
 625 630 635 640  
 Asp Asn Val Lys Thr Gln Asn Tyr Pro Asn Met Leu Val Thr Thr Gly  
 645 650 655  
 Leu His Asp Ser Gln Val Gln Tyr Phe Glu Pro Met Lys Trp Val Ala  
 660 665 670  
 Lys Leu Arg Glu Met Lys Thr Asp Asn Val Leu Leu Phe Lys Thr  
 675 680 685  
 Asp Met Glu Ala Gly His Gly Gly Ala Ser Gly Arg Phe Lys Arg Leu  
 690 695 700  
 Lys Glu Asp Ala Leu Glu Tyr Ala Phe Phe Leu Asp Leu Leu Glu Thr  
 705 710 715 720  
 Lys

<210> 87  
 <211> 1848  
 <212> DNA  
 <213> Unknown

<220>  
 <223> obtained from an environmental sample.

<400> 87

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ggcctgggag	ccggcggtggc	ggtcgcgggc	gtgtccgcga	ccgcacaggg	cacacccgtc	120
gcgcaggggtg	ccgttggttg	agacaagacc	gaccgcatca	tcgtcaagta	caaggacgaa	180
caggcgccgg	tggccgtgaa	gggcgggttcg	atcgccgcca	tggccaaggg	cacggccgag	240
ccgatgtcga	cggcgcgcaa	ggccaagctg	gaccgcgccg	gccagcagtt	cggcttcctg	300
atgaaggaat	cgcaccgcat	cgccaccggc	gcccgcgtcg	tcaagctgga	ccgcaaggtc	360
tcgctgcagg	aagccgcgca	agtggcgggc	gacctggccg	cgcgcgaccc	ggacgtcgaa	420
tacgccgaac	cggaccgcct	gctgcatccc	ctgatgacgc	cgaacgattc	gatgtacagc	480
cagcagtggg	acttcttcga	agccaccggc	ggcatgaaca	tcccggcgcc	ctgggacaag	540
tcgaccggct	ccggcatccg	cgtggccgtg	atcgataccg	gctaccgtcc	gcacgcccag	600
ctgtcggggc	agatcctggc	cggctatgac	ttcatttcgg	acgccaccat	cggcaacgac	660
ggcaacggcc	gcgacagcga	cgccagcgac	ccgggcgact	ggaccgcggc	cggcgaatgc	720
ggcgccggcg	agccggcgctc	caactcgagc	tggcacggca	cccacgtggc	cggcaccatc	780
gccgcgtcga	ccaacaacgg	cagcggcggtg	gccggcatcg	cctacggcgc	caagatcgtg	840
ccggtacgcg	tgctcggcaa	atgcggcggc	tacacctcgg	acatcgccga	cggcatcatc	900
tgggcttccg	gcggcaccgt	ctcgggcgtg	ccaacatcg	cggcgcgcg	gcaggtgatc	960
aacatgtcgc	tgggcggcg	cggcgcttcg	ggcaccacga	cccagaacgc	gatcaacagc	1020
gcccgcctcg	cgggcaccgt	ggtcgtggctg	cggcgccgga	acgagtcgca	gaacgccagc	1080
aacagcaacc	cggccaactg	ctcgggcgtg	atcacggtgg	cggcgacgaa	ccgttcggc	1140
ggacgcgcat	cctactcgaa	ctacggcacc	gtggtcgacg	tggcgggcgc	gggcggcgac	1200

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agcggcgcg	ccatcctgtc	gacgctgaac	gccggcacca	aggcaccggg	cgccgacagc	1260
tatgccggct	acatgggcac	ctcgatggcc	accccgcacg	tggccggcgt	ggtcgcgctg	1320
atgctggcca	agaacgcgtc	gatgaccccg	gaccaggctcg	aagccgcgct	gaagtcgacc	1380
gcgcgcgcct	tcccggcctc	gtgcagcggc	tgcggcgccg	gcatcgtgaa	cgctcgggcc	1440
gcggctcgatg	cggccatcgg	cggcgggcgg	accacgacgg	gcccgacggg	gtcgggaaacc	1500
gagtcgaaca	acacgatcag	caccgccaac	agcgtgacga	ccacgggtac	cacgggtcaac	1560
ggcaccatgg	ccagcagcac	ggacaccgat	tacttcgtgg	tccagggtccc	ggccggcaag	1620
acgctgagcg	ccaccctgac	cccgggttcg	agcgccgact	acgacctgta	tatctacaac	1680
agcgcgggca	cccagctggc	gaccagccag	aacggcaccg	gcgcgggtcga	cagcgccagc	1740
tcggccaact	ccaccacggc	cgctcggca	cgctacgtgc	gcgtgggtgta	ctacagcggc	1800
ggcaccggct	cgaccaacgg	caagtacacg	ctgaaactgt	cgtggtaa		1848

<210> 88  
 <211> 615  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Obtained from an environmental sample.

<221> SIGNAL  
 <222> (1)...(35)

<400> 88

Met	Lys	Ser	Lys	Gln	Ser	Met	Tyr	Pro	Ala	Val	Leu	Lys	Leu	Cys	Ala
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Ala	Ala	Val	Leu	Gly	Leu	Gly	Ala	Gly	Val	Ala	Val	Ala	Gly	Val	Ser
			20					25					30		
Ala	Thr	Ala	Gln	Gly	Thr	Pro	Val	Ala	Gln	Gly	Ala	Val	Val	Ala	Asp
			35				40					45			
Lys	Thr	Asp	Arg	Ile	Ile	Val	Lys	Tyr	Lys	Asp	Glu	Gln	Ala	Pro	Val
	50					55					60				
Ala	Val	Lys	Gly	Gly	Ser	Ile	Ala	Ala	Met	Ala	Lys	Ala	Thr	Ala	Glu
65					70				75						80
Pro	Met	Ser	Thr	Ala	Arg	Lys	Ala	Lys	Leu	Asp	Arg	Ala	Gly	Gln	Gln
				85					90					95	
Phe	Gly	Phe	Leu	Met	Lys	Glu	Ser	His	Arg	Ile	Ala	Thr	Gly	Ala	Arg
			100					105					110		
Val	Val	Lys	Leu	Asp	Arg	Lys	Val	Ser	Leu	Gln	Glu	Ala	Ala	Gln	Val
		115					120					125			
Ala	Ala	Asp	Leu	Ala	Ala	Arg	Asp	Pro	Asp	Val	Glu	Tyr	Ala	Glu	Pro
	130					135					140				
Asp	Arg	Leu	Leu	His	Pro	Leu	Met	Thr	Pro	Asn	Asp	Ser	Met	Tyr	Ser
145					150					155					160
Gln	Gln	Trp	Asp	Phe	Phe	Glu	Ala	Thr	Gly	Gly	Met	Asn	Ile	Pro	Ala
				165					170					175	
Ala	Trp	Asp	Lys	Ser	Thr	Gly	Ser	Gly	Ile	Arg	Val	Ala	Val	Ile	Asp
			180					185					190		
Thr	Gly	Tyr	Arg	Pro	His	Ala	Asp	Leu	Ser	Gly	Gln	Ile	Leu	Ala	Gly
		195					200					205			
Tyr	Asp	Phe	Ile	Ser	Asp	Ala	Thr	Ile	Gly	Asn	Asp	Gly	Asn	Gly	Arg
	210					215					220				
Asp	Ser	Asp	Ala	Ser	Asp	Pro	Gly	Asp	Trp	Thr	Ala	Ala	Gly	Glu	Cys
225					230					235					240
Gly	Ala	Gly	Glu	Pro	Ala	Ser	Asn	Ser	Ser	Trp	His	Gly	Thr	His	Val
				245					250					255	
Ala	Gly	Thr	Ile	Ala	Ala	Leu	Thr	Asn	Gly	Ser	Gly	Val	Ala	Gly	
			260					265					270		
Ile	Ala	Tyr	Gly	Ala	Lys	Ile	Val	Pro	Val	Arg	Val	Leu	Gly	Lys	Cys
		275					280					285			
Gly	Gly	Tyr	Thr	Ser	Asp	Ile	Ala	Asp	Gly	Ile	Ile	Trp	Ala	Ser	Gly
	290					295					300				
Gly	Thr	Val	Ser	Gly	Val	Pro	Asn	Ile	Ala	Ala	Arg	Ala	Gln	Val	Ile
305					310					315					320
Asn	Met	Ser	Leu	Gly	Gly	Gly	Gly	Ala	Cys	Gly	Thr	Thr	Thr	Gln	Asn
				325					330					335	
Ala	Ile	Asn	Ser	Ala	Arg	Ser	Arg	Gly	Thr	Val	Val	Val	Val	Ala	Ala
			340					345					350		

## 10336256.txt

Gly Asn Glu Ser Gln Asn Ala Ser Asn Ser Asn Pro Ala Asn Cys Ser  
 355 360 365  
 Gly Val Ile Thr Val Ala Ala Thr Asn Arg Ser Gly Gly Arg Ala Ser  
 370 375 380  
 Tyr Ser Asn Tyr Gly Thr Val Val Asp Val Ala Ala Pro Gly Gly Asp  
 385 390 395 400  
 Ser Gly Ala Ala Ile Leu Ser Thr Leu Asn Ala Gly Thr Lys Ala Pro  
 405 410 415  
 Gly Ala Asp Ser Tyr Ala Gly Tyr Met Gly Thr Ser Met Ala Thr Pro  
 420 425 430  
 His Val Ala Gly Val Val Ala Leu Met Leu Ala Lys Asn Ala Ser Met  
 435 440 445  
 Thr Pro Asp Gln Val Glu Ala Ala Leu Lys Ser Thr Ala Arg Ala Phe  
 450 455 460  
 Pro Ala Ser Cys Ser Gly Cys Gly Ala Gly Ile Val Asn Ala Ser Ala  
 465 470 475 480  
 Ala Val Asp Ala Ala Ile Gly Gly Gly Gly Thr Thr Thr Gly Pro Thr  
 485 490 495  
 Val Ser Glu Thr Glu Ser Asn Asn Thr Ile Ser Thr Ala Asn Ser Val  
 500 505 510  
 Thr Thr Thr Gly Thr Thr Val Asn Gly Thr Met Ala Ser Ser Thr Asp  
 515 520 525  
 Thr Asp Tyr Phe Val Val Gln Val Pro Ala Gly Lys Thr Leu Ser Ala  
 530 535 540  
 Thr Leu Thr Pro Gly Ser Ser Ala Asp Tyr Asp Leu Tyr Ile Tyr Asn  
 545 550 555 560  
 Ser Ala Gly Thr Gln Leu Ala Thr Ser Gln Asn Gly Thr Gly Ala Val  
 565 570 575  
 Asp Ser Ala Ser Ser Ala Asn Ser Thr Thr Ala Ala Ser Ala Arg Tyr  
 580 585 590  
 Val Arg Val Val Tyr Tyr Ser Gly Gly Thr Gly Ser Thr Asn Gly Lys  
 595 600 605  
 Tyr Thr Leu Lys Leu Ser Trp  
 610 615

<210> 89  
 <211> 1791  
 <212> DNA  
 <213> Unknown

<220>  
 <223> Obtained from an environmental sample.

<400> 89  
 atgcagaaac acaagctaac ctggaaggcg ctgcgatact gcctgctgat cgccctggcc 60  
 ctggcccaaa ccggctttgg ggcgccagca gcggcggcac agtccggcga ggccatgccg 120  
 ccggcagcca gcggggctgc ggacgacctg ccgaccgatc agattattat tctgtacgaa 180  
 gaaattgcct ccggcgcgcc ggccatgcag cagctgagct ttgccgccgg ggccgggctg 240  
 acccaggtgc gcgaattgtc gggcggtggg gcggtcatgc agctgccaga cccgctgccc 300  
 gccgaagagg tcgaggttct tgcgcggcgg ctgatgaacc tgcccgaggt ggcgtatgcc 360  
 gagcccgatc acatcaacct gccggccgtg ctgcccaatg actcgttctt ctccgcgtac 420  
 caatggagcc ttaccgcgcc caagaacaat atctacggca tcgacgcccc cgccgcctgg 480  
 gaaatttcga ccggctcgcc tgacatagtg gtggccgtgc tcgatacggg catcctcaac 540  
 caccgccgatt tgaacgggcg aaccgtcgcc ggctatgatt tcatcacaaa tgcttggatg 600  
 gccaacgacg gcgacgggcg cgaccccaac ccacggacc ccggcgactg gctgaccacc 660  
 aatgacattg caaccattg ttattatgcg ccggtgatgg acagctcgtg gcacggcacg 720  
 catgtggcgg gcataatcgg cgcgccagc aataacagtc ttggcataatc cggcatcaac 780  
 tggacgtcga aaatcctgcc ggtgcgctg ctgggcaagt gcggcgggta cgattcagac 840  
 atcatcgacg ccatccgctg gtcggccggc ctgccgttac ccggcgcgcc agccaacccc 900  
 aaccgggcca aagtaatcaa cctcagcctg ggcgcccaa atactgtcag ctcggtcatg 960  
 cagtcggcca tcaatgacgc gtacgagcag ggggtcacgg ttggtggtcgc cgccggcaac 1020  
 agcagcatgg ttcgcgcggg ctttcgcgg gcctctgca gcaatgtgat ccgctggggc 1080  
 gcgaccggcc cgactggctc gcgcgcgtgg tacagcaact acggcgctac cgtggccatc 1140  
 tccgcgcggg gcggcgacgg cagcagcgct atctattcgc tgcacaattc cggcaagacc 1200  
 acgcccgtag ccgattccta ccagtacatg atgggaccca gccaggccgc gccgcacgctc 1260  
 agcgggggtg tttcgtcgtc ctattcgtc caacccgcgc tgacccccga ccaggcgcg 1320  
 gccgttctga ccagcaccgc cacggccttc ccggcgggca gcagctgcgc caccggctcg 1380  
 tgcggggcgg gcatcctcaa tgccgggcag gccgtgcagg ccatgaccac cccgcccggc 1440

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accttccaga	agatcgcgcc	gctgaacaat	gccgcccggcc	tgccgggtcaa	cagcgtgggtc	1500
ctggagtgga	gccccagcag	cggggcgggcc	tcgtacgagt	actgctacta	cgcccccgcg	1560
cttcaggcag	cctgcgccag	ctggatcagc	gccggggcgga	gcaccaaagc	cacgctcacc	1620
aatctgctcc	ccgccgtgac	ctactcctgg	caggtgcggg	cggtaaatgc	cgcaatcacc	1680
gccaccgacg	ccgatttcgt	cgccaacagc	ggaacctggt	ggacgttctc	gaccgaggcg	1740
gtcagcttca	acgtaaccta	caacgtgttt	atgccgtcgg	tcgtgcgcta	a	1791

<210> 90  
 <211> 596  
 <212> PRT  
 <213> Unknown

<220>  
 <223> obtained from an environmental sample.

<221> SIGNAL  
 <222> (1)...(32)

<400> 90

Met	Gln	Lys	His	Lys	Leu	Thr	Trp	Lys	Ala	Leu	Arg	Tyr	Cys	Leu	Leu
1				5					10					15	
Ile	Ala	Leu	Ala	Leu	Ala	Gln	Thr	Gly	Phe	Gly	Ala	Pro	Ala	Ala	Ala
			20					25					30		
Ala	Gln	Ser	Gly	Glu	Ala	Met	Pro	Pro	Ala	Ala	Ser	Gly	Ala	Ala	Asp
		35					40					45			
Asp	Leu	Pro	Thr	Asp	Gln	Ile	Ile	Ile	Leu	Tyr	Glu	Glu	Ile	Ala	Ser
	50					55					60				
Gly	Ala	Pro	Ala	Met	Gln	Gln	Leu	Ser	Phe	Ala	Ala	Gly	Ala	Gly	Leu
	65				70					75					80
Thr	Gln	Val	Arg	Glu	Leu	Ser	Gly	Gly	Gly	Ala	Val	Met	Gln	Leu	Pro
				85					90					95	
Asp	Pro	Leu	Pro	Ala	Glu	Glu	Val	Glu	Val	Leu	Ala	Arg	Arg	Leu	Met
			100					105					110		
Asn	Leu	Pro	Glu	Val	Ala	Tyr	Ala	Glu	Pro	Asp	His	Ile	Asn	Leu	Pro
		115					120					125			
Ala	Val	Leu	Pro	Asn	Asp	Ser	Phe	Phe	Ser	Ala	Tyr	Gln	Trp	Ser	Leu
	130					135					140				
Thr	Ala	Pro	Lys	Asn	Asn	Ile	Tyr	Gly	Ile	Asp	Ala	Pro	Ala	Ala	Trp
	145				150					155					160
Glu	Ile	Ser	Thr	Gly	Ser	Pro	Asp	Ile	Val	Val	Ala	Val	Leu	Asp	Thr
				165					170					175	
Gly	Ile	Leu	Asn	His	Ala	Asp	Leu	Asn	Gly	Arg	Thr	Val	Ala	Gly	Tyr
			180					185					190		
Asp	Phe	Ile	Thr	Asn	Ala	Trp	Met	Ala	Asn	Asp	Gly	Asp	Gly	Arg	Asp
	195						200					205			
Pro	Asn	Pro	Thr	Asp	Pro	Gly	Asp	Trp	Leu	Thr	Thr	Asn	Asp	Ile	Ala
	210					215					220				
Thr	His	Cys	Tyr	Tyr	Ala	Pro	Val	Met	Asp	Ser	Ser	Trp	His	Gly	Thr
	225				230					235					240
His	Val	Ala	Gly	Ile	Ile	Gly	Ala	Ala	Ser	Asn	Asn	Ser	Leu	Gly	Ile
				245					250					255	
Ser	Gly	Ile	Asn	Trp	Thr	Ser	Lys	Ile	Leu	Pro	Val	Arg	Val	Leu	Gly
			260					265					270		
Lys	Cys	Gly	Gly	Tyr	Asp	Ser	Asp	Ile	Ile	Asp	Ala	Ile	Arg	Trp	Ser
		275					280					285			
Ala	Gly	Leu	Pro	Val	Pro	Gly	Ala	Pro	Ala	Asn	Pro	Asn	Pro	Ala	Lys
	290					295					300				
Val	Ile	Asn	Leu	Ser	Leu	Gly	Gly	Pro	Asn	Thr	Cys	Ser	Ser	Val	Met
	305				310					315					320
Gln	Ser	Ala	Ile	Asn	Asp	Ala	Tyr	Glu	Gln	Gly	Val	Thr	Val	Val	Val
				325				330						335	
Ala	Ala	Gly	Asn	Ser	Ser	Met	Asp	Ala	Ala	Gly	Phe	Ser	Pro	Ala	Ser
			340					345					350		
Cys	Ser	Asn	Val	Ile	Ala	Val	Gly	Ala	Thr	Gly	Pro	Thr	Gly	Ser	Arg
		355					360					365			
Ala	Trp	Tyr	Ser	Asn	Tyr	Gly	Ala	Thr	Val	Ala	Ile	Ser	Ala	Pro	Gly
	370					375					380				
Gly	Asp	Gly	Ser	Ser	Ala	Ile	Tyr	Ser	Leu	His	Asn	Ser	Gly	Lys	Thr

## 10336256.txt

```

385      390      395      400
Thr Pro Val Ala Asp Ser Tyr Gln Tyr Met Met Gly Thr Ser Gln Ala
Ala Pro His Val Ser Gly Val Val Ser Leu Leu Tyr Ser Leu Asn Pro
Ala Leu Thr Pro Asp Gln Ala Arg Ala Val Leu Thr Ser Thr Ala Thr
Ala Phe Pro Ala Gly Ser Ser Cys Ala Thr Gly Leu Cys Gly Ala Gly
Ile Leu Asn Ala Gly Gln Ala Val Gln Ala Met Thr Thr Pro Pro Gly
Thr Phe Gln Lys Ile Ala Pro Leu Asn Asn Ala Ala Gly Leu Pro Val
Asn Ser Val Val Leu Glu Trp Ser Pro Ser Ser Gly Ala Ala Ser Tyr
Glu Tyr Cys Tyr Tyr Ala Pro Ala Leu Gln Ala Ala Cys Ala Ser Trp
Ile Ser Ala Gly Ala Ser Thr Lys Ala Thr Leu Thr Asn Leu Leu Pro
Ala Val Thr Tyr Ser Trp Gln Val Arg Ala Val Asn Ala Ala Ile Thr
Ala Thr Asp Ala Asp Phe Val Ala Asn Ser Gly Thr Trp Trp Thr Phe
Ser Thr Glu Ala Val Ser Phe Asn Val Thr Tyr Asn Val Phe Met Pro
Ser Val Val Arg
595

```

<210> 91  
 <211> 1425  
 <212> DNA  
 <213> Unknown

<220>  
 <223> obtained from an environmental sample.

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<400> 91
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aaaagtggaa ttttttataa tttctcagct aaaactctac cttcttttga ttatgatact      120
gcaggaaaaac atattgcacg ggaaaattcc acatggaatg ggaagtatgt tattgggcaa      180
gcggcagaag tgacatattc attcccaact tgggctggta aaaagtttaa tgattttggt      240
gataaaaaatc cctatggatt taattcagcg caaaaagatc atgcaagaca atcttttagat      300
gcatggtctg atattgcaaa tatcaaattt accgaagtgg caccaaattgt aaaatcagat      360
attactttttg gtaattattac tgatccatac ggcaacttcc aagcttatgc aactttgcca      420
aataacctata gttatggccg tgatctttca gggcaagctt ggtttagtga ttattatgat      480
gcaaaaaata caacacctga attaggtaat tatggtcgtt taactattat ccatgaaatt      540
ggatcatgcg ttggtttaat gcaccctggc gattacaacg cagggcaaaa cgtacctgga      600
tatttaaaat ctgactatgc tgaagatagt cgccaatata ctggttatgag ttattgggaa      660
gaatatgaaa caggtgcgca cttccaaggt gcttatgcgg gcgctccttt acttcatgat      720
atttcagcaa tgcaatatct ttatggcgca aataccacaa ccagaacagg tgatgatggt      780
tatggtttta actcaaacac tgggtattaat tattacacgg caacaagtag cagtataaaa      840
ttaatcttct cagtttgagg cagtgcgggg aacgatactt ttgacttctc aggatattat      900
caagatcaag ttattgactt acgtgagggt catttctctg atgttggcgg actacagaaa      960
aacgttttcta ttgcacaagg cgttacaata gaaaatgcaa tcggtggctc tggtaatgat     1020
actatctatg gaaatgatgc tgataatatt ctcatcgggt gtggcggtaa caacatactg     1080
tatggtggcg gtggtcaaga tatattatgg ggtggtacag gtagcaatac ctttgtttat     1140
aaaaagatca ccgactcttt aacctctgct gctgacaaga taatggactt caaatcaggt     1200
attgataaga ttaatttatc agaattaatc gacgatacct ttggccataa attccttaac     1260
tttggtgata attttacagg tcgctcgggt gaagcaacca ttaaataatga tcaatcaaca     1320
aactcaagtg aacttgctat taatgcttat ggatatggat atagccctga tttcaaaatt     1380
gacattgtag gatttgtaa ttacgaaact gacattattg ttttaa      1425

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<210> 92  
 <211> 474  
 <212> PRT  
 <213> Unknown

<220>

10336256.txt

&lt;223&gt; Obtained from an environmental sample.

&lt;400&gt; 92

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Met Gly Ser Ser Leu Leu Lys Lys Ala Val Gly Leu Ser Asn Val Ser
 1      5      10      15
Asp Leu Leu Asp Lys Ser Gly Ile Phe Tyr Asn Phe Ser Ala Lys Thr
 20      25      30
Leu Pro Ser Phe Asp Tyr Asp Thr Ala Gly Lys His Ile Ala Arg Glu
 35      40      45
Asn Ser Thr Trp Asn Gly Lys Tyr Val Ile Gly Gln Ala Ala Glu Val
 50      55      60
Thr Tyr Ser Phe Pro Thr Trp Ala Gly Lys Lys Phe Asn Asp Phe Gly
 65      70      75
Asp Lys Asn Pro Tyr Gly Phe Asn Ser Ala Gln Lys Asp His Ala Arg
 80      85      90
Gln Ser Leu Asp Ala Trp Ser Asp Ile Ala Asn Ile Lys Phe Thr Glu
 100     105
Val Ala Pro Asn Val Lys Ser Asp Ile Thr Phe Gly Asn Ile Thr Asp
 115     120
Pro Tyr Gly Asn Phe Gln Ala Tyr Ala Thr Leu Pro Asn Thr Tyr Ser
 130     135
Tyr Gly Arg Asp Leu Ser Gly Gln Ala Trp Phe Ser Asp Tyr Tyr Asp
 145     150     155
Ala Lys Asn Thr Thr Pro Glu Leu Gly Asn Tyr Gly Arg Leu Thr Ile
 160     165     170
Ile His Glu Ile Gly His Ala Leu Gly Leu Met His Pro Gly Asp Tyr
 175     180     185
Asn Ala Gly Gln Asn Val Pro Gly Tyr Leu Lys Ser Asp Tyr Ala Glu
 190     195     200
Asp Ser Arg Gln Tyr Thr Val Met Ser Tyr Trp Glu Glu Tyr Glu Thr
 205     210     215
Gly Ala His Phe Gln Gly Ala Tyr Ala Gly Ala Pro Leu Leu His Asp
 220     225     230
Ile Ser Ala Met Gln Tyr Leu Tyr Gly Ala Asn Thr Thr Thr Arg Thr
 235     240     245
Gly Asp Asp Val Tyr Gly Phe Asn Ser Asn Thr Gly Ile Asn Tyr Tyr
 250     255     260
Thr Ala Thr Ser Ser Ser Asp Lys Leu Ile Phe Ser Val Trp Asp Ser
 265     270     275
Ala Gly Asn Asp Thr Phe Asp Phe Ser Gly Tyr Tyr Gln Asp Gln Val
 280     285     290
Ile Asp Leu Arg Glu Gly His Phe Ser Asp Val Gly Gly Leu Gln Lys
 295     300     305
Asn Val Ser Ile Ala Gln Gly Val Thr Ile Glu Asn Ala Ile Gly Gly
 310     315     320
Ser Gly Asn Asp Thr Ile Tyr Gly Asn Asp Ala Asp Asn Ile Leu Ile
 325     330     335
Gly Gly Gly Gly Asn Asn Ile Leu Tyr Gly Gly Gly Gly Gln Asp Ile
 340     345     350
Leu Trp Gly Gly Thr Gly Ser Asn Thr Phe Val Tyr Lys Lys Ile Thr
 355     360     365
Asp Ser Leu Thr Ser Ala Ala Asp Lys Ile Met Asp Phe Lys Ser Gly
 370     375     380
Ile Asp Lys Ile Asn Leu Ser Glu Leu Ile Asp Asp Thr Phe Gly His
 385     390     395
Lys Phe Leu Asn Phe Val Asp Asn Phe Thr Gly Arg Ser Gly Glu Ala
 400     405     410
Thr Ile Lys Tyr Asp Gln Ser Thr Asn Ser Ser Glu Leu Ala Ile Asn
 415     420     425
Ala Tyr Gly Tyr Gly Tyr Ser Pro Asp Phe Lys Ile Asp Ile Val Gly
 430     435     440
Phe Val Asn Tyr Glu Thr Asp Ile Ile Val
 445     450     455
465      470

```

&lt;210&gt; 93

&lt;211&gt; 984

&lt;212&gt; DNA

&lt;213&gt; Unknown

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&lt;220&gt;

&lt;223&gt; Obtained from an environmental sample.

&lt;400&gt; 93

atgggacttg	gcttttcgac	tgcattgcag	caacgcgcgc	accacccgat	agccggcatg	60
atcctggccg	tgcccgtttc	aatgattccg	ggttccgggtg	ttctggcgca	ggataaggct	120
cctttcaccc	ccgatcaggg	caggctcttc	ttgaacaacg	ccgccgagaa	ggcggaggaa	180
tcgcagaaga	cgaccaccaa	gacgtttgag	gaattcaaga	aatcgggtcac	caaggagccg	240
ttccagtacg	gcaaatacat	tgtcaatggc	gacaccccca	ttgccaacga	caaggatctt	300
gaggagtctt	acaagcagaa	cgtggagacc	gcggggcctg	tcgccgcaga	gtttgccatc	360
atgaacaagc	tcggcatcga	catcatctgg	aaggacgccg	acaagaagaa	tctcacatac	420
tgcgtgagca	acgccccggc	ggagtccggt	ggattcggaa	atcgctacaa	caccgtcgtg	480
agcgccatgg	ccgacgcgac	caaggcatgg	gaagcagttg	ccgacatcaa	gtttattcac	540
gtgactgccg	aggattcgaa	ctgcacgccg	accaacgaga	gcgtcaaatt	cgacgtcagg	600
ccggtcaatc	tcaacgcata	tctggcgcg	gcatttttcc	ccgacgatgt	gcgcaccgcg	660
cgtaacgtcc	tcacgcgcaa	ctcgtcggtt	gagcttcccg	ccggaggaaa	gctctcgttg	720
atcggcattc	tccgacatga	actcggacac	acgattgggtg	cgcgccatga	gcatacgcgg	780
ccccagtcgg	gaacctgctt	tgaggacaag	gattggagggg	gcgtgaccga	ctacgatgcg	840
ttgtcgggtc	tgcactatcc	gcagtgcac	ggaaagggcg	attggtcgtt	gaccttgacg	900
gtgcaggaca	agaacggcgt	cgcgtgcgtg	tacaaggcgg	ccccgggatt	cgtgatcgac	960
accaagatct	gcaagccgaa	gtag				984

&lt;210&gt; 94

&lt;211&gt; 327

&lt;212&gt; PRT

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; Obtained from an environmental sample.

&lt;221&gt; SIGNAL

&lt;222&gt; (1)...(36)

&lt;400&gt; 94

Met	Gly	Leu	Gly	Phe	Ser	Thr	Ala	Leu	Gln	Gln	Arg	Ala	His	His	Pro
1				5				10					15		
Ile	Ala	Gly	Met	Ile	Leu	Ala	Val	Ala	Val	Ser	Met	Ile	Pro	Gly	Ser
		20						25					30		
Gly	Val	Leu	Ala	Gln	Asp	Lys	Ala	Pro	Phe	Thr	Pro	Asp	Gln	Gly	Arg
		35					40					45			
Leu	Phe	Leu	Asn	Asn	Ala	Ala	Glu	Lys	Ala	Arg	Glu	Ser	Gln	Lys	Thr
	50					55					60				
Thr	Thr	Lys	Thr	Phe	Glu	Glu	Phe	Lys	Lys	Ser	Val	Thr	Lys	Glu	Pro
	65				70					75					80
Phe	Gln	Tyr	Gly	Lys	Tyr	Ile	Val	Asn	Gly	Asp	Thr	Pro	Ile	Ala	Asn
			85					90					95		
Asp	Lys	Asp	Leu	Glu	Glu	Phe	Tyr	Lys	Gln	Asn	Val	Glu	Thr	Ala	Gly
			100					105					110		
Leu	Val	Ala	Ala	Glu	Phe	Ala	Ile	Met	Asn	Lys	Leu	Gly	Ile	Asp	Ile
		115					120					125			
Ile	Trp	Lys	Asp	Ala	Asp	Lys	Lys	Asn	Leu	Thr	Tyr	Cys	Val	Ser	Asn
	130					135					140				
Ala	Pro	Ala	Glu	Ser	Gly	Gly	Phe	Gly	Asn	Arg	Tyr	Asn	Thr	Val	Val
	145				150					155					160
Ser	Ala	Met	Ala	Asp	Ala	Thr	Lys	Ala	Trp	Glu	Ala	Val	Ala	Asp	Ile
			165						170					175	
Lys	Phe	Ile	His	Val	Thr	Ala	Glu	Asp	Ser	Asn	Cys	Thr	Pro	Thr	Asn
			180					185					190		
Glu	Ser	Val	Lys	Phe	Asp	Val	Arg	Pro	Val	Asn	Leu	Asn	Ala	Tyr	Leu
		195					200					205			
Ala	Arg	Ala	Phe	Phe	Pro	Asp	Val	Arg	Thr	Ala	Arg	Asn	Val	Leu	
	210					215				220					
Ile	Asp	Asn	Ser	Ser	Phe	Glu	Leu	Pro	Ala	Gly	Gly	Lys	Leu	Ser	Leu
	225				230					235					240
Ile	Gly	Ile	Leu	Arg	His	Glu	Leu	Gly	His	Thr	Ile	Gly	Ala	Arg	His
			245						250					255	
Glu	His	Thr	Arg	Pro	Gln	Ser	Gly	Thr	Cys	Phe	Glu	Asp	Lys	Asp	Trp

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260  
 Arg Gly Val Thr Asp Tyr Asp Ala Leu Ser Val Met His Tyr Pro Gln  
 275  
 Cys Asn Gly Lys Gly Asp Trp Ser Leu Thr Leu Thr Val Gln Asp Lys  
 290  
 Asn Gly Val Ala Cys Val Tyr Lys Ala Ala Pro Gly Phe Val Ile Asp  
 305  
 Thr Lys Ile Cys Lys Pro Lys  
 325

<210> 95  
 <211> 1806  
 <212> DNA  
 <213> Unknown

<220>  
 <223> obtained from an environmental sample.

<400> 95  
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 actgtggcag cagcagatcg gggttattatt caggctcgaca atgccaacaa aggtatagtc 120  
 accgcattaa caaaacagct gggtggcgac gtaaaagtag atgcagatgg ttttatcgct 180  
 gctcagttca atggtaaact tgttgatgaa atcaaaggta ttctgaaaaa ccctcatatc 240  
 aaactgattg aagaagattt agtacgtaaa ccaatggcgt tatttaatga cgacgctggg 300  
 gatccaatgc aacaacaaat cacaccttat gctgtgtatc aatctcaggc caatcagggt 360  
 caatttaacc ctggcgaggg tatcaaagtc tgtgtcattg actcagggtt agaccagtct 420  
 aaccctgatt ttaactgggg cagcatcacg ggcgacaacg attcaggcac aggcaactgg 480  
 aatgtcaacg gtggcccaca cggcactcac gtcgccggta ccatagggtg ggcagacaac 540  
 ggttttgggt tgataggtat ggcccctggc gtagctatgc atatcatcaa agtatttaac 600  
 gctgaagggt ggggttattc gtcagatctg gcttatgccg cacaaaaatg taaaaacgca 660  
 ggctcagaca ttatcagcat gagcttaggc ggtgggtggg ccaataccac tgaatccaac 720  
 gcttttaaaa cctttaccga cgctgggtgg ttagttatag ccgcagcagg taacgacggc 780  
 aacaatgtgc gctcttaccg ggctgggttac cttctgtca tgatgatagg agccaacgac 840  
 aataacaaca atatcgcaga cttctcccaa ttcccaagct gtacagccaa cggcaaaaaca 900  
 gatgagacta ttgtgtgga agccacagct ggtgggtgtag acaccttgct cacctaccct 960  
 gccgatatgg caaccagcgc caccttgagt gccaacggta ctccttatgc cacctctgcg 1020  
 atggaaaatc cgggttcagc cagtgcagct acattcttta tgggcacagc ggaaactgtc 1080  
 aactcaggcg cagccggtaa gatttgtatg attgaccgtg gtgtgatctc tttccacgac 1140  
 aaagtgaaaa actgccaata ctctgggtgg gtaggtgctg tcatcattaa caacacagct 1200  
 ggcattgtgt acggcacttt ggtgaagggt tctgctaaca ctacatcaat ccctgcagta 1260  
 ggtgcggttt ttgaagacag gactgcgctg ttggccgcta ctactgcac catcaacatc 1320  
 ggcaccagcg attatgggtc gatgagcgga acttctatgg caacgccggc tgtttcagg 1380  
 attgcagctc tgggtgtgtc aaatcacccg ggctgtactg gtactcaaat ccgtaatgcg 1440  
 ttaaaagcga cggcaaaaaga cgcaggtgct ctgggcaaa atgtgtactt cggttatggt 1500  
 attgtgcagg ccgtgctgc gcatcagtac ctgacgacca atgggtgtgg tgggtggcact 1560  
 acaactccgg gcatcagcct gactttacag ggcgtatcca gcaaaggtaa acgttatgtc 1620  
 gacctgacat gggccagtg caccaccagc tcagttgata tttaccgcaa caacgtcaaa 1680  
 gtactgacca caaccaatga cggcgacat cgtgatggcc cgttaaaccg tggcagctat 1740  
 agttataaag tctgtgaagc ggcaagcacc accaagtgtg gtgccagcac ttctatcagt 1800  
 ctgtaa 1806

<210> 96  
 <211> 601  
 <212> PRT  
 <213> Unknown

<220>  
 <223> obtained from an environmental sample.

<221> SIGNAL  
 <222> (1)...(24)

<400> 96  
 Met Lys Ile Asn Lys Leu Ser Lys Ile Ser Phe Ala Thr Phe Met Ala  
 1 5 10 15  
 Leu Gly Cys Thr Thr Val Ala Ala Ala Asp Arg Val Ile Ile Gln Val  
 20 25 30  
 Asp Asn Ala Asn Lys Gly Ile Val Thr Ala Leu Thr Lys Gln Leu Gly

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Gly Asp Val Lys Val Asp Ala Asp Gly Phe Ile Ala Ala Gln Phe Asn  
 50 55 60  
 Gly Lys Ser Val Asp Glu Ile Lys Gly Ile Leu Lys Asn Pro His Ile  
 65 70 75 80  
 Lys Leu Ile Glu Glu Asp Leu Val Arg Lys Pro Met Ala Leu Phe Asn  
 85 90 95  
 Asp Asp Ala Gly Asp Pro Met Gln Gln Ile Thr Pro Tyr Ala Val  
 100 105 110  
 Tyr Gln Ser Gln Ala Asn Gln Val Gln Phe Asn Pro Gly Ala Gly Ile  
 115 120 125  
 Lys Val Cys Val Ile Asp Ser Gly Leu Asp Gln Ser Asn Pro Asp Phe  
 130 135 140  
 Asn Trp Gly Ser Ile Thr Gly Asp Asn Asp Ser Gly Thr Gly Asn Trp  
 145 150 155 160  
 Asn Val Asn Gly Gly Pro His Gly Thr His Val Ala Gly Thr Ile Gly  
 165 170 175  
 Ala Ala Asp Asn Gly Phe Gly Val Ile Gly Met Ala Pro Gly Val Ala  
 180 185 190  
 Met His Ile Ile Lys Val Phe Asn Ala Glu Gly Trp Gly Tyr Ser Ser  
 195 200 205  
 Asp Leu Ala Tyr Ala Ala Gln Lys Cys Lys Asn Ala Gly Ser Asp Ile  
 210 215 220  
 Ile Ser Met Ser Leu Gly Gly Gly Gly Ala Asn Thr Thr Glu Ser Asn  
 225 230 235 240  
 Ala Phe Lys Thr Phe Thr Asp Ala Gly Gly Leu Val Ile Ala Ala Ala  
 245 250 255  
 Gly Asn Asp Gly Asn Asn Val Arg Ser Tyr Pro Ala Gly Tyr Pro Ser  
 260 265 270  
 Val Met Met Ile Gly Ala Asn Asp Asn Asn Asn Ile Ala Asp Phe  
 275 280 285  
 Ser Gln Phe Pro Ser Cys Thr Ala Asn Gly Lys Thr Asp Glu Thr Ile  
 290 295 300  
 Cys Val Glu Ala Thr Ala Gly Gly Val Asp Thr Leu Ser Thr Tyr Pro  
 305 310 315 320  
 Ala Asp Met Ala Thr Ser Ala Thr Leu Ser Ala Asn Gly Thr Pro Tyr  
 325 330 335  
 Ala Thr Ser Ala Met Glu Asn Pro Gly Ser Ala Ser Ala Ala Thr Phe  
 340 345 350  
 Phe Met Gly Thr Ala Glu Thr Val Asn Ser Gly Ala Ala Gly Lys Ile  
 355 360 365  
 Cys Met Ile Asp Arg Gly Val Ile Ser Phe His Asp Lys Val Lys Asn  
 370 375 380  
 Cys Gln Asn Ser Gly Gly Val Gly Ala Val Ile Ile Asn Asn Thr Ala  
 385 390 395 400  
 Gly Met Leu Tyr Gly Thr Leu Gly Glu Gly Ser Ala Asn Thr Thr Ser  
 405 410 415  
 Ile Pro Ala Val Gly Ala Ala Phe Glu Asp Arg Thr Ala Leu Leu Ala  
 420 425 430  
 Ala Thr Thr Ala Ser Ile Asn Ile Gly Thr Ser Asp Tyr Gly Leu Met  
 435 440 445  
 Ser Gly Thr Ser Met Ala Thr Pro Ala Val Ser Gly Ile Ala Ala Leu  
 450 455 460  
 Val Trp Ser Asn His Pro Gly Cys Thr Gly Thr Gln Ile Arg Asn Ala  
 465 470 475 480  
 Leu Lys Ala Thr Ala Lys Asp Ala Gly Ala Ala Gly Lys Asp Val Tyr  
 485 490 495  
 Phe Gly Tyr Gly Ile Val Gln Ala Ala Ala His Gln Tyr Leu Thr  
 500 505 510  
 Thr Asn Gly Cys Gly Gly Gly Thr Thr Thr Pro Gly Ile Ser Leu Thr  
 515 520 525  
 Leu Gln Gly Val Ser Ser Lys Gly Lys Arg Tyr Val Asp Leu Thr Trp  
 530 535 540  
 Ala Ser Ala Thr Thr Ser Ser Val Asp Ile Tyr Arg Asn Asn Val Lys  
 545 550 555 560  
 Val Leu Thr Thr Thr Asn Asp Gly Ala His Arg Asp Gly Pro Leu Asn  
 565 570 575  
 Arg Gly Ser Tyr Ser Tyr Lys Val Cys Glu Ala Ala Ser Thr Thr Lys

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Cys Ser Ala 580 Ser Thr Ser Ile Ser 585 Leu 590  
595 600

<210> 97  
<211> 681  
<212> DNA  
<213> Unknown

<220>  
<223> obtained from an environmental sample.

<400> 97  
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acgcccggca cgcgcattccc cagccacggc acggatatgc tcggccagcg ctacgcttat 120  
gattttatcg gcgtagcgcc aggaggcagc agcctgaagt tctaccgcat gagcccaactg 180  
cgctatttgc tgttcggcgc gcgcctggcg gactgctacg gctggggcca gccgatctac 240  
gcggcggcgg acggtacggg ggcgacggc ggccgagcg caaccgggtg 300  
cacctcgccc gggatctgtt catgctcttt aagaacggcc tgtcgatccg ctcaaccgag 360  
gggctcgacc tgcgcattcct gaccggcaat tacgtcatcg tagagagcag cgcgggctat 420  
atgctctacg cccacgcgca gaacggctcg gtgcgcgtcg cgccgggcga gaagggtgacc 480  
accgggcagc acctggcgaa tgtaggccat tcgggcaatt ccaccgcgcc ccacctgcac 540  
ttccatatca tggatcagct cgacccgtgg aaagcgcagg gcatcgccctg ctgtttccgc 600  
gaatatgagg tctggcagaa cggcggctgg cagccggtgc gcaacggcat cccaccgcc 660  
gccgaacgca tccggcggtg g 681

<210> 98  
<211> 226  
<212> PRT  
<213> Unknown

<220>  
<223> obtained from an environmental sample.

<400> 98  
Met Met Asp Asn Pro Val Val Val Asp Phe Pro Leu Arg Gly Glu Trp  
1 5 10 15  
Asn Ala Pro Asn Thr Pro Gly Thr Arg Ile Pro Ser His Gly Thr Asp  
20 25 30  
Met Leu Gly Gln Arg Tyr Ala Tyr Asp Phe Ile Gly Val Ala Pro Gly  
35 40 45  
Gly Ser Ser Leu Lys Phe Tyr Arg Met Ser Pro Leu Arg Tyr Leu Leu  
50 55 60  
Phe Gly Ala Arg Leu Ala Asp Cys Tyr Gly Trp Gly Gln Pro Ile Tyr  
65 70 75 80  
Ala Ala Ala Asp Gly Thr Val Ala Gln Ala Gly Asp Gly Trp Pro Glu  
85 90 95  
Arg Asn Pro Val His Leu Ala Arg Asp Leu Phe Met Leu Phe Lys Asn  
100 105 110  
Gly Leu Ser Ile Arg Ser Thr Glu Gly Leu Asp Leu Arg Ile Leu Thr  
115 120 125  
Gly Asn Tyr Val Ile Val Glu Ser Ser Ala Gly Tyr Met Leu Tyr Ala  
130 135 140  
His Ala Gln Asn Gly Ser Val Arg Val Ala Pro Gly Glu Lys Val Thr  
145 150 155 160  
Thr Gly Gln His Leu Ala Asn Val Gly His Ser Gly Asn Ser Thr Ala  
165 170 175  
Pro His Leu His Phe His Ile Met Asp Gln Leu Asp Pro Trp Lys Ala  
180 185 190  
Gln Gly Ile Ala Cys Cys Phe Arg Glu Tyr Glu Val Trp Gln Asn Gly  
195 200 205  
Gly Trp Gln Pro Val Arg Asn Gly Ile Pro Thr Ala Glu Arg Ile  
210 215 220  
Arg Arg  
225

<210> 99  
<211> 1944

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&lt;212&gt; DNA

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; Obtained from an environmental sample.

&lt;400&gt; 99

atggcctttc	ttgctgccc	tccgaaggac	gcgctatttt	cctcgcagtg	gcattctttcc	60
tcgttgcggt	cggatgtttc	gctgaatctt	cgagacgttt	ggaccgacta	caaggggtgct	120
gggattaggc	tagcggtcct	tgatgacggc	ttcgaccgcc	atcatgctga	cctgcgtgca	180
aactacaacg	tcaacatcga	ccgtgatattt	gtcggccgtg	gtgactttga	cgcgattcat	240
gagcgcgga	actggcatgg	tactgctgtg	atgggcgtgg	ccggcgctga	cgacaatgga	300
gttgggggta	caggtgttgc	cacagacgtg	accctgatgg	gcctgcgtat	cggctttggc	360
tctgccggca	atccggcgca	gtacgcggcg	gctctcagcg	agagcgcaaa	agctgacgtt	420
gcaaacagtt	catggggggt	tggtggcttc	ttcattgaca	attttgatag	tcatcatttc	480
cgtgccgccc	aaagcgtct	gaagttttcg	gttgacaatg	gccgtgggtg	ccttggtact	540
gttcaagttt	ttgctgctgg	taactcgcga	gcgtcgggtg	acgacgtgaa	cttcacacaac	600
ttccagaatt	caatctatac	gatggcagtg	ggtgcgacgg	acaccgccgg	tcgggtagct	660
tcattctcga	cgccgggctg	tgcgcttcat	gtctctgcgc	cgggtgtgtc	gattctgaca	720
actgacgtct	cgggccgtga	cggctatagc	tctggcaatg	aggcggtggg	gcaaggcacg	780
tcctttgccc	ccccgtcggt	tgaggcatt	gtctcactca	tgctcgatgc	taatgcccgt	840
cttggatggc	gagatgttca	agagatctta	gcttattctg	cgaaggagac	gacagccggg	900
atttccgatc	cattcttgat	cacgaataag	gcagacaact	ggaatgggtg	cggccttacc	960
catagcaaga	attatggcct	cggtctgggt	gatgcccatg	ctgcggtccg	ccttgccgag	1020
acttggaccg	agcagcagac	ttcgcacaa	atgatgactg	catcttttgg	agctgcgccc	1080
cgggcaacgc	tgccgggacgc	aggccgttgg	gagacgacgt	tcacgatcaa	ccgtgacatc	1140
accattgacc	gtgttgagct	tgagattgat	ctcaagcaca	actggattgg	agatctccgc	1200
ataggtcttg	tgtagccga	aggcacaacg	agttgggttg	tcgatcgtcc	gggctgtggc	1260
cctggcgccg	cggggaaacg	ttcggggcta	aaaaatat	ggttcgactt	cacgaccagt	1320
cagttctggg	gcgaggaagc	gcgtggtacc	tggaagctgg	tcacgagga	cgtaagcgt	1380
ggcaatat	gtcggcttga	ctggttccaa	gtcaacatct	ttggcgatcg	cccagcaac	1440
gatgactctt	acatctacac	caacgagttt	gcccgcctcg	gcgctcaatc	cggtcgtacg	1500
gtgatcaacg	acgcccgaag	gcgtgatgcc	atcaacgcct	cagcggtaac	cagcgatagc	1560
gttcttgatc	ttctccacgg	ctcgatcatt	gccggccggc	aggtttctta	cggggctggc	1620
accatcatcg	agcgggcttt	tgctggtgac	ggcaacgacc	aagtcctgtg	caacaccatg	1680
gataaccttc	ttcggggcgg	tcgcggcaat	gatgtccttg	agggtcgcgg	tggttccgat	1740
atcttcgcct	ttggcgtagc	ttcgggacgc	gatataattc	tagactttga	cgcgaaacgac	1800
cgaattctcc	taacggacgg	ggtgagtgtc	cgagctcttt	cgggcagcgt	cgccacgctc	1860
tccgacgggt	tcaccattac	tgacgctaac	ggttggcag	ggcagatgtc	caatttctac	1920
caaggcgatt	tgctctttgc	ttga				1944

&lt;210&gt; 100

&lt;211&gt; 647

&lt;212&gt; PRT

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; Obtained from an environmental sample.

&lt;400&gt; 100

Met	Ala	Phe	Leu	Ala	Arg	Pro	Lys	Asp	Ala	Leu	Phe	Ser	Ser	Gln
1				5				10					15	
Trp	His	Leu	Ser	Ser	Leu	Arg	Ser	Val	Ser	Leu	Asn	Leu	Arg	Asp
			20					25				30		
Val	Trp	Thr	Asp	Tyr	Lys	Gly	Ala	Gly	Ile	Arg	Leu	Ala	Val	Leu
			35				40					45		
Asp	Gly	Phe	Asp	Arg	His	His	Ala	Asp	Leu	Arg	Ala	Asn	Tyr	Asn
			50			55					60			
Asn	Ile	Asp	Arg	Asp	Phe	Val	Gly	Arg	Gly	Asp	Phe	Asp	Ala	Ile
			65			70				75				80
Glu	Arg	Gly	Asn	Trp	His	Gly	Thr	Ala	Val	Met	Gly	Val	Ala	Gly
			85						90				95	
Asp	Asp	Asn	Gly	Val	Gly	Val	Thr	Gly	Val	Ala	Thr	Asp	Val	Thr
			100					105					110	
Met	Gly	Leu	Arg	Ile	Gly	Phe	Gly	Ser	Ala	Gly	Asn	Pro	Ala	Gln
			115				120					125		
Ala	Ala	Ala	Leu	Ser	Glu	Ser	Ala	Lys	Ala	Asp	Val	Ala	Asn	Ser
			130			135						140		

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Trp Gly Phe Gly Gly Phe Phe Ile Asp Asn Phe Asp Ser His His Phe  
 145 Arg Ala Ala Glu Ser 150 Ala Leu Lys Phe Ser 155 Val Asp Asn Gly Arg 160  
 Gly Leu Gly Thr Val Gln Val Phe Ala Ala Gly Asn Ser Arg Ala Ser  
 165 170 175  
 Gly Asp Asp Val Asn Phe His Asn Phe Gln Asn Ser Ile Tyr Thr Met  
 180 185 190 200 205  
 Ala Val Gly Ala Thr Asp Thr Ala Gly Arg Val Ala Ser Phe Ser Thr  
 210 215 220  
 Pro Gly Val Ala Leu His Val Ser Ala Pro Gly Val Ser Ile Leu Thr  
 225 230 235 240  
 Thr Asp Val Ser Gly Arg Asp Gly Tyr Ser Ser Gly Asn Glu Ala Trp  
 245 250 255  
 Val Gln Gly Thr Ser Phe Ala Ala Pro Ser Val Ala Gly Ile Val Ser  
 260 265 270  
 Leu Met Leu Asp Ala Asn Ala Arg Leu Gly Trp Arg Asp Val Gln Glu  
 275 280 285  
 Ile Leu Ala Tyr Ser Ala Lys Glu Thr Thr Ala Gly Ile Ser Asp Pro  
 290 295 300  
 Phe Leu Ile Thr Asn Lys Ala Asp Asn Trp Asn Gly Gly Gly Leu Thr  
 305 310 315 320  
 His Ser Lys Asn Tyr Gly Phe Gly Leu Val Asp Ala His Ala Ala Val  
 325 330 335  
 Arg Leu Ala Glu Thr Trp Thr Glu Gln Thr Ser His Asn Met Met  
 340 345 350  
 Thr Ala Ser Phe Gly Ala Ala Pro Arg Ala Thr Leu Arg Asp Ala Gly  
 355 360 365  
 Arg Trp Glu Thr Thr Phe Thr Ile Asn Arg Asp Ile Thr Ile Asp Arg  
 370 375 380  
 Val Glu Leu Glu Ile Asp Leu Lys His Asn Trp Ile Gly Asp Leu Arg  
 385 390 395 400  
 Ile Gly Leu Val Ser Ala Glu Gly Thr Thr Ser Trp Leu Val Asp Arg  
 405 410 415  
 Pro Gly Val Ala Pro Gly Ala Ala Gly Asn Gly Ser Gly Leu Lys Asn  
 420 425 430  
 Ile Trp Phe Asp Phe Thr Thr Ser Gln Phe Trp Gly Glu Glu Ala Arg  
 435 440 445  
 Gly Thr Trp Lys Leu Val Ile Glu Asp Val Lys Arg Gly Asn Ile Gly  
 450 455 460  
 Arg Leu Asp Trp Phe Gln Val Asn Ile Phe Gly Asp Arg Pro Ser Asn  
 465 470 475 480  
 Asp Asp Ser Tyr Ile Tyr Thr Asn Glu Phe Ala Arg Leu Gly Ala Gln  
 485 490 495  
 Ser Gly Arg Thr Val Ile Asn Asp Ala Gln Gly Arg Asp Ala Ile Asn  
 500 505 510  
 Ala Ser Ala Val Thr Ser Asp Ser Val Leu Asp Leu Leu His Gly Ser  
 515 520 525  
 Ile Ile Ala Gly Arg Gln Val Ser Tyr Gly Ala Gly Thr Ile Ile Glu  
 530 535 540  
 Arg Ala Phe Ala Gly Asp Gly Asn Asp Gln Val Arg Gly Asn Thr Met  
 545 550 555 560  
 Asp Asn Leu Leu Trp Gly Gly Arg Gly Asn Asp Val Leu Glu Gly Arg  
 565 570 575  
 Gly Gly Ser Asp Ile Phe Ala Phe Gly Val Arg Ser Gly Arg Asp Ile  
 580 585 590  
 Ile Leu Asp Phe Asp Ala Asn Asp Arg Ile Leu Leu Thr Asp Gly Val  
 595 600 605  
 Ser Val Arg Ser Leu Ser Gly Ser Val Ala Thr Leu Ser Asp Gly Ala  
 610 615 620  
 Thr Ile Thr Ala Ala Asn Gly Trp Gln Trp Gln Met Ser Asn Phe Tyr  
 625 630 635 640  
 Gln Gly Asp Leu Leu Phe Ala

<210> 101  
 <211> 1125  
 <212> DNA

10336256.txt

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; Obtained from an environmental sample.

&lt;400&gt; 101

gtgctgagaa	aaaccttggt	cgctcgtcgtt	gcggcgctgt	tggcctcggc	tcaacccgctc	60
gcagcgcaac	gcatggagaa	cggaacgta	cgcccggtga	acgacggcat	agtgcaggaa	120
gtcagcaagg	tgctgcagcc	gctaagcggg	cagccgcaat	cgccaagat	gcacgtcgac	180
agcgcggggg	cgaagagcat	tcgctgcagg	atcggcgttg	ccagcaatgc	ggcgccacgc	240
tcggattaca	ctgtcgccgt	cagggatcga	aacggcgggc	tgggtggcgcg	atacccggct	300
gcggagcttc	gcgccaagcc	ggtctggagt	cctcctgtcc	cgggcgccctc	ggtcgagggtc	360
gaggtcgagg	tcgagggcgc	ggcggcggat	acggccggca	ttgcggtcgc	ggtgaccggc	420
atcatcgggc	agcgcacgcc	ggcgatccg	atgctctcgg	tgctgggcga	tacgttcgac	480
ctggaaccga	tcgagtcggt	tcggctggaa	aagcccagaa	tattcaaggc	cgggctcgcg	540
gtagccaagc	tgatgctggt	gcgtgacggc	aagtctctgg	cgtgcacggg	cttcatgac	600
gacgatgatc	gcatgctgac	caacgagcat	tgcatcaata	gccaggccat	ctgcgacagc	660
gcagtcgcac	tgttcggata	cgactcgaac	gcgggtatga	cgagcgacat	ggtgcgcgag	720
cagtcgcgcc	cctgtctgga	attcaagagc	atggacgaga	agctcgacgt	agcgatgatt	780
cggttgggcca	acagcccggg	caagcgggtg	ggacgactga	agctcgctgt	cgctgcgccc	840
gacgaactgt	cgatgctgat	ccaccatccc	aatggagatc	cgaagtatgt	cacgcgagag	900
gactgcttcg	ttggcaagct	gcccgttgac	ggcgcgccca	aggacaccga	tttcagccac	960
cggtgcgaca	cgatgggagg	tagctcgggc	tcgccggtcc	tgagccgaag	gagcctggaa	1020
gtcatcggct	tgcacacct	tggcatcgac	ctcgtgatc	cggttggcg	ggatcaaaat	1080
cgcgcggtgc	gaatggagct	catccgcgcc	gcgctggggc	tttga		1125

&lt;210&gt; 102

&lt;211&gt; 374

&lt;212&gt; PRT

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; Obtained from an environmental sample.

&lt;221&gt; SIGNAL

&lt;222&gt; (1)...(22)

&lt;400&gt; 102

Met	Leu	Arg	Lys	Thr	Leu	Phe	Val	Val	Val	Ala	Ala	Leu	Leu	Ala	Ser
1				5					10					15	
Ala	Gln	Pro	Val	Ala	Ala	Gln	Arg	Met	Glu	Asn	Gly	Asn	Val	Arg	Pro
		20						25					30		
Val	Asn	Asp	Gly	Ile	Val	Gln	Glu	Val	Ser	Lys	Val	Leu	Gln	Pro	Leu
		35					40					45			
Ser	Gly	Gln	Pro	Gln	Ser	Ala	Lys	Met	His	Val	Asp	Ser	Ala	Gly	Ala
	50					55				60					
Lys	Ser	Ile	Arg	Val	Arg	Ile	Gly	Val	Ala	Ser	Asn	Ala	Ala	Pro	Arg
	65				70					75				80	
Ser	Asp	Tyr	Thr	Val	Ala	Val	Arg	Asp	Arg	Asn	Gly	Gly	Leu	Val	Ala
			85						90					95	
Arg	Tyr	Pro	Ala	Ala	Glu	Leu	Arg	Ala	Lys	Pro	Val	Trp	Ser	Pro	Pro
			100					105					110		
Val	Pro	Gly	Ala	Ser	Val	Glu	Val	Glu	Val	Glu	Val	Glu	Ala	Ala	Ala
		115					120					125			
Ala	Asp	Thr	Ala	Gly	Ile	Ala	Val	Ala	Val	Thr	Gly	Ile	Ile	Gly	Gln
	130					135					140				
Arg	Thr	Pro	Gly	Asp	Pro	Leu	Ser	Val	Leu	Gly	Asp	Thr	Phe	Asp	
	145				150				155					160	
Leu	Glu	Pro	Ile	Glu	Ser	Phe	Arg	Leu	Glu	Lys	Pro	Glu	Ile	Phe	Lys
			165						170					175	
Ala	Gly	Leu	Ala	Val	Ala	Lys	Leu	Met	Leu	Val	Arg	Asp	Gly	Lys	Ser
			180					185					190		
Leu	Ala	Cys	Thr	Gly	Phe	Met	Ile	Asp	Asp	Asp	Arg	Met	Leu	Thr	Asn
		195					200					205			
Glu	His	Cys	Ile	Asn	Ser	Gln	Ala	Ile	Cys	Asp	Ser	Ala	Val	Ala	Leu
	210					215					220				
Phe	Gly	Tyr	Asp	Ser	Asn	Ala	Gly	Met	Thr	Ser	Asp	Met	Val	Arg	Glu
	225				230					235					240

## 10336256.txt

Gln Ser Ala Ala Cys Leu Glu Phe Lys Ser Met Asp Glu Lys Leu Asp  
 Val Ala Met Ile Arg Leu Ala Asn Ser Pro Gly Lys Arg Trp Gly Arg  
 Leu Lys Leu Ala Val Ala Ala Pro Asp Glu Leu Ser Ile Val Ile His  
 His Pro Asn Gly Asp Pro Lys Tyr Val Thr Arg Glu Asp Cys Phe Val  
 Gly Lys Leu Pro Val Asp Gly Arg Ala Lys Asp Thr Asp Phe Ser His  
 Arg Cys Asp Thr Met Gly Gly Ser Ser Gly Ser Pro Val Leu Ser Arg  
 Arg Ser Leu Glu Val Ile Gly Leu His His Leu Gly Ile Asp Leu Ala  
 Asp Pro Ala Trp Arg Asp Gln Asn Arg Ala Val Arg Met Glu Leu Ile  
 Arg Ala Ala Leu Gly Leu

<210> 103  
 <211> 897  
 <212> DNA  
 <213> Unknown

<220>  
 <223> Obtained from an environmental sample.

<400> 103  
 atgaaagagt taaaggtaat gcaaaaacat caagaccaga tttttaacct gccaaatata 60  
 gtcggtgtag gtatcggctg caaagtgaag gatggtatta tttctcaaga acctgccatt 120  
 gtcgcttttg ttgttaagaa agtggacaaa gcttatttgc cggaagcaag catggttccg 180  
 gctgaattgg atggtgtagt taccgatgtc agagaagtag gggaaattaa acttcttggg 240  
 cgtaccgata aacaacggcc ggcatgtcct ggcacagca ttggtcatta taaaattacc 300  
 gccggtactt tcggcgcaat gggttacgac aatcaaacag gtgatccgct tattctgtca 360  
 aataatcacg ttctggccaa tgaactaat gggcgtgacg gcagaagcgc tattggtgat 420  
 gcaatatatc aaccgggtag ttatgacgga ggtacgtcgg cagataccat tgcccacttg 480  
 caccgggttg taccagtta ttacggttca agttcgaag cgaatctggt tgactgtgca 540  
 gtagctaagc cgataagcaa tgatcctatc atcgacgaga tcatggaaat tggcaaagt 600  
 gccggggtcg ctcaggccga ggtaggtatg aatgtcaaga aaagcggccg gactaccgga 660  
 ctaacaacag gactatcga cactgtgcat accacagtaa aggtgaacat gggcgtcgg 720  
 acagctactt tcaaagatca aatcgtggcc ggtgcaatgt cccagggcgg cgacagcggg 780  
 tcattgggtg ttaatgagca aaacgaagcg ataggattat tgtttgccgg ttctgattat 840  
 accactatat tcaatgatat ccagaatgtt ttgaacgcac tgaaggttaag gttttag 897

<210> 104  
 <211> 298  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Obtained from an environmental sample.

<400> 104  
 Met Lys Glu Leu Lys Val Met Gln Lys His Gln Asp Gln Ile Phe Asn  
 1 5 10 15  
 Leu Pro Asn Ile Val Gly Val Gly Ile Gly Cys Lys Val Lys Asp Gly  
 20 25 30  
 Ile Ile Ser Gln Glu Pro Ala Ile Val Ala Leu Val Val Lys Lys Val  
 35 40 45  
 Asp Lys Ala Tyr Leu Pro Glu Ala Ser Met Val Pro Ala Glu Leu Asp  
 50 55 60  
 Gly Val Val Thr Asp Val Arg Glu Val Gly Glu Ile Lys Leu Leu Gly  
 65 70 75 80  
 Arg Thr Asp Lys Gln Arg Pro Ala Cys Pro Gly Ile Ser Ile Gly His  
 85 90 95  
 Tyr Lys Ile Thr Ala Gly Thr Phe Gly Ala Met Val Tyr Asp Asn Gln  
 100 105 110  
 Thr Gly Asp Pro Leu Ile Leu Ser Asn Asn His Val Leu Ala Asn Val

## 10336256.txt

115 120 125  
 Thr Asn Gly Arg Asp Gly Arg Ser Ala Ile Gly Asp Ala Ile Tyr Gln  
 130 135 140  
 Pro Gly Ser Tyr Asp Gly Gly Thr Ser Ala Asp Thr Ile Ala His Leu  
 145 150 155 160  
 His Arg Phe Val Pro Val Tyr Tyr Gly Ser Ser Ser Lys Ala Asn Leu  
 165 170 175  
 Val Asp Cys Ala Val Ala Lys Pro Ile Ser Asn Asp Leu Ile Ile Asp  
 180 185 190  
 Glu Ile Met Glu Ile Gly Lys Val Ala Gly Val Ala Gln Ala Glu Val  
 195 200 205  
 Gly Met Asn Val Lys Lys Ser Gly Arg Thr Thr Gly Leu Thr Thr Gly  
 210 215 220  
 Thr Ile Asp Thr Val His Thr Thr Val Lys Val Asn Met Gly Val Gly  
 225 230 235 240  
 Thr Ala Thr Phe Lys Asp Gln Ile Val Ala Gly Ala Met Ser Gln Gly  
 245 250 255  
 Gly Asp Ser Gly Ser Leu Val Leu Asn Glu Gln Asn Glu Ala Ile Gly  
 260 265 270  
 Leu Leu Phe Ala Gly Ser Asp Tyr Thr Thr Ile Phe Asn Asp Ile Gln  
 275 280 285  
 Asn Val Leu Asn Ala Leu Lys Val Arg Phe  
 290 295

<210> 105  
 <211> 2091  
 <212> DNA  
 <213> Unknown

<220>  
 <223> obtained from an environmental sample.

<400> 105  
 gtgagcgcgc tgcacgtctg gcgccagtag acctgggttc tggaacaagc caagacccag 60  
 caggagtgcg atgaacccca gaccgcgtcag gaaggggaca agaccatcag ctatcgggtg 120  
 tgccgtcaga ccctgcccgc cgccagcgaa gtgcaggtgg tcttgaagga caccggctat 180  
 caatacccg tggggggcag cgaatggcag accctgcccg aaacaaccga gtggcaggag 240  
 aaccgggtgc tcaaccgccc catcgtgctg gccagcaagg aagagcagct cgactgtcgc 300  
 cgtgccgacg gccgcgcctg ttccgagccg gatctgcccg gcaccgaact gctggacgcc 360  
 gaagcggcca agatagtgcg ggatgccagt ggccagcccg ccccggtctg gcaggagaac 420  
 tatggtcacg atgacaccaa gctgctggcc gtgtcgcgcg gcatccagag cctgctggcg 480  
 gccaatcagc cgcccattcc ggccatgaag ctgctgctgg aatacgtgcg tgcccacaac 540  
 taccacaact acggcaagca caaggaagac ggcccggctg ccgcccaggc gctggccgag 600  
 gcattgaccg cgtggggcgc ccatccgctg ctcttcccgg agcaggccag cgacgaggta 660  
 ggcgcgctca tgggtgcctg gagcatcgcc ctgcacggtc ttcaaccaga tgctggccta cagcaccgcg 720  
 cagagccgct ttggcacctt gctcggcgag ttcaaccaga tgctggccta cagcaccgcg 780  
 catgccagcg agatcaacgg tcagcacgcc tggggcgacc gtctgttcga tctgtcaaac 840  
 ttctctgact tcgccagcga ctacagcgat cccttcgcca acgacttccg ccaacaggac 900  
 ggcgagctgc gcaagcagct gcacgccctc ggcatgagcg agctcgcgtt gtggaaggga 960  
 cgggatggcg ccgatctggt cctgctcaac aacgtgctgg atgcttacac ccgcctctac 1020  
 cgggtcgccc gctatacccg cccggacgag ctgcacggct accgcaagct gctggatgac 1080  
 tccgtcatcg cactggttcg ccaccacgac ctgatccccg gtggccagca gagccaggat 1140  
 ctgctggaag acatgtcgtg gacctctccc acctactacc ggaccgcacc 1200  
 agcgaagcct gcattcagcg cgactttgcc gggctctgca cccctgtccg ggtagaggac 1260  
 gtgctgcccgt tcgagcacac ctgctcgccg accctgcgcc tgccgggcca ggatctcacc 1320  
 atggatcagg ccgaggggat ctgccgtgaa ctgggtgccc aagagcagca gttccaccag 1380  
 cagatggaga ccggctggca gcccgtggcg gacgatcaca acgaggcgct ggaactggtg 1440  
 gtcttcaact cctccgcccga ctggaaaacgc tacggcagtg ccctgttcgg cggcgtctcc 1500  
 accgacaacg gcggcatcta cctcgaaggg gatccggctc gccccggcaa ccaggcccgc 1560  
 ttctttgcct acgaggcgga gtggaagcgc ccagcgttcc aggtgtggaa cctgcgccac 1620  
 gagtacgtgc actacctgga cggccgcttc aaccagtacg gcagcttcgg ccactaccgc 1680  
 ctcaaccgta ccacctggtg gtcggaaagg ctcggcggat tcgtcgccca cggtcagtgc 1740  
 ttgcgccgcg gtctggacaa cgtcgccggc cgtccggcca gtgagcgtcc ggccctggcc 1800  
 gacatcctgc acctggatta cgacaagggc ggcgagatgg tctactcctg gtcctacacg 1860  
 gtgcaccgct tccctgaacga gaccggtcgc ggcgaccagc ggctggccat ggcccaggcc 1920  
 ctgcgcaacc cggatcagca gcaggccatg agcgcttcg aagccgagct ggaccagctg 1980  
 attgccaatg acagcgaggc ctaccagcag tggctcgccc gccagctgct gccctggtgg 2040  
 gaagccaaca aggactccga cgagtgaag gccaacgact cctcccactg a 2091

10336256.txt

<210> 106  
 <211> 696  
 <212> PRT  
 <213> Unknown

<220>  
 <223> obtained from an environmental sample.

<400> 106  
 Met Ser Glu Leu His Val Trp Arg Gln Tyr Thr Trp Leu Leu Glu Gln  
 1 5 10 15  
 Ala Lys Thr Gln Gln Glu Cys Asp Glu Pro Gln Thr Arg Gln Glu Gly  
 20 25 30  
 Asp Lys Thr Ile Ser Tyr Arg Val Cys Arg Gln Thr Leu Pro Ala Gly  
 35 40 45  
 Ser Glu Val Gln Val Val Leu Lys Asp Thr Gly Tyr Gln Tyr Pro Val  
 50 55 60  
 Gly Gly Ser Glu Trp Gln Thr Leu Pro Glu Thr Thr Glu Trp Gln Glu  
 65 70 75 80  
 Asn Arg Val Leu Asn Arg Pro Ile Val Leu Ala Ser Lys Glu Glu Gln  
 85 90 95  
 Leu Asp Cys Arg Arg Ala Asp Gly Arg Ala Cys Ser Glu Pro Asp Leu  
 100 105 110  
 Pro Gly Thr Glu Leu Leu Asp Ala Glu Ala Ala Lys Ile Val Gln Asp  
 115 120 125  
 Ala Ser Gly Gln Pro Ala Pro Val Trp Gln Glu Asn Tyr Gly His Asp  
 130 135 140  
 Asp Thr Lys Leu Leu Ala Val Ser Arg Gly Ile Gln Ser Leu Leu Ala  
 145 150 155 160  
 Ala Asn Gln Pro Ala His Pro Ala Met Lys Leu Leu Leu Glu Tyr Val  
 165 170 175  
 Arg Ala His Asn Tyr His Asn Tyr Gly Lys His Lys Glu Asp Gly Pro  
 180 185 190  
 Ala Ala Ala Glu Ala Leu Ala Glu Ala Leu Thr Ala Leu Gly Ala His  
 195 200 205  
 Pro Leu Leu Phe Pro Glu Gln Ala Ser Asp Glu Val Gly Ala Val Met  
 210 215 220  
 Gly Ala Trp Ser Ile Ala Leu His Gly Gln Phe Lys Ser Pro Ala Val  
 225 230 235 240  
 Gln Ser Arg Phe Gly Thr Leu Leu Gly Glu Phe Asn Gln Met Leu Ala  
 245 250 255  
 Tyr Ser Thr Arg His Ala Ser Glu Ile Asn Gly Gln His Ala Trp Ala  
 260 265 270  
 Thr Gly Leu Phe Asp Leu Leu Asn Phe Leu Asp Phe Ala Ser Asp Tyr  
 275 280 285  
 Ser Asp Pro Phe Ala Asn Asp Phe Arg Gln Gln Asp Gly Glu Leu Arg  
 290 295 300  
 Lys Gln Leu His Ala Leu Gly Met Ser Glu Leu Ala Leu Trp Lys Gly  
 305 310 315 320  
 Arg Asp Gly Ala Asp Leu Phe Leu Leu Asn Asn Val Leu Asp Ala Tyr  
 325 330 335  
 Thr Arg Leu Tyr Arg Val Ala Arg Tyr Thr Arg Pro Asp Glu Leu Asp  
 340 345 350  
 Gly Tyr Arg Lys Leu Leu Asp Asp Ser Val Ile Ala Leu Val Arg His  
 355 360 365  
 His Asp Leu Ile Pro Gly Gly Gln Gln Ser Gln Asp Leu Leu Glu Asp  
 370 375 380  
 Met Ser Leu Thr Leu Ser Thr Tyr Tyr Leu Thr Tyr Thr Asp Arg Thr  
 385 390 395 400  
 Ser Glu Ala Cys Ile Ser Gly Asp Phe Ala Gly Leu Cys Thr Pro Val  
 405 410 415  
 Arg Val Glu Asp Val Leu Pro Phe Glu His Thr Cys Ser Pro Thr Leu  
 420 425 430  
 Arg Leu Arg Ala Gln Asp Leu Thr Met Asp Gln Ala Glu Gly Ile Cys  
 435 440 445  
 Arg Glu Leu Gly Ala Glu Glu Gln Gln Phe His Gln Gln Met Glu Thr  
 450 455 460

10336256.txt

Gly 465	Trp	Gln	Pro	Val	Ala 470	Asp	Asp	His	Asn 475	Glu	Ala	Leu	Glu	Leu	Val 480
Val	Phe	Asn	Ser 485	Ser	Ala	Asp	Trp	Lys	Arg 490	Tyr	Gly	Ser	Ala	Leu 495	Phe
Gly	Gly	Val	Ser 500	Thr	Asp	Asn	Gly	Gly 505	Ile	Tyr	Leu	Glu	Gly 510	Asp	Pro
Ala	Arg	Pro 515	Gly	Asn	Gln	Ala	Arg 520	Phe	Phe	Ala	Tyr	Glu 525	Ala	Glu	Trp
Lys	Arg 530	Pro	Ala	Phe	Gln	Val 535	Trp	Asn	Leu	Arg	His 540	Glu	Tyr	Val	His
Tyr 545	Leu	Asp	Gly	Arg	Phe 550	Asn	Gln	Tyr	Gly	Ser 555	Phe	Gly	His	Tyr	Pro 560
Leu	Asn	Arg	Thr 565	Thr	Trp	Trp	Ser	Glu	Gly 570	Leu	Ala	Glu	Phe	Val 575	Ala
His	Gly	Gln	Cys 580	Phe	Ala	Arg	Gly	Leu 585	Asp	Asn	Val	Ala	Gly 590	Arg	Pro
Ala	Ser	Glu 595	Arg	Pro	Ala	Leu	Ala 600	Asp	Ile	Leu	His	Leu 605	Asp	Tyr	Asp
Lys	Gly 610	Gly	Glu	Met	Val	Tyr 615	Ser	Trp	Ser	Tyr	Thr	Val	His	Arg	Phe
Leu 625	Asn	Glu	Thr	Gly	Arg 630	Gly	Ala	Ser	Trp	Leu	Ala 635	Met	Ala	Gln	Ala 640
Leu	Arg	Asn	Pro	Asp 645	Gln	Gln	Gln	Ala	Met	Ser	Ala	Phe	Glu	Ala 655	Glu
Leu	Asp	Gln	Leu 660	Ile	Ala	Asn	Asp	Ser 665	Glu	Ala	Tyr	Gln	Gln 670	Trp	Leu
Gly	Arg	Glu 675	Leu	Leu	Pro	Trp	Trp 680	Glu	Ala	Asn	Lys	Asp 685	Ser	Asp	Glu
Cys	Lys	Ala	Asn	Asp	Ser	Ser 695	His								

<210> 107  
 <211> 1116  
 <212> DNA  
 <213> Unknown

<220>  
 <223> Obtained from an environmental sample.

<400> 107	
atggctacat	atatacgttac
ggcaaagtag	gtaagccgca
aagcaaacac	tagagggtat
cctgaagaag	cacgtcctac
tcacgcagca	acacaacata
gtagatgatg	gtatgagaga
agaaatgttg	acgggtgtgc
tctttatttg	gggcagcctt
gcagatacaa	ttaaagctat
ccttccgtgt	tgaatttatc
gacagagctt	ttagttaggg
tccctaaaaa	gattccctgc
gatatggtaa	gagcttctta
cacgatggaa	gagcggcgtc
tcattccgctg	cacctgttat
ctgacgaacg	tagaggttcg
ggtcgagttg	gatacgctca
cctgaaccag	agcctattga
gcaatgcaaa	ccttcattctc
attagaagag	ggtcaaacaa
atctgtacct	gaatgcgtta
agatggcggt	gtcagtgtaa
taataataaac	tggttcctag
cataccaacc	cgttcgggca
atcacacaga	gatttctcag
aagggcacat	ggtacttttg
tgaagcagaa	atctatatgg
ggatgcttgt	attgaccact
attcacatca	atgtcctccg
tatgactgtt	gtagcagcag
aaatccttgat	aacgtaatat
cagtaactac	ggagaactgg
agccgtagat	aacaactcag
agctgggtgtc	tgtgcaatga
taaagaactt	atgacaaatg
agttacaaat	acagcacctc
tacgtcagca	atagaacaag
tagtttgaat	aagtga
gagattgcct	actaggttgt
ttgttgacac	cctgcttact
tagaggatca	tcctgtgcag
accgtatcca	caaccaacag
aggggggatg	tatctatatc
gacgtgtagc	acaaacgatt
ttgcaagttg	tgcagcaggg
ctgaaacatt	gtggacgtat
atatccaaaa	tggacgtaaa
caggatatag	agtagttata
caggcaacca	taacgacgat
cagtaggatg	cttgactaaa
tgatatatg	ggcacctgga
cgagaatggc	cacaggcact
ttcttgaagg	gaaccctaac
gttcattacc	ctttgcacta
ttcccgaacc	agaaccttgc
cattagcaga	ttttaatgct

60  
120  
180  
240  
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660  
720  
780  
840  
900  
960  
1020  
1080  
1116

<210> 108  
 <211> 371  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Obtained from an environmental sample.

## 10336256.txt

<400> 108  
 Met Ala Thr Tyr Ile Val Thr Leu Glu Glu Gly Gln Thr Arg Asp Cys  
 1 5 10 15  
 Leu Leu Gly Cys Gly Lys Val Gly Lys Pro Gln Ser Val Pro Glu Cys  
 20 25 30  
 Val Ile Val Asp Thr Leu Leu Thr Lys Gln Thr Leu Glu Gly Ile Asp  
 35 40 45  
 Gly Val Val Ser Val Ile Glu Asp His Pro Val Gln Pro Glu Glu Ala  
 50 55 60  
 Arg Pro Thr Asn Asn Asn Trp Phe Leu Asp Arg Ile His Asn Gln Gln  
 65 70 75 80  
 Ser Arg Ser Asn Thr Thr Tyr Ile Pro Thr Arg Ser Gly Lys Gly Val  
 85 90 95  
 Cys Ile Tyr Ile Val Asp Asp Gly Met Arg Glu Ser His Arg Asp Phe  
 100 105 110  
 Ser Gly Arg Val Ala Gln Thr Ile Arg Asn Val Asp Gly Val Ser Arg  
 115 120 125  
 Ala His Gly Thr Leu Val Ala Ser Cys Ala Ala Gly Ser Leu Phe Gly  
 130 135 140  
 Ala Ala Phe Glu Ala Glu Ile Tyr Met Ala Glu Thr Leu Trp Thr Tyr  
 145 150 155 160  
 Ala Asp Thr Ile Lys Ala Met Asp Ala Cys Ile Asp His Tyr Ile Gln  
 165 170 175  
 Asn Gly Arg Lys Pro Ser Val Leu Asn Leu Ser Phe Thr Ser Met Ser  
 180 185 190  
 Ser Ala Gly Tyr Arg Val Val Ile Asp Arg Ala Phe Ser Glu Gly Met  
 195 200 205  
 Thr Val Val Ala Ala Ala Gly Asn His Asn Asp Asp Ser Leu Lys Arg  
 210 215 220  
 Phe Pro Ala Asn Leu Asp Asn Val Ile Ser Val Gly Cys Leu Thr Lys  
 225 230 235 240  
 Asp Met Val Arg Ala Ser Tyr Ser Asn Tyr Gly Glu Leu Val Asp Ile  
 245 250 255  
 Trp Ala Pro Gly His Asp Gly Arg Ala Ala Ser Ala Val Asp Asn Asn  
 260 265 270  
 Ser Ala Arg Met Ala Thr Gly Thr Ser Ser Ala Ala Pro Val Ile Ala  
 275 280 285  
 Gly Val Cys Ala Met Ile Leu Glu Gly Asn Pro Asn Leu Thr Asn Val  
 290 295 300  
 Glu Val Arg Lys Glu Leu Met Thr Asn Gly Ser Leu Pro Phe Ala Leu  
 305 310 315 320  
 Gly Arg Val Gly Tyr Ala Gln Val Thr Asn Thr Ala Pro Leu Pro Glu  
 325 330 335  
 Pro Glu Pro Cys Pro Glu Pro Glu Pro Ile Asp Thr Ser Ala Ile Glu  
 340 345 350  
 Gln Ala Leu Ala Asp Phe Asn Ala Ala Met Gln Thr Phe Ile Ser Ser  
 355 360 365  
 Leu Asn Lys  
 370

<210> 109  
 <211> 1215  
 <212> DNA  
 <213> Unknown

<220>  
 <223> Obtained from an environmental sample.

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 acggcaaaaga ttattgctga cttagattgt gtggaatcta ttgagaaaga ttctgtatgt 180  
 acatctgatg aggaatttta caagtcattct cgtactactg ataattgggc attgacacga 240  
 ttcaatttta cagaacctca acgagagtat cctgagagtt accgttacaa tcgcacaggc 300  
 aaagggtgtg gcattctacgt tattgacagt ggtgtacgta ctactcatca agagttagta 360  
 ggacgtgtag aaactatcta cagtaccctt gaaggtaagc attttgacag tgataatgag 420  
 ctaaaccatta accgtagtca tggtagagcc gtagcgtag cagcagcagg gaagaagcta 480  
 ggtattgcaa gtgaagctac tgtctacaac ttattcgtag atttttctat gtcagacatt 540

## 10336256.txt

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cgtgtgccac	atacacgttt	tgacattgaa	ccattcaagt	ttcctaaacc	ttctcctgta	1080
gaaaaaattg	tacaaaaggt	gtctgacaat	aaggaatcgt	caactatttc	agacaaaggt	1140
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&lt;210&gt; 110

&lt;211&gt; 404

&lt;212&gt; PRT

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; Obtained from an environmental sample.

&lt;400&gt; 110

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Phe	Asn	Phe	Thr	Glu	Pro	Gln	Arg	Glu	Tyr	Pro	Glu	Ser	Tyr	Arg	Tyr
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Asn	Arg	Thr	Gly	Lys	Gly	Val	Gly	Ile	Tyr	Val	Ile	Asp	Ser	Gly	Val
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Gly	Ile	Ala	Ser	Glu	Ala	Thr	Val	Tyr	Asn	Leu	Phe	Val	Asp	Phe	Ser
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Met	Ser	Asp	Ile	Ile	Lys	Ala	Phe	Asp	Thr	Val	Leu	His	His	Tyr	Lys
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Lys	Ser	Lys	Ser	Ala	Ala	Val	Leu	Val	Thr	Ser	Phe	Ser	Thr	Leu	Ser
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Leu	Ala	Met	Lys	Pro	Ile	Ser	Asp	Ala	Leu	Tyr	Gln	Ala	Gly	Leu	Val
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					230					235					240
Ala	Ala	Phe	Pro	Gln	Thr	Ile	Ser	Val	Gly	Ala	Thr	Asp	Lys	Gln	Asp
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Pro	Gly	Val	Asn	Val	Lys	Val	Ala	Asp	His	Ala	Arg	Asp	Val	Arg	Thr
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Arg	Ile	Ala	Arg	Gly	Thr	Ser	Phe	Ser	Ala	Pro	Tyr	Val	Ala	Gly	Ile
					295					300					
Ile	Ala	Leu	Met	Leu	Glu	Gly	Ser	Asp	Lys	Pro	Arg	Lys	Ser	Glu	His
					310					315					320
Val	Asp	Thr	Ile	Arg	Gln	Ser	Phe	Leu	Asp	Asn	Ala	Ala	Ser	Ala	Ser
				325					330					335	
Lys	Ala	Asp	Lys	Arg	Val	Pro	His	Thr	Arg	Phe	Asp	Ile	Glu	Pro	Phe
			340					345					350		
Lys	Phe	Pro	Lys	Pro	Ser	Pro	Val	Glu	Lys	Ile	Val	Gln	Lys	Val	Ser
		355					360					365			

10336256.txt

Asp Asn Lys Glu Ser Ser Thr Ile Ser Asp Lys Gly Ser Lys Lys Asn  
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 Tyr Val Lys Glu Ile Val Ala Gly Val Ile Leu Val Ala Thr Ile Ala  
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 Ala Ile Leu Leu

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 <211> 1596  
 <212> DNA  
 <213> Unknown

<220>  
 <223> Obtained from an environmental sample.

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 gccgccaacg tgcgcgccta catcatcgat tcgggcgtgc tgaccgcgca cagccagttc 540  
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 aatggccacg gcacacatgt ggccgggacg gtcgccggca gtacatgggg cgtggccaag 660  
 ggctgtgatcg tgcattccagt gcgcgtgttc ggctgtctcg gcggctcggc ctggctcgacg 720  
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 <211> 531  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Obtained from an environmental sample.

<221> SIGNAL  
 <222> (1)...(36)

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 Thr Ala Val Ala Ser Glu Leu Arg Thr Ser Glu Asp Pro Ile Glu Gly  
 35 40 45  
 Arg Tyr Ile Val Val Leu Arg Glu Gln Ala Ala Arg Leu Ser Ser Glu  
 50 55 60  
 Phe Thr Gly Arg Ala Asp Val Pro Ala Ile Ala Asp Val Ala Arg Thr  
 65 70 75 80  
 Leu Ala Ser Arg His Gly Ala Thr Leu Leu Phe Ser Tyr Glu His Ala  
 85 90 95

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Leu Arg Gly Phe Val Val Asp Ala Asp Asp Arg Thr Leu Ala Gln Leu  
 100 105 110  
 Leu Ala Asp Pro Arg Val Glu Tyr Val Glu Glu Asp Gly His Val Leu  
 115 120 125  
 Leu Asn Ser Thr Thr Gln Pro Asn Ala Thr Trp Gly Leu Asp Arg Val  
 130 135 140  
 Asp Gln Arg Phe Leu Pro Leu Asn Ser Thr Tyr Val Tyr Asp Thr Thr  
 145 150 155 160  
 Ala Ala Asn Val Arg Ala Tyr Ile Ile Asp Ser Gly Val Leu Thr Ala  
 165 170 175  
 His Ser Gln Phe Gly Gly Arg Ile Gly Asn Gly Phe Ser Ala Ile Asn  
 180 185 190  
 Asp Gly Arg Gly Val Gln Asp Cys Asn Gly His Gly Thr His Val Ala  
 195 200 205  
 Gly Thr Val Ala Gly Ser Thr Trp Gly Val Ala Lys Gly Val Ile Val  
 210 215 220  
 His Pro Val Arg Val Phe Gly Cys Ser Gly Gly Ser Ala Trp Ser Thr  
 225 230 235 240  
 Ile Ile Ala Gly Ile Asp Trp Val Arg Gly Asn His Val Lys Pro Ala  
 245 250 255  
 Val Ala Asn Met Ser Leu Gly Gly Gly Asn Ser Ser Ala Asp Thr  
 260 265 270  
 Ala Thr Asn Asn Leu Ile Asn Ala Gly Val Thr Val Val Ala Ala  
 275 280 285  
 Gly Asn Ser Asn Asp Asn Ala Cys Leu Tyr Ser Pro Ala Arg Val Ala  
 290 295 300  
 Asn Ala Ile Thr Val Gly Ser Thr Gln Ser Asn Asp Ala Arg Ser Trp  
 305 310 315 320  
 Phe Ser Asn Trp Gly Asn Cys Leu Asp Leu Phe Ala Pro Gly Ser Ala  
 325 330 335  
 Ile Thr Ser Ala Trp Trp Thr Ser Thr Ala Ser His Thr Ile Asp  
 340 345 350  
 Gly Thr Ser Met Ala Ala Pro His Val Ala Gly Ala Ala Leu Tyr  
 355 360 365  
 Leu Ala Asn Asn Pro Gly Ala Ser Pro Ala Thr Val Arg Asn Ala Ile  
 370 375 380  
 Ile Thr Asn Ala Thr Thr Asn Val Val Ser Asn Pro Gly Ala Gly Ser  
 385 390 395 400  
 Pro Asn Arg Leu Leu Tyr Thr Arg Phe Ala Ala Pro Pro Pro Pro  
 405 410 415  
 Pro Pro Gly Cys Gly Arg Leu Asn Gly Gly Gln Thr Leu Gln Thr Gly  
 420 425 430  
 Gln Ser Ala Val Ser Cys Asp Gly Arg Phe Thr Phe Val Ile Gln Gly  
 435 440 445  
 Asp Gly Asn Leu Val Leu Tyr Gln Ala Gly Val Gly Ala Ile Trp Ala  
 450 455 460  
 Asn His Val Tyr Gly Ser Gly His Arg Leu Ser Met Gln Gly Asp Gly  
 465 470 475 480  
 Asn Leu Val Val Tyr Asn Ser Val Asn Gln Ala Arg Trp His Thr Gly  
 485 490 495  
 Thr His Gly His Pro Gly Ala Trp Leu Ala Val Gln Asn Asp Gly Asn  
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 Cys Cys Arg  
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<210> 113  
 <211> 4818  
 <212> DNA  
 <213> Unknown

<220>  
 <223> Obtained from an environmental sample.

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<210> 114  
 <211> 1606  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Obtained from an environmental sample.

<221> SIGNAL  
 <222> (1)...(32)

<400> 114

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			20					25					30		
Ala	Leu	Leu	Lys	Gln	Pro	Phe	Lys	Thr	Asn	Pro	Gln	Asp	Ala	Ser	Ala
		35					40					45			
Leu	Gln	Gln	Lys	Ala	Ala	Ile	Ala	Gln	Gln	Thr	Ser	Leu	Leu	Glu	Gly
	50					55					60				
Asp	Ala	Arg	Leu	His	Lys	Asp	Leu	Gln	Gly	Leu	Ser	Gly	Ser	Gln	Glu
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Val	Pro	Val	Ile	Ile	His	Leu	Ser	Glu	Lys	Ala	Val	Gly	Leu	Glu	Gln
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Gly	Ile	His	Lys	Leu	Asn	Gly	Lys	Lys	Met	Ser	Gln	Ser	Glu	Ile	Thr
			100					105					110		
Leu	Lys	Lys	Gly	Lys	Ile	Gln	Ala	Gln	Gln	Asn	Thr	Ala	Arg	Lys	Glu
		115					120					125			
Met	Thr	Val	Lys	Lys	Val	Lys	Phe	Asp	Gln	Val	Tyr	Ser	Tyr	Asp	Thr
	130					135					140				
Val	Leu	Asn	Gly	Leu	Ser	Gly	Thr	Val	Gln	Ala	Asn	Asp	Leu	Lys	Lys
	145				150					155				160	
Leu	Leu	Thr	Ile	Ser	Gly	Val	Lys	Tyr	Val	Glu	Pro	Asp	Thr	Thr	Val
			165						170					175	
Tyr	Ala	Gln	Glu	Gly	Leu	Gln	Lys	Val	Asp	Pro	Lys	Val	Asp	Ala	Lys
		180						185					190		
Met	Asp	Thr	Ser	Ile	Pro	Phe	Leu	Gly	Ile	Asn	Lys	Leu	Trp	Glu	Glu
		195					200					205			
Gly	Ile	Glu	Gly	Gln	Gly	Val	Lys	Val	Ala	Val	Leu	Asp	Thr	Gly	Ile
	210					215					220				
Asp	Ala	Ser	His	Pro	Asp	Leu	Lys	Ala	Val	Tyr	Lys	Gly	Gly	Lys	Asn
	225				230					235					240
Phe	Val	Pro	His	Val	Asp	Gly	Glu	Tyr	Ala	Arg	Pro	Arg	Ala	Asp	Asp
			245						250					255	
Asp	Gly	Ser	Glu	Thr	Ser	Pro	Leu	Asp	Arg	Pro	Ala	Asn	Lys	Pro	Glu
		260						265					270		
Val	Asn	Glu	Arg	Gly	Ser	Ser	Phe	Tyr	Thr	Thr	His	Gly	Thr	His	Val
		275					280					285			
Ala	Gly	Thr	Ile	Val	Ala	Gln	Gly	Asn	Asn	Glu	Phe	Gly	Ile	Lys	Gly
	290					295					300				
Ile	Ala	Pro	Lys	Val	Asp	Leu	Tyr	Ser	Tyr	Arg	Val	Leu	Gly	Ala	Tyr
	305				310					315				320	
Gly	Ser	Gly	Ala	Thr	Ser	Gly	Ile	Ile	Lys	Ala	Ile	Asp	Thr	Ala	Val
			325						330					335	
Ile	Glu	Lys	Ile	Asp	Val	Ile	Asn	Leu	Ser	Leu	Gly	Gly	Gly	Ala	Asn
		340						345					350		

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Ser Glu Thr Asp Gly Ala Ser Phe Ala Ile Asn Asn Ala Met Leu Ala  
 Gly Thr 355 Ser Val Val Ala 360 Thr Gly Asn Ser Gly 365 Pro Asn Arg Gly  
 Thr Met Gly Thr Pro Ala 375 Thr Ser Arg Leu Gly 380 Ile Ala Val Gly Asn  
 385 Thr Thr Asn Pro Glu 390 Thr His Phe Gln Ala 395 Asn Val Asn Val Lys Ala  
 Gly Glu Phe Thr Tyr Ser Lys Val Asn 410 Asp Leu Met Ala Thr Thr Phe  
 Gly Lys Asp Val Glu Thr Gln Leu 425 Ala Gly Gly Tyr Asp 430 Leu Ile Ala  
 Val Pro 435 Gly Ala Gly Ala Glu 440 Lys Asp Tyr Ala Asp 445 Leu Asp Val Thr  
 Gly Lys Val Ala Leu Val 455 Ala Arg Ser Glu Ile Ala Phe Val Asp Lys  
 465 Val Ala Ala Ala Lys 470 Asn Gly Ala Val 475 Ala Ile Ile Val His Asn  
 Phe Ala Gly Gly Thr Asn Ala Pro Asn Lys Ser Asp Val Phe 480 Leu Gly  
 Asp Ala Phe 500 Glu Phe Ile Pro Thr 505 Phe Asp Met Ser Val 510 Thr Asp Gly  
 Glu Ala Leu Arg Ala Ala Leu 520 Ala Ala Pro Ser 525 Thr Ile Ser Phe  
 Asp 530 Gln Phe Ser Ser Ile 535 Lys Thr Thr Gly Asp 540 Asp Val Asn Asp Ser  
 545 Ser Ser Arg Gly Pro 550 Ser Thr Pro Asn Phe 555 Asp Ile Lys Pro Asp Val  
 Ser Ala Pro Gly 565 Thr Asn Ile Met Ser 570 Thr Ile Pro Met Tyr Gly Asn  
 Asp Phe Pro 580 Asp Ala Asp Tyr Ser 585 Glu Ala Tyr Ser Arg 590 Lys Thr Gly  
 Thr Ser 595 Met Ala Thr Pro His 600 Ile Ala Gly Ile Ala Ala Leu Val Lys  
 Gln 610 Ala Asn Pro Thr Trp 615 Asn Ala Phe Asp Val 620 Lys Val Ala Leu Ser  
 625 Asn Thr Ala Thr Val 630 Leu Asp Thr Lys Lys Tyr Asp Val Phe Ala Gln  
 Gly Ala Gly Arg 645 Val Asp Ala Tyr Lys 650 Ala Ala Arg Ala Asp Val Leu  
 Ala Tyr Ala Ile Asp Thr Ala Ser 665 Asn Asp Gly Thr Glu 670 Val Glu Asn  
 Leu Lys 675 Gly Thr Val Thr Phe 680 Gly Pro Gln Lys Leu 685 Asp Lys Asn Ile  
 Ser Val Thr Lys Lys Ile Asn Val Lys Asp Leu 700 Lys Ser Ala Gly Gly  
 705 Asp Tyr Thr Val Ser 710 Val Asp Val Thr Lys 715 Gly Phe Gly Asp Ala Lys  
 Val Thr Val Asp Gln Ser Glu Phe Thr 730 Leu Asn Gly Glu Gln 735 Leu Leu  
 Asn Val Thr 740 Leu Thr Ala Ser Lys 745 Ala Glu Thr Lys Ala Gly Asp Glu  
 Ile Leu Gly Tyr Ile His Ile 760 Lys Gly Asn Gly Lys 765 Asp Leu Ser Leu  
 Pro Phe Ala Ala Asp Phe 775 Gly Gly Ala Ala Ala Val Ala Val Lys Asp  
 785 Met Glu Ile Thr Lys 790 Thr Asp Leu Ser Phe 795 Asn Gly Asp Gly Val Asn  
 Asp Asp Ala Met Leu Tyr Phe Thr Ile 805 Thr Gly Asp Val Gly 815 Phe Asn  
 Thr Ile Glu 820 Leu Trp Asp Ile Met 825 Asn Pro Thr Gly Gly 830 Lys Tyr Ser  
 Asp Gly Tyr Ile Gly Tyr Leu His Ala Ser Asp Thr 845 Leu Thr Ala Gly  
 Ser Tyr Gln Leu Pro Ile 855 Leu Gly Lys Tyr Thr 860 Gln Trp Gly Gly Thr  
 865 Ala ser Glu Val Ile 870 Pro Asp Gly Leu Tyr 875 Thr Ile Asp Phe Ser 880 Ala  
 885 890 895

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Glu Thr Lys Ser Gly Asn Pro Lys Thr Ile Ala Asp Tyr Val Gly Pro  
 Val Val Val<sup>900</sup> Lys Ser Thr Ala Gly<sup>905</sup> Thr Ile Glu Gly Ala Val Ala Asp  
 Gly Lys Val<sup>915</sup> Thr Gly Lys Ile Thr Asp Lys Tyr Val<sup>925</sup> Asp Tyr Gln Lys  
 Glu<sup>930</sup> Leu Val Lys Tyr Gly<sup>935</sup> Met Gly Tyr Asp Leu<sup>940</sup> Asn Thr Lys Leu Ser  
 Ala<sup>945</sup> Thr Tyr Glu Val<sup>950</sup> Thr Ala Asn Asp Ala<sup>955</sup> Val Val Asp Ser Gly<sup>960</sup> Ala  
 Val Lys Leu Ala<sup>965</sup> Gln Asp Gly Thr Phe Ala<sup>970</sup> Phe Asp Leu Pro Thr Phe  
 Asp Lys Thr<sup>980</sup> Lys Asn Asn Val Thr<sup>985</sup> Val Lys Tyr Ala Asp Ala Ala Gly  
 Asn Lys Ala<sup>995</sup> Glu Glu Val Ile Tyr Thr Ala Ile Asp Glu Pro Val Asp  
 Thr<sup>1010</sup> Val Ser Val Ala Val<sup>1015</sup> Asp Gln Thr Ala Leu Asp Leu Lys Val Gly  
 Asp<sup>1025</sup> Thr Ala Gln Leu<sup>1030</sup> Leu Val Thr Glu Thr<sup>1035</sup> Thr Thr Lys Pro Asp Gly  
 Thr Ser Thr Asp<sup>1045</sup> Arg Asp Val Thr Ala<sup>1050</sup> Glu Ala Thr Phe Ala Ser Ser  
 Asp Ala Ala Val<sup>1060</sup> Ala Thr Val Val<sup>1065</sup> Asn Gly Lys Val Thr Ala Val Ala  
 Ala Gly Lys Ala Glu Ile Thr Val Thr Tyr Asn Asp<sup>1070</sup> Phe Thr Gln Thr  
 Val<sup>1075</sup> Pro Val Thr Val Thr<sup>1080</sup> Ala Glu Pro Val Lys Glu Glu Ile Ser Tyr  
 Ala<sup>1090</sup> Leu Asn Lys Lys<sup>1095</sup> Ser Leu Ser Leu Gly Val Gly Gln Gln Glu Gln  
 Leu Thr Ile Thr<sup>1100</sup> Glu Thr Lys Val Lys Ala Asp Gly Thr Val Val Lys  
 Thr Asp Val Thr<sup>1110</sup> Pro Thr Val Ser Phe Asn Val Val Asp Asn Ser Ile  
 Ala Thr Val His Lys Gly Leu Val Thr Ala His Lys Ala Gly Lys Thr  
 Gln Val Arg Val Met Ile Pro Gly Gln Asp Thr Arg Phe Val Tyr Leu  
 Glu Val Lys Asp Leu<sup>1125</sup> Pro Gln Asp Val Val<sup>1130</sup> Thr Tyr Ser Val Asp Lys  
 Thr Ala Leu Lys Leu Gly Val Gly Gln Gln Glu Gln Leu Thr Val Lys  
 Gln Thr Thr Val Lys Pro Asp Gly Thr Val Val Glu Lys Asp Phe Thr  
 Pro Ser Thr Ser Phe Asn Val Val Asp Lys Lys Ile Ala Thr Val Ser  
 Lys Gly Leu Val Thr Ala His Lys Ala Gly Lys Thr Gln Val Arg Val  
 Met Ile Pro Gly Glu Asp Thr Ile Phe Val Tyr Leu Glu Val Val Thr  
 Pro Pro Gln Asn Ile Val Thr Tyr Ser Val Asp Lys Thr Asp Val Lys  
 Met Gln Val Asn Gln Gln Thr Gln Ile Lys Ile Thr Glu Lys Thr Val  
 Thr Pro Asp Gly Lys Ile Thr Glu Lys Asp Val Thr Gly Ala Ser Lys  
 Phe Ser Val Val Asn Asn Lys Ile Ala Thr Val Asn Lys Gly Leu Ile  
 Ser Ala Leu Thr Pro Gly Lys Thr Gln Val Lys Val Val Leu Pro Asn  
 Gly Glu Ser Leu Val Tyr Leu Ala Val Lys Gly Glu Pro Ala Pro  
 Ile Ile Thr Tyr Ser Leu Asp Lys Asp Ser Val Ser Leu Lys Ala Gly  
 Asp Ser Ala Asn Val Gln Leu Val Glu Thr Thr Thr Lys Ala Asp Gly  
 Thr Ser Thr Thr Lys Asp Val Thr Thr Glu Ala Thr Tyr Gln Thr Asn  
 1425 1430 1435 1440

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Asn Ala Asp Val Ala Thr Val Thr Gln Gly Lys Ile Ser Ala Ile Ala
1445 1450 1455
Ala Gly Asp Thr Glu Ile Ser Val Thr Leu Gly Ala Phe Glu Thr Thr
1460 1465 1470
Val Lys Val His Val Glu Ala Val Ala Pro Lys Ala Ile Val Val Thr
1475 1480 1485
Asp Glu Met Ile Asn Ala Phe Ile Ala Asp Lys Lys Ala Lys Gln Ile
1490 1495 1500
Ile Ile Glu Val Pro Ala Ala Val Gly Leu Met Asp Val Glu Phe Ser
1505 1510 1515 1520
Lys Ala Ile Leu Lys Lys Ile Glu Lys Ser Glu Lys Asp Leu Val Leu
1525 1530 1535
Lys Ala Gly Asn Ala Val Tyr Thr Leu Glu Asp Asp Ala Val Glu Glu
1540 1545 1550
Leu Met Asn Arg Ser Gly Gly Asp Ala Val Ile Thr Leu Gly Thr Ser
1555 1560 1565
Ser Ser Ala Asn Val Lys Asp Ala Val Ser Glu Val Tyr Thr Ile Glu
1570 1575 1580
Phe Ser Thr Gly Thr Ala Ala Asn Lys Ser Ala Leu Lys Lys Phe Asp
1585 1590 1595 1600
Glu Glu Ile Leu Val Ala
1605

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<210> 115  
 <211> 2487  
 <212> DNA  
 <213> Unknown

<220>  
 <223> Obtained from an environmental sample.

<400> 115

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gccatgagca	tgggcctgct	gtcgcagccg	gccggcgcgag	ccgggaacac	cggtctccgtc	120
gcgcacgtcg	cggcggacga	cccggaggac	gcaggacccc	caccgtagc	gcagtcccc	180
acagccgaga	cggagcacgt	cgcgacgga	cgacgaagg	tgtccgagct	tccgccactg	240
gccgcgagca	aggaccgct	caaggaggtg	tacggcaaga	ccggaaggc	gccgggtccgt	300
ccctcgaagt	cgatggagaa	ggcggttgcc	ggcaagaccg	gcaagtccc	tgcgcttgcc	360
gccgcgtgca	acgtctccga	cttcaccagc	cgaagcggcg	gcgcgctggg	ccagcagatc	420
aaggcgctcta	caaccgactg	cgtaaacacc	ctgttcaacc	tgaccgggtc	ggacgcctac	480
tacgccttcc	gcgagtcgca	gatggcctcg	gtcgcctacg	ccctgcgcga	cggtctcgacg	540
tcctacccgg	gtaacgcctc	caccggtagt	ccgcagctcg	tgctctacct	gcgcgcccgc	600
tactacgtcc	actactacaa	cgcaagcacg	gtgggctcct	acggcagcag	cctgcagacc	660
gcgatacgcg	ccgggctcga	cgcttcttc	gccagcccgc	gctcacgcga	cgtaaacgac	720
gccaacggcg	agacgctcgc	cgaggcggtc	acgctcatcg	acagtgccga	ggagaacgcc	780
cgctacatcc	acgtcgtcaa	gcgcctgctg	gcggattacg	actccacctg	gaactcctcc	840
tggtggatgc	tcaacgcggt	caacaacgtg	tacaccgtga	ccttcgcggg	ccatcagggtg	900
cccgcgttcg	tgagtgcggt	gcagtcggag	cccggctctga	tcgacgcgct	ctacaacttc	960
gcgagcggcg	acctcgcgct	gctgggaacg	acctcacgtc	ccaaggtccg	gaacgcggga	1020
cgcgaaactcg	gcaggttcct	gcagcactcc	ccactgcgct	ccccgctgtg	ccccctggcc	1080
gcgggcctgc	tcaactccag	ctccatcaag	ggccgaacgg	ccccgctgtg	ggtcgggtgtg	1140
gccgagatga	ccgactacta	cgacaaggcc	aactgctcct	actacggcac	ctgcgacctc	1200
caggcccaac	tggcccgtc	cgctcctgacg	gtgacctacc	cctgcagctc	cagcatcacc	1260
atcaaggcgc	agcagatgac	ctcgggagag	ctgtcctcca	gctgcagcag	cctgcgcaac	1320
caggacgcct	acttccacaa	cgtaggcccgt	gacaacggcc	ccgtcgcgaa	cgacaacaac	1380
agcaccatcg	aggtcgtggt	cttcgactcc	agcaccgact	accagacctc	cgccggcgcc	1440
atgtacggga	tcgacaccaa	caacggcgcg	atgtacctgg	aagggaaccc	gtcggcgggc	1500
ggcaaccagc	gcagattcat	cgcttacgag	gccgattggc	tgccggcccga	cttcagatc	1560
tggaacctca	accacgagta	cacgcactac	ctcgacggtc	gcttcaacat	gtacggcgac	1620
ttcaacgcca	acatcaccac	cccgaacctc	tggtggatcg	aaggcttcgc	cgagtacgtc	1680
tcctactcct	accgcggtct	cccctatacg	gaggcgacga	ccgaagcagg	ccgtcgcacg	1740
tacgcgtgga	gcaccttggt	cgacaccacg	tacagccacg	acaccacgcg	catctaccgc	1800
tggggctacc	tcgcccgtgcg	gtacatgctc	gagaaccacc	gcgccgacat	ggacaccgtc	1860
ctcggctact	accgcgcggg	aaactggaac	gccgcacgtt	cctacctgac	cggcaccatc	1920
ggcaccgcgt	acgacaacga	ctggtacacc	tggtggcgcg	cctgcgcggc	cggaactgc	1980
ggaggcgggg	gcaccaaccc	gcccggcaac	caggcgccca	ccgccgcgtt	caccaccgcc	2040
gtccagggcc	tggacgtcac	cttcaccgac	cagtcacagg	acgccgacgg	caccatcgcc	2100
tcccggctct	ggagcttcgg	tgacggcacc	acctccacgg	ccaccaacc	cgtcaagagg	2160

## 10336256.txt

tacggggtcgg	ccgggtccta	cacgggtgaag	ctgaccgtca	ccgacgacaa	gggagccacc	2220
gccaccgcaa	cgaggacggt	caccgtagcc	agcggcggag	gcggcggcac	cgagtgcacc	2280
ggaaccgaca	cccgggaact	gggccagaac	tgccaacgcg	gcaaccagtc	cgccaccgcc	2340
ggcaactacg	cctacctgta	cctctacgtc	ccggccggca	ccacccagct	gaagatcacc	2400
acctccggcg	ggacgggcca	cgcggacctc	tactacagca	ccagcggctg	gcccggcacc	2460
acgagctaca	cgacgcgtgc	gacggga				2487

<210> 116  
 <211> 829  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Obtained from an environmental sample.

<221> SIGNAL  
 <222> (1)...(33)

<400> 116

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Ala	Leu	Thr	Val	Ala	Met	Ser	Met	Gly	Leu	Leu	Ser	Gln	Pro	Ala	Gly
			20					25					30		
Ala	Ala	Gly	Asn	Thr	Gly	Ser	Val	Ala	His	Val	Ala	Ala	Asp	Asp	Pro
		35					40				45				
Glu	Asp	Ala	Gly	Pro	Pro	Pro	Val	Ala	Gln	Ser	Pro	Thr	Ala	Glu	Thr
	50					55					60				
Glu	His	Val	Ala	His	Gly	Arg	Thr	Lys	Val	Ser	Glu	Leu	Pro	Pro	Leu
65					70				75						80
Ala	Ala	Ser	Lys	Asp	Pro	Leu	Lys	Glu	Val	Tyr	Gly	Lys	Thr	Ala	Lys
			85					90						95	
Ala	Pro	Val	Arg	Pro	Ser	Lys	Ser	Met	Glu	Lys	Ala	Val	Ala	Gly	Lys
			100					105					110		
Thr	Gly	Lys	Ser	Arg	Ala	Leu	Ala	Ala	Cys	Asn	Val	Ser	Asp	Phe	
		115				120					125				
Thr	Ser	Arg	Ser	Gly	Gly	Ala	Leu	Val	Gln	Gln	Ile	Lys	Ala	Ser	Thr
	130					135					140				
Thr	Asp	Cys	Val	Asn	Thr	Leu	Phe	Asn	Leu	Thr	Gly	Ser	Asp	Ala	Tyr
145					150				155						160
Tyr	Ala	Phe	Arg	Glu	Ser	Gln	Met	Ala	Ser	Val	Ala	Tyr	Ala	Leu	Arg
				165					170					175	
Asp	Gly	Ser	Thr	Ser	Tyr	Pro	Gly	Asn	Ala	Ser	Thr	Gly	Met	Pro	Gln
			180					185					190		
Leu	Val	Leu	Tyr	Leu	Arg	Ala	Gly	Tyr	Tyr	Val	His	Tyr	Tyr	Asn	Ala
		195					200					205			
Ser	Thr	Val	Gly	Ser	Tyr	Gly	Ser	Ser	Leu	Gln	Thr	Ala	Ile	Arg	Ala
	210					215					220				
Gly	Leu	Asp	Ala	Phe	Phe	Ala	Ser	Pro	Arg	Ser	Arg	Asp	Val	Asn	Asp
225					230					235					240
Ala	Asn	Gly	Glu	Thr	Leu	Ala	Glu	Ala	Val	Thr	Leu	Ile	Asp	Ser	Ala
			245						250					255	
Glu	Glu	Asn	Ala	Arg	Tyr	Ile	His	Val	Val	Lys	Arg	Leu	Leu	Ala	Asp
		260						265					270		
Tyr	Asp	Ser	Thr	Trp	Asn	Ser	Ser	Trp	Trp	Met	Leu	Asn	Ala	Val	Asn
		275				280						285			
Asn	Val	Tyr	Thr	Val	Thr	Phe	Arg	Gly	His	Gln	Val	Pro	Ala	Phe	Val
	290					295					300				
Ser	Ala	Val	Gln	Ser	Asp	Pro	Gly	Leu	Ile	Asp	Ala	Leu	Tyr	Asn	Phe
305					310					315					320
Ala	Ser	Gly	His	Leu	Ala	Leu	Leu	Gly	Thr	Asp	Gln	Ser	Tyr	Leu	Thr
			325						330					335	
Ser	Asn	Ala	Gly	Arg	Glu	Leu	Gly	Arg	Phe	Leu	Gln	His	Ser	Pro	Leu
		340						345					350		
Arg	Ser	Lys	Val	Arg	Pro	Leu	Ala	Ala	Gly	Leu	Leu	Asn	Ser	Ser	Ser
		355					360					365			
Ile	Lys	Gly	Arg	Thr	Ala	Pro	Leu	Trp	Val	Gly	Val	Ala	Glu	Met	Thr
	370					375					380				
Asp	Tyr	Tyr	Asp	Lys	Ala	Asn	Cys	Ser	Tyr	Tyr	Gly	Thr	Cys	Asp	Leu

## 10336256.txt

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385      390      395      400
Gln Ala Gln Leu Ala Arg Ser Val Leu Thr Val Thr Tyr Pro Cys Ser
      405
Ser Ser Ile Thr Ile Lys Ala Gln Gln Met Thr Ser Gly Glu Leu Ser
      420
Ser Ser Cys Ser Ser Leu Arg Asn Gln Asp Ala Tyr Phe His Asn Val
      435
Ala Arg Asp Asn Gly Pro Val Ala Asn Asp Asn Asn Ser Thr Ile Glu
      450
Val Val Val Phe Asp Ser Ser Thr Asp Tyr Gln Thr Tyr Ala Gly Ala
      465
Met Tyr Gly Ile Asp Thr Asn Asn Gly Gly Met Tyr Leu Glu Gly Asn
      485
Pro Ser Ala Ala Gly Asn Gln Pro Arg Phe Ile Ala Tyr Glu Ala Glu
      500
Trp Leu Arg Pro Asp Phe Gln Ile Trp Asn Leu Asn His Glu Tyr Thr
      515
His Tyr Leu Asp Gly Arg Phe Asn Met Tyr Gly Asp Phe Asn Ala Asn
      530
Ile Thr Thr Pro Thr Ile Trp Trp Ile Glu Gly Phe Ala Glu Tyr Val
      545
Ser Tyr Ser Tyr Arg Gly Leu Pro Tyr Thr Glu Ala Thr Thr Glu Ala
      565
Gly Arg Arg Thr Tyr Ala Leu Ser Thr Leu Phe Asp Thr Thr Tyr Ser
      580
His Asp Thr Arg Ile Tyr Arg Trp Gly Tyr Leu Ala Val Arg Tyr
      595
Met Leu Glu Asn His Arg Ala Asp Met Asp Thr Val Leu Gly Tyr Tyr
      610
Arg Ala Gly Asn Trp Asn Ala Ala Arg Ser Tyr Leu Thr Gly Thr Ile
      625
Gly Thr Arg Tyr Asp Asn Asp Trp Tyr Thr Trp Leu Ala Ala Cys Ala
      645
Ala Gly Asn Cys Gly Gly Gly Gly Thr Asn Pro Pro Gly Asn Gln Ala
      660
Pro Thr Ala Phe Thr Thr Ala Val Gln Gly Leu Asp Val Thr Phe
      675
Thr Asp Gln Ser Thr Asp Ala Asp Gly Thr Ile Ala Ser Arg Ser Trp
      690
Ser Phe Gly Asp Gly Thr Thr Ser Thr Ala Thr Asn Pro Val Lys Arg
      705
Tyr Gly Ser Ala Gly Ser Tyr Thr Val Lys Leu Thr Val Thr Asp Asp
      725
Lys Gly Ala Thr Ala Thr Ala Thr Arg Thr Val Thr Val Ala Ser Gly
      740
Gly Gly Gly Gly Thr Glu Cys Thr Gly Thr Asp Thr Arg Glu Leu Gly
      755
Gln Asn Cys Gln Arg Gly Asn Gln Ser Ala Thr Ala Gly Asn Tyr Ala
      770
Tyr Leu Tyr Leu Tyr Val Pro Ala Gly Thr Thr Gln Leu Lys Ile Thr
      785
Thr Ser Gly Gly Thr Gly Asp Ala Asp Leu Tyr Tyr Ser Thr Ser Gly
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Trp Pro Gly Thr Thr Ser Tyr Thr Gln Arg Ala Thr Gly
      820

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<210> 117  
 <211> 1356  
 <212> DNA  
 <213> Unknown

<220>  
 <223> Obtained from an environmental sample.

<400> 117  
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 actggaaccg gcgcaccgg acttgactgc ccgggttcagc gcctgatcga cgcggcgctt 120  
 gaacatccgc agggccatac cggccgctac atcgcgatca tgcgtgagga tgccgaaggc 180

## 10336256.txt

gataactgaag	cggtgatgtc	gaattccttt	gccgccacct	cggtcaaacag	ccgtgacttc	240
ggcaccgcgc	gtttcgcgat	ggatgagatt	tcgggggcgc	actcgcctgg	gctgaacacg	300
ctggggcatgg	cggttctggg	cggttccgcc	gccgacgcgc	cgcgcgaaag	catgacgcgc	360
tctggcgaca	gtttcgggac	tgctgccgag	ttgccctatg	tgctcgaacc	cgaaccatc	420
gaatgggtgc	tgatcgacct	ggccagctat	ctcatgggct	ttcgtgctgc	ctcggaccgg	480
atcgcgaccg	atcttctggg	gcaacctgtg	ccgtcgcagt	tcgaaccggc	ccccgccgac	540
gtcactgctg	ctgccggcgc	gatgacctgg	ggcctttcgc	cgaccgcgct	cggtgccagc	600
acggcgaccg	ggcgcgcat	ccgcgtggcg	atccttgata	ccgggcttga	tctcggccac	660
ccggatttcg	cgggccgcag	gatcctggcg	cagtcgttca	tcgcgggcga	gacaccgcag	720
gatgtcaacg	cccacggcac	tcacgtgacc	ggcaccgctt	gcggcccgcg	ggtgcccgcg	780
accggcgcca	accgctatgg	catcgccac	gagtgcgaaa	tcctggctcg	caagggtgctg	840
agcaacgccg	gtgccggacc	gggccttggc	atcgtgatgg	gcatcgactg	ggcgctggcg	900
aacggcgcg	atatcatcaa	catgtctctt	ggcagcccgc	cagcggcggc	caatctcaag	960
tacacccagg	ccgctaagcg	ggccttgacc	cgcggcgctg	tgattgtcgc	ggcggcgggc	1020
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gtgaactcgt	tcctgcagaa	gtcgggcttt	tcaaacttcg	gcaaggctga	acttgccgca	1140
ccggggctct	ccatcgattc	gtccctgccc	cgtccgcgca	ggcgcggggt	cctcagcggt	1200
accagctagg	ccgcccgcga	gttcacgggg	attgctgccc	ttcatgccc	ggccactggc	1260
ctgcgcggca	aggcgctgtg	ggcccatctc	gagtcctcgc	ccaaggcgct	gtcgtgccc	1320
ccccagaacc	gtggggcagg	gctggtgcag	gcatga			1356

&lt;210&gt; 118

&lt;211&gt; 451

&lt;212&gt; PRT

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; Obtained from an environmental sample.

&lt;400&gt; 118

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Gly	Thr	Asp	Asp	Thr	Gly	Thr	Gly	Ala	Pro	Gly	Leu	Asp	Cys	Pro	Val
			20					25					30		
Gln	Arg	Leu	Ile	Asp	Ala	Ala	Leu	Glu	His	Pro	Gln	Gly	His	Thr	Gly
		35					40					45			
Arg	Tyr	Ile	Ala	Ile	Met	Arg	Glu	Asp	Ala	Glu	Gly	Asp	Thr	Glu	Ala
	50				55						60				
Val	Met	Ser	Asn	Ser	Phe	Ala	Ala	Thr	Ser	Ala	Asn	Ser	Arg	Asp	Phe
65					70				75					80	
Gly	Thr	Arg	Gly	Phe	Ala	Met	Asp	Glu	Ile	Ser	Gly	Ala	Asp	Ser	Leu
			85						90					95	
Val	Leu	Asn	Thr	Leu	Gly	Met	Ala	Val	Leu	Gly	Gly	Ser	Ala	Ala	Asp
			100					105					110		
Ala	Ala	Arg	Glu	Ser	Met	Thr	Arg	Ser	Gly	Asp	Ser	Phe	Gly	Thr	Ala
		115					120					125			
Ala	Glu	Leu	Pro	Tyr	Val	Leu	Glu	Pro	Glu	Thr	Ile	Glu	Trp	Val	Leu
	130					135					140				
Ile	Asp	Pro	Ala	Ser	Tyr	Leu	Met	Gly	Phe	Arg	Ala	Ala	Ser	Asp	Arg
145					150				155					160	
Ile	Ala	Thr	Asp	Leu	Leu	Gly	Gln	Pro	Val	Pro	Ser	Gln	Phe	Glu	Pro
			165						170					175	
Ala	Pro	Ala	Asp	Val	Thr	Ala	Ala	Ala	Gly	Gly	Met	Thr	Trp	Gly	Leu
			180					185					190		
Ser	Ala	Thr	Arg	Val	Gly	Ala	Ser	Thr	Ala	Thr	Gly	Arg	Gly	Ile	Arg
		195					200					205			
Val	Ala	Ile	Leu	Asp	Thr	Gly	Leu	Asp	Leu	Gly	His	Pro	Asp	Phe	Ala
	210					215					220				
Gly	Arg	Arg	Ile	Leu	Ala	Gln	Ser	Phe	Ile	Ala	Gly	Glu	Thr	Pro	Gln
225					230				235					240	
Asp	Val	Asn	Gly	His	Gly	Thr	His	Val	Thr	Gly	Thr	Ala	Cys	Gly	Pro
			245						250					255	
Arg	Val	Pro	Ala	Thr	Gly	Gly	Asn	Arg	Tyr	Gly	Ile	Ala	His	Glu	Cys
			260					265					270		
Glu	Ile	Leu	Val	Gly	Lys	Val	Leu	Ser	Asn	Ala	Gly	Ala	Gly	Pro	Gly
	275						280					285			
Leu	Gly	Ile	Val	Met	Gly	Ile	Asp	Trp	Ala	Leu	Ala	Asn	Gly	Ala	His
	290					295					300				

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```

Ile Ile Asn Met Ser Leu Gly Ser Pro Ala Ala Ala Asn Leu Lys
305 310 315 320
Tyr Thr Gln Ala Gly Lys Arg Ala Leu Thr Arg Gly Ala Leu Ile Val
325 330 335
Ala Ala Ala Gly Asn Asp Asn Ala Pro Thr Gly Gln Pro Ala Asn Ser
340 345 350
Pro Thr Ile Leu Ser Val Ala Ser Val Asn Ser Phe Leu Gln Lys Ser
355 360 365
Gly Phe Ser Asn Phe Gly Lys Val Glu Leu Ala Ala Pro Gly Ser Ser
370 375 380
Ile Asp Ser Ser Leu Pro Arg Pro Arg Arg Arg Gly Phe Leu Ser Gly
385 390 395 400
Thr Ser Met Ala Ala Pro His Val Thr Gly Ile Ala Ala Leu His Ala
405 410 415
Gln Ala Thr Gly Leu Arg Gly Lys Ala Leu Trp Ala His Leu Glu Ser
420 425 430
Arg Ala Lys Ala Leu Ser Leu Pro Pro Gln Asn Arg Gly Ala Gly Leu
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Val Gln Ala
450

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<210> 119  
 <211> 1590  
 <212> DNA  
 <213> Unknown

<220>  
 <223> obtained from an environmental sample.

<400> 119

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gcgacacttc	gcactcgtct	gcagaaaacg	atttctgcag	gagccagtgc	ggtgcggggg	180
gccggaaaca	aattgaaact	gaaagctgaa	aaggcgcaga	aatcagcctt	tgaaatcgct	240
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cgcaaattga	aaattaccgt	gctccgggagc	gatacgcagc	agccggtgtc	aggtgttgac	480
atcattgggt	ttacgaattt	cgaacaacga	gaggggagtag	aggggggtcac	gtcggcgagc	540
ggcaagggtga	cgctgacagt	ttccgggagt	ctgaaattcc	agcgggtcta	tgtacaacat	600
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ggaggggaatg	cggatggtac	cggcgtcaag	gttgggggtga	ttgattcggg	aattgccctc	780
aatcatcctg	atcttcgggt	gagtggcgga	ttgggctgcg	ttcctggcga	accagaaagt	840
gattttggtc	cccgcggcgg	aattcacggc	tcacacgttg	cggaataaat	tgccgggacgt	900
ggcaacgctc	caaccggaat	gcgcggggcag	gctcccaatg	cggaatctt	ctcgtatcgc	960
gtttttggaa	acacctcttc	gtcgggggtca	aattttgccc	tcgtgaaagc	gattcagcga	1020
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ggcgttcctc	aagtctgatgc	cgcggtgcag	gaggcaatcc	gcgaggcaca	tcagaagggc	1140
gtgctgggtga	tcgcggcggc	aggggaatgat	ggacgtcgct	cggttaagtta	tccagccatg	1200
gatgacatgg	ttgttgcggt	ttccgcagtg	gggcgaaaag	ggacgtttcc	ggcgaaatcc	1260
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<210> 120  
 <211> 529  
 <212> PRT  
 <213> Unknown

<220>  
 <223> obtained from an environmental sample.

<400> 120  
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			20							25						30			
Met	Ser	Leu	Asn	Ala	Gly	Ser	Ala	Ala	Thr	Leu	Arg	Thr	Arg	Leu	Gln				
		35					40												
Lys	Thr	Ile	Ser	Ala	Gly	Ala	Ser	Ala	Val	Arg	Gly	Ala	Gly	Asn	Lys				
		50				55													
Leu	Lys	Leu	Lys	Ala	Glu	Lys	Ala	Gln	Lys	Ser	Ala	Phe	Glu	Ile	Val				
		65			70					75									
Ser	Ser	Leu	Asn	Glu	Asp	Gly	Val	Lys	Leu	Val	Ser	Ala	Thr	Pro	80				
			85						90										
Met	Ile	Ala	Ala	Met	Arg	Phe	Asp	Gln	Pro	Gly	Leu	Arg	Val	Val	Pro				
			100					105											
Glu	Ala	Phe	Cys	Ser	Pro	Ala	Arg	Ala	Val	Val	Arg	Leu	110	Arg	Thr				
		115						120											
Val	Thr	Lys	Thr	Ala	Ala	Ala	Ala	Thr	Ala	Val	Gln	Arg	Lys	Leu	Lys				
		130						135											
Ile	Thr	Val	Leu	Arg	Ser	Asp	Thr	Gln	Gln	Pro	Val	Ser	Gly	Val	Asp				
		145			150					155									
Ile	Ile	Gly	Phe	Thr	Asn	Phe	Glu	Gln	Arg	Glu	Gly	Val	Gln	Gly	Val				
			165						170										
Thr	Ser	Ala	Ser	Gly	Lys	Val	Thr	Leu	Thr	Val	Ser	Gly	Ser	Leu	Lys				
			180					185											
Phe	Gln	Arg	Leu	Tyr	Val	Gln	His	Glu	Gln	Val	Gly	Leu	Trp	Ser	Phe				
		195					200												
Leu	Gly	Lys	Asn	Val	Ser	Thr	Asp	Gly	Thr	Leu	Thr	Ile	Thr	Leu	Gln				
		210				215													
Ala	Leu	Ser	Leu	Ala	Thr	Val	Asp	Ser	Leu	Arg	His	Phe	His	Gly	Leu				
		225			230					235									
Gly	Gly	Asn	Ala	Asp	Gly	Thr	Gly	Val	Lys	Val	Gly	Val	Ile	Asp	Ser				
			245						250										
Gly	Ile	Ala	Leu	Asn	His	Pro	Asp	Leu	Arg	Val	Ser	Gly	Gly	Leu	Gly				
		260						265											
Cys	Val	Pro	Gly	Glu	Pro	Glu	Ser	Asp	Phe	Gly	Pro	Arg	Gly	Gly	Ile				
		275						280											
His	Gly	Ser	His	Val	Ala	Gly	Ile	Ile	Ala	Gly	Arg	Gly	Asn	Ala	Pro				
		290				295													
Thr	Gly	Met	Arg	Gly	Gln	Ala	Pro	Asn	Ala	Glu	Ile	Phe	Ser	Tyr	Arg				
		305			310					315									
Val	Phe	Gly	Asn	Thr	Ser	Ser	Ser	Gly	Ser	Asn	Phe	Ala	Leu	Val	Lys				
			325						330										
Ala	Ile	Gln	Arg	Gly	Val	Ala	Asp	Gly	Cys	Asp	Leu	Leu	Asn	Met	Ser				
			340					345											
Leu	Ser	Phe	Asp	Pro	Asp	Val	Asn	Gly	Val	Pro	Gln	Val	Asp	Ala	Ala				
		355					360												
Val	Gln	Glu	Ala	Ile	Arg	Glu	Ala	His	Gln	Lys	Gly	Val	Leu	Val	Ile				
		370				375													
Ala	Ala	Ala	Gly	Asn	Asp	Gly	Arg	Arg	Ser	Val	Ser	Tyr	Pro	Ala	Met				
		385			390					395									
Asp	Asp	Met	Val	Val	Ala	Val	Ser	Ala	Val	Gly	Arg	Lys	Gly	Thr	Phe				
			405						410										
Pro	Ala	Lys	Ser	Gly	Glu	Ser	Gly	Asp	Val	Leu	Ala	Pro	Phe	Gly	Ala				
			420					425											
Ala	Pro	Lys	Asp	Phe	Leu	Ala	Ala	Phe	Ser	Asn	Val	Gly	Thr	Glu	Leu				
		435					440												
Asp	Val	Thr	Gly	Ala	Gly	Val	Gly	Val	Val	Ser	Thr	Ala	Pro	Gly	Gly				
		450				455													
Tyr	Ile	Pro	Met	Ser	Gly	Thr	Ser	Met	Ala	Cys	Pro	Ala	Val	Thr	Gly				
		465			470					475									
Val	Leu	Ala	Arg	Leu	Leu	Ala	Asn	Thr	Pro	Ala	Val	Leu	Asn	Met	Gln				
			485						490										
Arg	Asp	Ser	Asn	Arg	Thr	Asp	Ala	Ile	Lys	Ala	Leu	Leu	Phe	Ser	Asn				
			500					505											
Ala	Gln	Thr	Leu	Gly	Phe	Asp	Leu	Arg	Phe	Glu	Gly	Lys	Gly	Leu	Pro				
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Lys																			

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<210> 121  
 <211> 1557  
 <212> DNA  
 <213> Unknown

<220>  
 <223> obtained from an environmental sample.

<400> 121  
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 gtagtgctga aggaatcggc agcccgttc agcagcgaag cgtcgatcgc ccaccggcgc 180  
 aatgtgccgg aggtggcgca ggtggccagc caattggccg ctggcgggcg gggcatgcgg 240  
 gtatcgcgca gcttcaacaa tgcgtgcgc gggtttgcg ctgataacac cagtgacgcc 300  
 gatctggcgc gcctgctgca ggacccgcgg gtcgactacg tcgaagaaga cggcgtgggtg 360  
 catgcctttg ccaccagag cggggcgacc tggggcctgg accggatcga tcagacggcg 420  
 ctgccgtga atggtcaata tgtctatgac agcaccgcca gcaatgtgaa tgcctacatc 480  
 atcgataccg gcatccgcgc cagtcacagc gatttcggcg gccgggtcag cggcggttat 540  
 gacgcggtca acgacggcaa cggcaccaat gactgccagg gccatggcac ccattgctgcc 600  
 ggcacggctc gcagcgccac ctatggcgtc gccaaaggcg tgcacctggg tccggtagcg 660  
 gtgctggggt gtgatggttc cggcaccaac tcgggctgca tctccggcat cgaactgggt 720  
 cggagcaacc acagcgccc ggcggtggcc aatatgagcc tgggcggcgg cgcctcaacg 780  
 gcggttgaca gcgcggtggc caatctcagc gccgcccggc tcgtgggtgg ggtcgccgcc 840  
 ggcaacgaca ataccagcgc ctgcgactat tcaccggcgc gggcgccaag cgcgatcacg 900  
 gtcggctcca ccaccaatac cgatgcgcgc tcgtcgttct ccaactacgg ccagtgtctg 960  
 gatatcttcg cgcccggctc caacatcctg tcgactgcca acagcagcaa cagcgccacc 1020  
 accacgatga gtggcacgtc gatggcctcg ccgcatgttg ctggcgccgc cgcgctctac 1080  
 ctggccagta accccagcgc atcgccggcc gcggtggcga cggcgttggg caaccaggcg 1140  
 gtcgccaatg cggtagcaaa tccgggctcc ggctcaccga accgactact gcaaagtcgc 1200  
 gccggcgga gcaaccggcc accgcccacc ccgcccggcg gcggtgaccc ctgcacggcc 1260  
 tgcgccaagt acagtggcag cttgtattac agcggcgact acggctacca acctgacggg 1320  
 aacttctact atgcctccag cggccaacaa cagggctggc tgcgcgggcc cgccagcacc 1380  
 gacttcgacc tcgaactgct gcgctggagt ggctatgggt ggaccaaggt ggcgcagagc 1440  
 gtgggctcga ccagcagcga acaggtcagc tactacggca gcgctggcta ctacatgtgg 1500  
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<210> 122  
 <211> 518  
 <212> PRT  
 <213> Unknown

<220>  
 <223> obtained from an environmental sample.

<221> SIGNAL  
 <222> (1)...(25)

<400> 122  
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 Val Met Ala Thr Gln Ser Ala Asp Ala Ala Asp Leu Arg Leu Thr Gln  
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 Thr Pro Val Ser Gly Arg Tyr Ile Val Val Leu Lys Glu Ser Ala Ala  
 35 40 45  
 Arg Phe Ser Ser Glu Ala Ser Ile Ala His Arg Arg Asn Val Pro Glu  
 50 55 60  
 Val Ala Gln Val Ala Ser Gln Leu Ala Ala Gly Arg Gly Met Arg  
 65 70 75 80  
 Val Ser Arg Ser Phe Asn Asn Ala Leu Arg Gly Phe Val Ala Asp Asn  
 85 90 95  
 Thr Ser Asp Ala Asp Leu Ala Arg Leu Gln Asp Pro Arg Val Asp  
 100 105 110  
 Tyr Val Glu Glu Asp Gly Val Val His Ala Phe Ala Thr Gln Ser Gly  
 115 120 125  
 Ala Thr Trp Gly Leu Asp Arg Ile Asp Gln Thr Ala Leu Pro Leu Asn  
 130 135 140  
 Gly Gln Tyr Val Tyr Asp Ser Thr Ala Ser Asn Val Asn Ala Tyr Ile  
 145 150 155 160

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Ile Asp Thr Gly Ile Arg Ala Ser His Ser Asp Phe Gly Gly Arg Val
165 170 175
Ser Gly Gly Tyr Asp Ala Val Asn Asp Gly Asn Gly Thr Asn Asp Cys
180 185 190
Gln Gly His Gly Thr His Val Ala Gly Thr Val Gly Ser Ala Thr Tyr
195 200 205
Gly Val Ala Lys Gly Val His Leu Val Pro Val Arg Val Leu Gly Cys
210 215 220
Asp Gly Ser Gly Thr Asn Ser Gly Val Ile Ser Gly Ile Asp Trp Val
225 230 235 240
Arg Ser Asn His Ser Arg Pro Ala Val Ala Asn Met Ser Leu Gly Gly
245 250 255
Gly Ala Ser Thr Ala Val Asp Ser Ala Val Ala Asn Leu Ser Ala Ala
260 265 270
Gly Val Val Val Val Val Ala Ala Gly Asn Asp Asn Thr Ser Ala Cys
275 280 285
Asp Tyr Ser Pro Ala Arg Ala Pro Ser Ala Ile Thr Val Gly Ser Thr
290 295 300
Thr Asn Thr Asp Ala Arg Ser Ser Phe Ser Asn Tyr Gly Gln Cys Leu
305 310 315 320
Asp Ile Phe Ala Pro Gly Ser Asn Ile Leu Ser Thr Ala Asn Ser Ser
325 330 335
Asn Ser Ala Thr Thr Thr Met Ser Gly Thr Ser Met Ala Ser Pro His
340 345 350
Val Ala Gly Ala Ala Ala Leu Tyr Leu Ala Ser Asn Pro Ser Ala Ser
355 360 365
Pro Ala Ala Val Ala Thr Ala Leu Gly Asn Gln Ala Val Ala Asn Ala
370 375 380
Val Ser Asn Pro Gly Ser Gly Ser Pro Asn Arg Leu Leu Gln Ser Arg
385 390 395 400
Ala Gly Gly Ser Asn Pro Pro Pro Pro Gly Gly Gly Asp
405 410 415
Pro Cys Thr Ala Cys Ala Lys Tyr Ser Gly Ser Leu Tyr Tyr Ser Gly
420 425 430
Asp Tyr Gly Tyr Gln Pro Asp Gly Asn Phe Tyr Tyr Ala Ser Ser Gly
435 440 445
Gln Gln Gln Gly Trp Leu Arg Gly Pro Ala Ser Thr Asp Phe Asp Leu
450 455 460
Glu Leu Leu Arg Trp Ser Gly Tyr Gly Trp Thr Lys Val Ala Gln Ser
465 470 475 480
Val Gly Ser Thr Ser Ser Glu Gln Val Ser Tyr Tyr Gly Ser Ala Gly
485 490 495
Tyr Tyr Met Trp Arg Val Val Ser Tyr Ser Gly Ser Gly Asn Phe Asp
500 505 510
Phe Tyr Leu Ser Ile Pro
515

```

&lt;210&gt; 123

&lt;211&gt; 1656

&lt;212&gt; DNA

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; obtained from an environmental sample.

&lt;400&gt; 123

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gttttcttat	tcctaattgat	tataccgacg	gatagaaccg	tagggcaagc	aatcagtttt	180
ggagcgcagt	aggagtttagc	gagtggttaac	ggagatgaaa	ttccttactt	atTTTTTggc	240
gatgtcgcagg	acacccctct	tgagtatgat	ggttacatca	ttgagttaca	cgaaaaaccc	300
ctcgcgcaag	taatagctat	gcaagagaa	attccttcag	gtgattttgg	agctatgagc	360
acttcatcaa	gcgcagtgat	taatcacgaa	gcaattattg	tatcagaaca	acaaaacgcg	420
ctagcggaca	taactatgcg	acttagtcaa	gcacagtcct	catcgggaatt	cggagcgcaa	480
gcaaccacat	catcccagga	attaattggt	cgagagtcct	acagcgttgt	tttcaacgga	540
ttctctctcg	acattacaga	tgaacaagca	ctagcaataa	atcaatcacc	ctacgtgaaa	600
aacgtacatc	ctaaccgtcg	cgtgagcatt	gcgcttcaag	atgccgtacc	cctcatccaa	660
gacggaattc	tcgcaggcag	agtggatgaa	gacgggaatg	attgtgaact	aacacaaaaa	720

## 10336256.txt

ccctgttttaa	caggtgaagg	cgttaccatc	gctattatag	atacaggcgt	tgattacacg	780
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attggagggt	atgatttcac	taataatgat	gatgatgcc	tggatgataa	tggtcatgga	900
acacacgtcg	cagggattgc	tgagggaat	ggcttactaa	aaggcgttgc	gcccgcgcg	960
aaaatactag	cgtataaagt	tttaggtgct	gggtggttatg	gaacctggga	aggaataatt	1020
gctggaatag	aacaagcagt	tattgatggc	gcggatattt	taagtttaag	tcttggttgt	1080
gttcactctt	cctgtaatcc	tgatgatatc	gcttctcaag	cagttgataa	cgcagtactt	1140
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agtcctggga	ctgcacgaaa	agcaataact	gttgggttcta	caactaaatc	agatattatt	1260
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cctgaaatga	tgtttgataa	tagaatttgt	gctgcttggc	ttaataaaga	atatcttgcc	1440
atttcaggta	catcaatggc	aacaccttta	gtttccggag	caatagcatt	acttaaacaa	1500
aaacatcccc	attggacacc	tgaagaaatt	aaaggagcag	taaaagggaac	cgcgattaat	1560
ttaggttatg	acccaacga	gcaaggcgt	ggaagaatta	atgtgagaga	aatgattggt	1620
ttggagggaaa	gagcacttat	tgcttcaatt	ctttgg			1656

&lt;210&gt; 124

&lt;211&gt; 552

&lt;212&gt; PRT

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; Obtained from an environmental sample.

&lt;221&gt; SIGNAL

&lt;222&gt; (1)...(56)

&lt;400&gt; 124

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			20					25					30		
Ile	Ser	Phe	Leu	Leu	Ile	Val	Gly	Val	Phe	Leu	Phe	Leu	Met	Ile	Ile
			35				40					45			
Pro	Thr	Asp	Arg	Thr	Val	Gly	Gln	Ala	Ile	Ser	Phe	Gly	Ala	Ser	Glu
						55					60				
Glu	Leu	Ala	Ser	Val	Asn	Gly	Asp	Glu	Ile	Pro	Tyr	Leu	Phe	Phe	Gly
65					70					75					80
Asp	Val	Glu	Asp	Thr	Pro	Leu	Glu	Tyr	Asp	Gly	Tyr	Ile	Ile	Glu	Leu
				85					90					95	
His	Glu	Lys	Pro	Leu	Ala	Gln	Val	Ile	Ala	Met	Gln	Glu	Asn	Ile	Pro
			100					105					110		
Ser	Gly	Asp	Phe	Gly	Ala	Met	Ser	Thr	Ser	Ser	Ser	Ala	Val	Ile	Asn
		115					120					125			
His	Glu	Ala	Ile	Ile	Val	Ser	Glu	Gln	Gln	Asn	Ala	Leu	Ala	Asp	Ile
						135					140				
Thr	Met	Arg	Leu	Ser	Gln	Ala	Gln	Ser	Ser	Ser	Glu	Phe	Gly	Ala	Gln
145					150					155					160
Ala	Thr	Thr	Ser	Ser	Gln	Glu	Leu	Ile	Val	Arg	Glu	Ser	Tyr	Ser	Val
				165					170					175	
Val	Phe	Asn	Gly	Phe	Ser	Leu	Asp	Ile	Thr	Asp	Glu	Gln	Ala	Leu	Ala
			180					185					190		
Ile	Asn	Gln	Ser	Pro	Tyr	Val	Lys	Asn	Val	His	Pro	Asn	Arg	Arg	Val
		195					200					205			
Ser	Ile	Ala	Leu	Gln	Asp	Ala	Val	Pro	Leu	Ile	Gln	Asp	Gly	Ile	Leu
		210					215					220			
Ala	Gly	Arg	Val	Asp	Glu	Asp	Gly	Asn	Asp	Cys	Glu	Leu	Thr	Gln	Lys
225					230					235					240
Pro	Cys	Leu	Thr	Gly	Glu	Gly	Val	Thr	Ile	Ala	Ile	Ile	Asp	Thr	Gly
				245					250					255	
Val	Asp	Tyr	Thr	His	Pro	Asp	Leu	Gly	Gly	Cys	Thr	Thr	Gln	Glu	Phe
			260					265					270		
Leu	Gly	Gly	Ala	Cys	Glu	Lys	Val	Ile	Gly	Gly	Tyr	Asp	Phe	Ile	Asn
		275					280					285			
Asn	Asp	Asp	Asp	Ala	Met	Asp	Asp	Asn	Gly	His	Gly	Thr	His	Val	Ala
		290				295					300				
Gly	Ile	Ala	Ala	Gly	Asn	Gly	Leu	Leu	Lys	Gly	Val	Ala	Pro	Asp	Ala

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305	Lys	Ile	Leu	Ala	Tyr	310	Lys	Val	Leu	Gly	Ala	315	Gly	Gly	Tyr	Gly	Thr	Trp	320
	Glu	Gly	Ile	Ile	325	Gly	Ile	Glu	Gln	Ala	330	Val	Ile	Asp	Gly	Ala	Asp	335	
	Ile	Leu	Ser	Leu	340	Ser	Leu	Gly	Cys	Val	His	Ser	Ser	Cys	Asn	Pro	Asp	350	
	Asp	Ile	Ala	Ser	355	Gln	Ala	Val	Asp	Asn	Ala	Val	Leu	Ala	Gly	Lys	Val	365	
	Val	Val	Val	Ala	370	Ala	Gly	Asn	Ser	Gly	Pro	Ser	Ser	Arg	Thr	Ile	Gly	380	
	Ser	Pro	Gly	Thr	385	Arg	Lys	Ala	Ile	Thr	Val	Gly	Ser	Thr	Thr	Lys	400		
	Ser	Asp	Ile	Ile	405	Ser	Trp	Phe	Ser	Ser	Arg	Gly	Pro	Val	Val	Trp	Met	415	
	Asp	Glu	Ala	Gly	420	Ile	Glu	Gln	Ala	Ile	Met	Lys	Pro	Asp	Val	Leu	Ala	430	
	Pro	Gly	Gly	Thr	435	Asp	Ser	Gly	Ser	Glu	Phe	Cys	Asn	Pro	Glu	Met	Met	445	
	Phe	Asp	Asn	Arg	450	Ile	Cys	Ala	Ala	Trp	Leu	Asn	Lys	Glu	Tyr	Leu	Ala	460	
	Ile	Ser	Gly	Thr	465	Ser	Met	Ala	Thr	Pro	Leu	Val	Ser	Gly	Ala	Ile	Ala	475	
	Leu	Leu	Lys	Gln	485	Lys	His	Pro	Asp	Trp	Thr	Pro	Glu	Glu	Ile	Lys	Gly	490	
	Ala	Val	Lys	Gly	500	Thr	Ala	Ile	Asn	Leu	Gly	Tyr	Asp	Pro	Asn	Glu	Gln	510	
	Gly	Ala	Gly	Arg	515	Ile	Asn	Val	Arg	Glu	Met	Ile	Gly	Leu	Glu	Glu	Arg	525	
	Ala	Leu	Ile	Ala	530	Ser	Ile	Leu	Trp	540								550	

<210> 125  
 <211> 1215  
 <212> DNA  
 <213> Unknown

<220>  
 <223> Obtained from an environmental sample.

<400> 125

atgaagtaca	ttgtcattct	aaagaaaggt	tacaatagag	attcacttac	agactactgc	60
acaaaagtag	gtaagccatg	tgagctacac	aatctcgtta	tcattaacac	tgacgaagct	120
acagcaaaaa	ttgttgctga	ttagatttgt	gtagaatcta	ttgagaaaga	ttctgtatgt	180
acatctgatg	aggaatttta	caagtcattct	cgtactactg	ataattgggc	attgacacga	240
ttcaatttta	cagaacctca	acgagagtat	cctgagaggt	accggttaca	tcgcacagga	300
aaaggtgtgg	gcatctacgt	tattgacagt	ggtgtccgta	ctactcatca	agagtttagta	360
ggacgtgtag	agactgtcta	cagtgttctc	gaaggtaagc	aatttgacag	tgataatgag	420
ctaaacatta	accgtagcca	tgccacagca	gtggcgtcag	cagcagcagg	gaagaagcta	480
ggtattgcaa	gtgaagctac	tgtctacaac	ttattcgtag	atttttctat	gtcagacatt	540
atcaaagcgt	ttgatactgt	attgcaccat	tacaaaaagt	ctaagagtgc	tgctgtactt	600
gtgacatcat	tctcaacttt	gtcactagca	atgaaaccta	tctcagacgc	actctaccaa	660
gcaggtctcg	ttcatgtatc	tagtgcaggc	aatcagtcta	cagatactcc	aagataccct	720
gctgcattcc	ctcagactat	ctctgtaggt	gctactgaca	agcaggacaa	taaagcatca	780
ttcagtaact	ttggcaatac	cgtagacgta	tatgcacccg	gagtgaatgt	gaaggtagcg	840
gatcatgcaa	gagatgttcg	tactcgtatt	gcaagaggga	cttctttctc	tgacacctat	900
gttgctggta	tcattgacct	catgctagaa	gattcagaca	agcctcgtaa	gcgcgagcat	960
tcgatgacca	tacgacaatc	cttcctagac	aattgctaca	gtattttcaa	ggcagataag	1020
cgtgtgccac	atacacgttt	tgacattgaa	ccgttcaagt	ttcctaaacc	ttctcctgta	1080
gaaaaaattg	tacaaaagggt	gtctgacaat	aaggatacgt	caagtatttc	agacaaaaaa	1140
cgtaaaaaga	gttacacgaa	acagattgta	gcaggcgtta	tcctagcagc	tactatagtt	1200
gcaattcttg	tgttaa					1215

<210> 126  
 <211> 404  
 <212> PRT  
 <213> Unknown

10336256.txt

&lt;220&gt;

&lt;223&gt; obtained from an environmental sample.

&lt;400&gt; 126

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Met Lys Tyr Ile Val Ile Leu Lys Lys Gly Tyr Asn Arg Asp Ser Leu
 1      5      10      15
Thr Asp Tyr Cys Thr Lys Val Gly Lys Pro Cys Glu Leu His Asn Leu
      20      25      30
Val Ile Ile Asn Thr Asp Glu Ala Thr Ala Lys Ile Val Ala Asp Leu
      35      40      45
Asp Cys Val Glu Ser Ile Glu Lys Asp Ser Val Cys Thr Ser Asp Glu
      50      55      60
Glu Phe Tyr Lys Ser Ser Arg Thr Thr Asp Asn Trp Ala Leu Thr Arg
65      70      75      80
Phe Asn Phe Thr Glu Pro Gln Arg Glu Tyr Pro Glu Ser Tyr Arg Tyr
      85      90      95
Asn Arg Thr Gly Lys Gly Val Gly Ile Tyr Val Ile Asp Ser Gly Val
      100      105      110
Arg Thr Thr His Gln Glu Leu Val Gly Arg Val Glu Thr Val Tyr Ser
      115      120      125
Val Leu Glu Gly Lys Gln Phe Asp Ser Asp Asn Glu Leu Asn Ile Asn
      130      135      140
Arg Ser His Gly Thr Ala Val Ala Ser Ala Ala Ala Gly Lys Lys Leu
145      150      155      160
Gly Ile Ala Ser Glu Ala Thr Val Tyr Asn Leu Phe Val Asp Phe Ser
      165      170      175
Met Ser Asp Ile Ile Lys Ala Phe Asp Thr Val Leu His His Tyr Lys
      180      185      190
Lys Ser Lys Ser Ala Ala Val Leu Val Thr Ser Phe Ser Thr Leu Ser
      195      200      205
Leu Ala Met Lys Pro Ile Ser Asp Ala Leu Tyr Gln Ala Gly Leu Val
210      215      220
His Val Ser Ser Ala Gly Asn Gln Ser Thr Asp Thr Pro Arg Tyr Pro
225      230      235      240
Ala Ala Phe Pro Gln Thr Ile Ser Val Gly Ala Thr Asp Lys Gln Asp
      245      250      255
Asn Lys Ala Ser Phe Ser Asn Phe Gly Asn Thr Val Asp Val Tyr Ala
      260      265      270
Pro Gly Val Asn Val Lys Val Ala Asp His Ala Arg Asp Val Arg Thr
      275      280      285
Arg Ile Ala Arg Gly Thr Ser Phe Ser Ala Pro Tyr Val Ala Gly Ile
290      295      300
Ile Ala Leu Met Leu Glu Asp Ser Asp Lys Pro Arg Lys Arg Glu His
305      310      315      320
Val Asp Thr Ile Arg Gln Ser Phe Leu Asp Asn Ala Thr Ser Ile Ser
      325      330      335
Lys Ala Asp Lys Arg Val Pro His Thr Arg Phe Asp Ile Glu Pro Phe
      340      345      350
Lys Phe Pro Lys Pro Ser Pro Val Glu Lys Ile Val Gln Lys Val Ser
      355      360      365
Asp Asn Lys Asp Thr Ser Ser Ile Ser Asp Lys Lys Arg Lys Lys Ser
370      375      380
Tyr Thr Lys Gln Ile Val Ala Gly Val Ile Leu Ala Ala Thr Ile Val
385      390      395      400
Ala Ile Leu Val

```

&lt;210&gt; 127

&lt;211&gt; 1236

&lt;212&gt; DNA

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; Obtained from an environmental sample.

&lt;400&gt; 127

```

atgttcaacc gtcgttccat gcttgccgtc gccattggcg ccggcgtcct gagcaccttc
ggcgcggggg ccctgcaggc ctccgagctc cgcttcgcgg agaaccgat cgaaggccag

```

60  
120

## 10336256.txt

tacatcgctcg	tcctgaagga	tgacgccgcc	acgctcgagg	gagagacctc	gatcgcgtcc	180
aaccgtccca	acgtggccac	ggccgcacgc	aacctcgccc	gcgcgcaccg	cgccgaggtt	240
cgccacacct	acaaccgcgc	cctgcgcgga	ttcgtggccc	gtgccgacga	gcgtgccctg	300
gcccgcctgc	tgaggaccc	cagcgtcgcc	tatgtcgaag	aggacggcat	cgccaccacc	360
caggccacgc	agaccggcgc	gacctggggc	atcgaccgca	tcgaccagcg	caccctgccg	420
ctgaaccaga	cctacgtcta	cgacaccacc	gcgtcgaacg	tgaacgtcta	catcgtcgac	480
accggcatcc	gctcggcgca	caacgacttc	ggcggccgcg	tgcgctcggg	ctacaccgcc	540
atcaacgacg	gccagggcac	caacgactgc	aacggccacg	gcacccacgt	cgccctccacc	600
gccgcccgcg	ccacctatgg	cgtggccaag	gccgcccgcc	tgtatccggt	gcgcgtgctc	660
ggctgcaacg	gctcgggcac	caactccggc	gtgatcgccg	gcatggactg	ggcgcgcagc	720
aaccacgtca	agccggccgt	ggccaacatg	agcctgggcg	gcggcgccctc	gtccgccacc	780
gactcggccg	tcacccgcat	gcgcaatgcc	ggcgtgaccg	tggctcgtggc	cgccgggcaac	840
gacagcggca	ccacgtgcaa	ctactcgccg	gcgcgctcga	cctcggcgat	caccgtgggt	900
tccaccacca	gcaccgacgc	gcgctcgaac	ttctccaact	tcggcacctg	cgtgaacatc	960
ttcgcgccgg	gttcctcgat	cactgccgcg	tggcacacca	gcaacaccgc	gaccaacacc	1020
atcagcggca	cctcgatggc	ggcgccgcac	gtggccggcg	tggccgcgct	gttcctggcc	1080
accaacccca	acgccacccc	ggcccaggtc	gagcaggcga	tctacagcaa	ctccacgccc	1140
aaccgcgtca	ccaatccggg	cagcggctcg	ccaatcgcc	tgctgtactc	ccgattcggc	1200
ggcggcaccg	acccgggtcc	cgatccggat	ccaaag			1236

&lt;210&gt; 128

&lt;211&gt; 412

&lt;212&gt; PRT

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; Obtained from an environmental sample.

&lt;221&gt; SIGNAL

&lt;222&gt; (1)...(27)

&lt;400&gt; 128

Met	Phe	Asn	Arg	Arg	Ser	Met	Leu	Ala	Val	Ala	Ile	Gly	Ala	Gly	Val
1				5					10					15	
Leu	Ser	Thr	Phe	Gly	Ala	Gly	Ala	Leu	Gln	Ala	Ser	Glu	Leu	Arg	Phe
			20					25					30		
Ala	Glu	Asn	Pro	Ile	Glu	Gly	Gln	Tyr	Ile	Val	Val	Leu	Lys	Asp	Asp
		35					40					45			
Ala	Ala	Thr	Leu	Glu	Gly	Glu	Thr	Ser	Ile	Ala	Ser	Asn	Arg	Pro	Asn
	50					55					60				
Val	Ala	Thr	Ala	Ala	Arg	Asn	Leu	Ala	Arg	Ala	His	Arg	Ala	Glu	Val
65					70				75					80	
Arg	His	Thr	Tyr	Asn	Arg	Ala	Leu	Arg	Gly	Phe	Val	Ala	Arg	Ala	Asp
			85						90					95	
Glu	Arg	Ala	Leu	Ala	Arg	Leu	Leu	Gln	Asp	Pro	Ser	Val	Ala	Tyr	Val
			100					105					110		
Glu	Glu	Asp	Gly	Ile	Val	Thr	Thr	Gln	Ala	Thr	Gln	Thr	Gly	Ala	Thr
		115					120					125			
Trp	Gly	Ile	Asp	Arg	Ile	Asp	Gln	Arg	Thr	Leu	Pro	Leu	Asn	Gln	Thr
	130					135					140				
Tyr	Val	Tyr	Asp	Thr	Thr	Ala	Ser	Asn	Val	Asn	Val	Tyr	Ile	Val	Asp
145					150				155					160	
Thr	Gly	Ile	Arg	Ser	Ala	His	Asn	Asp	Phe	Gly	Gly	Arg	Val	Arg	Ser
			165						170					175	
Gly	Tyr	Thr	Ala	Ile	Asn	Asp	Gly	Gln	Gly	Thr	Asn	Asp	Cys	Asn	Gly
			180					185					190		
His	Gly	Thr	His	Val	Ala	Ser	Thr	Ala	Ala	Gly	Ala	Thr	Tyr	Gly	Val
		195					200					205			
Ala	Lys	Ala	Ala	Arg	Leu	Tyr	Pro	Val	Arg	Val	Leu	Gly	Cys	Asn	Gly
	210					215					220				
Ser	Gly	Thr	Asn	Ser	Gly	Val	Ile	Ala	Gly	Met	Asp	Trp	Val	Ala	Ser
	225				230					235				240	
Asn	His	Val	Lys	Pro	Ala	Val	Ala	Asn	Met	Ser	Leu	Gly	Gly	Gly	Ala
			245						250					255	
Ser	Ser	Ala	Thr	Asp	Ser	Ala	Val	Thr	Arg	Met	Arg	Asn	Ala	Gly	Val
		260						265					270		
Thr	Val	Val	Val	Ala	Ala	Gly	Asn	Asp	Ser	Gly	Asn	Ala	Cys	Asn	Tyr
		275					280					285			

## 10336256.txt

Ser Pro Ala Arg Ser Thr Ser Ala Ile Thr Val Gly Ser Thr Thr Ser  
 290 295 300  
 Thr Asp Ala Arg Ser Asn Phe Ser Asn Phe Gly Thr Cys Val Asn Ile  
 305 310 315  
 Phe Ala Pro Gly Ser Ile Thr Ala Ala Trp His Thr Ser Asn Thr  
 325 330 335  
 Ala Thr Asn Thr Ile Ser Gly Thr Ser Met Ala Ala Pro His Val Ala  
 340 345 350  
 Gly Val Ala Ala Leu Phe Leu Ala Thr Asn Pro Asn Ala Thr Pro Ala  
 355 360 365  
 Gln Val Glu Gln Ala Ile Tyr Ser Asn Ser Thr Pro Asn Arg Val Thr  
 370 375 380  
 Asn Pro Gly Ser Gly Ser Pro Asn Arg Leu Leu Tyr Ser Arg Phe Gly  
 385 390 395 400  
 Gly Gly Thr Asp Pro Gly Pro Asp Pro Asp Pro Lys  
 405 410

<210> 129  
 <211> 1248  
 <212> DNA  
 <213> Unknown

<220>  
 <223> Obtained from an environmental sample.

<400> 129  
 atggatctgg ccgcgcctgc gacgccgcgc gtgacggtgt gggaatactc gatggacgag 60  
 cgctaccgca atcccggttc gccgctgttc aagggtgctgc ccaacggcgc cagggtcgtg 120  
 cgccgcgacg gcgatgcggt gttcctgctgc ggcagcggcg cgaccgcgca gggcgaccgc 180  
 cccttcctcg atcgccacga cctgaagacc ggccagacca ggcgcctgtt ccgcagcgcg 240  
 ccgatgcct tcgagcgcgt cgccagcgtc tccgacgacg gccagcgcct gtacacgctg 300  
 cgcgaacccc cgaaggaccc gccgaacctg ttcgtgcgca cgctgggcgc gccggtcgcc 360  
 gatgccgcgc aaggcgaagc cgtcgtcgct tcctcgccgc ggcaggtcac gagctacgtc 420  
 gacccgaccc cggaagtgcg cggcatccag cgccggctgg tgacctacaa gcgcaaggac 480  
 ggctgggacc tgcgtttcac gctctacctg ccgctgggct accaggccgg gacgcgcgtg 540  
 cccgccgtgc tctacgccta tcccgcgcgc tatgccgatc cgggcaaggc cgggcaggtc 600  
 accgggtcgc agcagagctt caccgccttc ccggagtacc gcctgctgct gctcgccggc 660  
 tacgcgatca tcgacaacac ctctgtcccg atcgtcggcg acccgcgac cgctacgac 720  
 acctacctgc agcagctcgt cgacaacgcg caggcgggcg tcgacaaggc cgtcgagctg 780  
 ggctgtgtcg atcgcgaccg catcggcgtg accgggcaca gccatggcgc gctgatgacc 840  
 gccaacctgc tcgcgcactc ggacctgttc cgcccggtg tcgccagcag cggcggttac 900  
 aacaagacgc tcacgccctt cggtttccag aacgagcgcc gctcgctgtg gaacgccaag 960  
 cgcgtgtacg aagaggcgct gacctactac tacgccgaca aggtggacga gccgctgctg 1020  
 atcgtgcacg gcgaggacga tgccaacccc ggcaccgaac cgggtgcagtc gccgaagctc 1080  
 ttccaggcca tccgcggcaa cggcggcacc gcgcgcctgg tgatgctgcc cttcgagccg 1140  
 cactggtaca ccgcgaagga aaccaatgag cacttcgccg cggaaatgct gatgtggttc 1200  
 gaccgctggg tgaagaacgc cggcccgcgc gaggcgaaga aggagtga 1248

<210> 130  
 <211> 415  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Obtained from an environmental sample.

<400> 130  
 Met Asp Leu Ala Ala Pro Ala Thr Pro Pro Val Thr Val Trp Glu Tyr  
 1 5 10 15  
 Ser Met Asp Glu Arg Tyr Arg Asn Pro Gly Ser Pro Leu Phe Lys Val  
 20 25 30  
 Leu Pro Asn Gly Gly Arg Val Val Arg Arg Asp Gly Asp Ala Val Phe  
 35 40 45  
 Leu Arg Gly Ser Gly Ala Thr Ala Gln Gly Asp Arg Pro Phe Leu Asp  
 50 55 60  
 Arg His Asp Leu Lys Thr Gly Gln Thr Arg Arg Leu Phe Arg Ser Ala  
 65 70 75 80  
 Pro Asp Ala Phe Glu Arg Val Ala Ser Val Ser Asp Asp Gly Gln Arg

## 10336256.txt

85 90 95  
 Leu Tyr Thr Leu Arg Glu Thr Pro Lys Asp Pro Pro Asn Leu Phe Val  
 100 105 110  
 Arg Thr Leu Gly Ala Pro Val Ala Asp Ala Ala Glu Gly Glu Ala Val  
 115 120 125  
 Val Ala Ser Ser Pro Arg Gln Val Thr Ser Tyr Val Asp Pro Thr Pro  
 130 135 140  
 Glu Val Arg Gly Ile Gln Arg Arg Leu Val Thr Tyr Lys Arg Lys Asp  
 145 150 155 160  
 Gly Val Asp Leu Ser Phe Thr Leu Tyr Leu Pro Leu Gly Tyr Gln Ala  
 165 170 175  
 Gly Thr Arg Val Pro Ala Val Leu Tyr Ala Tyr Pro Ala Asp Tyr Ala  
 180 185 190  
 Asp Pro Gly Lys Ala Gly Gln Val Thr Gly Ser Gln Gln Ser Phe Thr  
 195 200 205  
 Arg Phe Pro Glu Tyr Arg Leu Leu Leu Ala Gly Tyr Ala Ile Ile  
 210 215 220  
 Asp Asn Thr Ser Phe Pro Ile Val Gly Asp Pro Arg Thr Ala Tyr Asp  
 225 230 235 240  
 Thr Tyr Leu Gln Gln Leu Val Asp Asn Ala Gln Ala Ala Val Asp Lys  
 245 250 255  
 Ala Val Glu Leu Gly Val Val Asp Arg Asp Arg Ile Gly Val Thr Gly  
 260 265 270  
 His Ser His Gly Ala Leu Met Thr Ala Asn Leu Leu Ala His Ser Asp  
 275 280 285  
 Leu Phe Arg Ala Gly Val Ala Ser Ser Gly Gly Tyr Asn Lys Thr Leu  
 290 295 300  
 Thr Pro Phe Gly Phe Gln Asn Glu Arg Arg Ser Leu Trp Asn Ala Lys  
 305 310 315 320  
 Arg Val Tyr Glu Glu Ala Ser Thr Tyr Tyr Ala Asp Lys Val Asp  
 325 330 335  
 Glu Pro Leu Leu Ile Val His Gly Glu Asp Asp Ala Asn Pro Gly Thr  
 340 345 350  
 Glu Pro Val Gln Ser Pro Lys Leu Phe Gln Ala Ile Arg Gly Asn Gly  
 355 360 365  
 Gly Thr Ala Arg Leu Val Met Leu Pro Phe Glu Pro His Trp Tyr Thr  
 370 375 380  
 Ala Lys Glu Thr Asn Glu His Phe Ala Ala Glu Met Leu Met Trp Phe  
 385 390 395 400  
 Asp Arg Trp Val Lys Asn Ala Gly Pro Arg Glu Ala Lys Lys Glu  
 405 410 415

<210> 131  
 <211> 903  
 <212> DNA  
 <213> Unknown

<220>  
 <223> Obtained from an environmental sample.

<400> 131  
 atgattatga ataagtggcc ccttctgcta ttgcttagtt ttctctcttc tttggcaaac 60  
 gcacaggaaa aagagagaca atcttacatt ataccatatg ttggttggaa tcaggaaaaa 120  
 ctcaactgga atattgctgg taatgaaaat ggacaatacc ccaatgtatt atctgaatta 180  
 aaatggcagc agttgctggg cccggaaatg ggaattatct ccgctgtatc aatttcacatca 240  
 aggtttcagg tgaggtggaa tttcagctac caggcaatta cctccggaac agtaaattgat 300  
 acagattacg caggcgataa cagagcgctt aaaactgctg aattcaattt acaagcagat 360  
 aaaggctata caattaaaac ccgtctggaa ttatcttattc ttctctggac taaccaaaaca 420  
 ttctctttta gaccacatgc aggatatttc ggaagttacc agaagcttta tatgctggat 480  
 ggtgatactc cgcttatttc cggaagaaagaa ttaaaaagca cctataaacc cgaatggcac 540  
 ggtgcagttc ttggcttaga aacaaacttc aaaaaggaaa actggaatgt taatctcgac 600  
 atcagcggca tgtattttcc ccaatattct gccactgcaa actggaatct tcgggaagaa 660  
 ctcagaaggc ctgtcagctt cgaacacaga tccaaaggaa aaggcttcga tactggactt 720  
 cgtattgggt accagctcgg tcaacgcatt cagcctttta tatctgcaag atatacacag 780  
 atagaagcag gaaaaggaac ggataaatta tatatggcaa acggagatat ttacaaaagc 840  
 aggtgaacg aagttaattc tacaagcatt agttttggca tcggtgttaa agtactattc 900  
 tag 903

10336256.txt

<210> 132  
 <211> 300  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Obtained from an environmental sample.

<221> SIGNAL  
 <222> (1)...(21)

<400> 132  
 Met Ile Met Asn Lys Trp Pro Leu Leu Leu Leu Ser Phe Leu Ser  
 1 5 10 15  
 Ser Leu Ala Asn Ala Gln Glu Lys Glu Arg Gln Ser Tyr Ile Ile Pro  
 20 25 30  
 Tyr Val Gly Trp Asn Gln Glu Lys Leu Asn Trp Asn Ile Ala Gly Asn  
 35 40 45  
 Glu Asn Gly Gln Tyr Pro Asn Val Leu Ser Glu Leu Lys Trp Gln Gln  
 50 55 60  
 Leu Arg Gly Pro Glu Met Gly Ile Ile Ser Ala Val Ser Ile Ser Ser  
 65 70 75 80  
 Arg Phe Gln Val Arg Trp Asn Phe Ser Tyr Gln Ala Ile Thr Ser Gly  
 85 90 95  
 Thr Val Asn Asp Thr Asp Tyr Ala Gly Asp Asn Arg Ala Leu Lys Thr  
 100 105 110  
 Ala Glu Phe Asn Leu Gln Ala Asp Lys Gly Tyr Thr Ile Lys Thr Arg  
 115 120 125  
 Leu Glu Leu Ser Tyr Leu Leu Trp Thr Asn Gln Thr Phe Ser Phe Arg  
 130 135 140  
 Pro His Ala Gly Tyr Phe Gly Ser Tyr Gln Lys Leu Tyr Met Leu Asp  
 145 150 155 160  
 Gly Asp Thr Pro Leu Ile Pro Gly Lys Glu Leu Lys Ser Thr Tyr Lys  
 165 170 175  
 Pro Glu Trp His Gly Ala Val Leu Gly Leu Glu Thr Asn Phe Lys Lys  
 180 185 190  
 Glu Asn Trp Asn Val Asn Leu Asp Ile Ser Gly Met Tyr Phe Pro Gln  
 195 200 205  
 Tyr Ser Ala Thr Ala Asn Trp Asn Leu Arg Glu Glu Leu Arg Arg Pro  
 210 215 220  
 Val Ser Phe Glu His Arg Ser Lys Gly Lys Gly Phe Asp Thr Gly Leu  
 225 230 235 240  
 Arg Ile Gly Tyr Gln Leu Gly Gln Arg Ile Gln Pro Phe Ile Ser Ala  
 245 250 255  
 Arg Tyr Thr Gln Ile Glu Ala Gly Lys Gly Thr Asp Lys Leu Tyr Met  
 260 265 270  
 Ala Asn Gly Asp Ile Tyr Lys Ser Arg Leu Asn Glu Val Asn Ser Thr  
 275 280 285  
 Ser Ile Ser Phe Gly Ile Gly Val Lys Val Leu Phe  
 290 295 300

<210> 133  
 <211> 939  
 <212> DNA  
 <213> Unknown

<220>  
 <223> Obtained from an environmental sample.

<400> 133  
 atgaaccccg tgtatcgcag cctcttcgcc ccggccctgc tggccggcgt gatgctggcc 60  
 catgtgccctg cagccctggc acagacggca ggccccgccc cgctccgcct cgccgacctg 120  
 cgcccgccca gcctgcagat cgaaggacgc gacccgccca tctcgatcgc gtcgcacgtg 180  
 ccgctgctgg agatcagcac cgaggacgcc tccttcacatc aggtgcattt cgaccacttc 240  
 tccctgcccc ccggcctggc cctgggtggc gagaaccccc acggcagcga ggcctaccgc 300  
 tacagcagcc accagcgcga cgccacacac ttcgaccgca gcctcggcca caacggcccg 360  
 accagtttct cggccatgtc gatcagcggc ccgctgctgc tgctgcgcct ggagggcacg 420  
 gccaccgagc gctggcggcc ccaccacggc atccgcgtga gcggatacca cgagggctac 480

## 10336256.txt

ccggacgaga	tgatcgagac	cctgcagtcg	gagggcctgc	tcgacgaggt	cggcaccag	540
gccatctgcg	gcagcaacga	caagcgcggc	gtggcctgct	acgccagctc	cgagcctgcc	600
gcggtcgacc	gctcgcgcc	ggtggccgc	ctgggtgatga	gcggctcgct	ctgcaccgcg	660
tggcgctgg	gcccgaacaa	ccgcatgttc	accaacaacc	actgcatgtc	cacggcggcg	720
cgcgtggccg	cctcggaagt	gtggttcaac	caccaggcgc	cctcctgcgg	tggcaccagc	780
gcaggcaccg	tggtcaaggt	ggccggtgac	cagatgctgg	ccaccaacag	ctcgtctggac	840
tacaccctgt	tcacgggtgcg	cgacttcgcc	tcgatcgcca	gcttcggcta	cctgggcctg	900
gacatcgcca	gcactggcgt	gggcgaccag	atccaaaga			939

&lt;210&gt; 134

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; Obtained from an environmental sample.

&lt;221&gt; SIGNAL

&lt;222&gt; (1)...(27)

&lt;400&gt; 134

Met	Asn	Pro	Val	Tyr	Arg	Ser	Leu	Phe	Ala	Pro	Ala	Leu	Leu	Ala	Gly
1				5				10						15	
Val	Met	Leu	Ala	His	Val	Pro	Ala	Ala	Leu	Ala	Gln	Thr	Ala	Gly	Pro
			20					25					30		
Ala	Pro	Leu	Arg	Ile	Ala	Asp	Leu	Arg	Pro	Ala	Ser	Leu	Gln	Ile	Glu
			35				40					45			
Gly	Arg	Asp	Pro	Pro	Met	Ser	Ile	Ala	Ser	His	Val	Pro	Leu	Leu	Glu
		50				55					60				
Ile	Ser	Thr	Glu	Asp	Ala	Ser	Phe	Ile	Lys	Val	His	Phe	Asp	His	Phe
65					70				75						80
Ser	Leu	Pro	Ala	Gly	Leu	Ala	Leu	Val	Val	Glu	Asn	Pro	Asp	Gly	Ser
			85					90					95		
Glu	Ala	Tyr	Arg	Tyr	Ser	Ser	His	Gln	Arg	Asp	Gly	His	Thr	Phe	Asp
			100					105					110		
Arg	Ser	Leu	Gly	His	Asn	Gly	Arg	Thr	Ser	Phe	Ser	Ala	Met	Ser	Ile
			115				120					125			
Ser	Gly	Pro	Arg	Ala	Val	Leu	Arg	Leu	Glu	Gly	Thr	Ala	Thr	Glu	Arg
			130			135					140				
Trp	Arg	Pro	His	His	Gly	Ile	Arg	Val	Ser	Gly	Tyr	His	Glu	Gly	Tyr
145					150					155					160
Pro	Asp	Glu	Met	Ile	Glu	Thr	Leu	Gln	Ser	Glu	Gly	Leu	Leu	Asp	Glu
				165					170					175	
Val	Gly	Thr	Gln	Ala	Ile	Cys	Gly	Ser	Asn	Asp	Lys	Arg	Gly	Val	Ala
			180					185					190		
Cys	Tyr	Ala	Ser	Ser	Glu	Pro	Ala	Ala	Val	Asp	Arg	Ser	Arg	Pro	Val
			195				200					205			
Ala	Arg	Leu	Val	Met	Ser	Gly	Ser	Leu	Cys	Thr	Ala	Trp	Arg	Val	Gly
			210			215					220				
Pro	Thr	Asn	Arg	Met	Phe	Thr	Asn	Asn	His	Cys	Met	Ser	Thr	Ala	Ala
225					230					235					240
Arg	Val	Ala	Ala	Ser	Glu	Val	Trp	Phe	Asn	His	Gln	Ala	Pro	Ser	Cys
				245					250					255	
Gly	Gly	Thr	Ser	Ala	Gly	Thr	Val	Val	Lys	Val	Ala	Gly	Asp	Gln	Met
			260					265					270		
Leu	Ala	Thr	Asn	Ser	Ser	Leu	Asp	Tyr	Thr	Leu	Phe	Thr	Val	Arg	Asp
			275				280					285			
Phe	Ala	Ser	Ile	Ala	Ser	Phe	Gly	Tyr	Leu	Gly	Leu	Asp	Ile	Ala	Ser
			290			295					300				
Thr	Gly	Val	Gly	Asp	Gln	Ile	Gln	Arg							
305					310										

&lt;210&gt; 135

&lt;211&gt; 3105

&lt;212&gt; DNA

&lt;213&gt; Unknown

&lt;220&gt;

10336256.txt

&lt;223&gt; Obtained from an environmental sample.

&lt;400&gt; 135

atgcttgcta	tagaaaaataa	taaaaatttc	aaactaggtg	aaaaagggtca	agatacagta	60
ataagtgc	taggtaaact	tataggggaac	gcctcttgta	atgctgaagt	agttaacaaa	120
acagttccta	tattagaaca	atattataga	gaaatgaaca	aatatccaaa	ggataaatta	180
aaagcggatg	ctgtatataa	tcttatgaaa	gagataaatt	atgatata	acaatatata	240
tatgatcata	atattagaga	tggtaaaaat	acaccttggt	ccagcaaaat	agatcctttc	300
ataaatacaa	tttcaaaatt	tcgaggata	tctaaagtta	cagaagataa	tggtctggatt	360
ataaataatg	gtatttatta	tactagttaa	ttcgctatat	atcatagcag	tccatctatt	420
cctcattcag	taatagacaa	atgtcttgaa	atccttcctg	cttatagtga	gcaatattat	480
attgcagtag	aaagaataaa	ggaagatttt	aattgtaaag	attcaaaagg	aaatgtttata	540
gacattgata	aattacttga	agatggtaaa	aaacattatt	tacctaanaac	ttatactttt	600
gataacggaa	aaatgattat	aaaagctgga	gataaagtag	aagaatcaaa	aattcaaaag	660
ctttattggg	catctaaaga	agtaaaatcc	caatttcata	ggataaagg	taataataaa	720
cctttagaag	caggtaatgc	tgatgatgtc	ctaactatgg	taatatataa	tagtccagaa	780
gaatataaac	taaatagaac	tttatatgga	tatagtgtag	acaatgggtg	aatatatatt	840
gaaggaaattg	gtacttttct	tacttatgaa	agaactccag	aggaaagcat	atatagtcta	900
gaagaacttt	tccgtcatga	gtttactcat	tacttaacag	gacgttattt	agtaccagga	960
ttattttaatg	aagggtgattt	ttataaaagga	aatagcggaa	gaatcacatg	gtttgaagaa	1020
ggttctgccc	aatttttttgc	aggctcaact	agaacttctg	tattaccaag	aaaatcaatg	1080
gttgggtggac	tttctgaaaa	ccctaagaaa	agatttagtg	cagataagat	attacattca	1140
aaatatgatg	atggatggga	attctacaaa	tatggatatg	ctttctcaga	ttatatgtat	1200
aataacaaca	aaaaactatt	tagcgattta	gtatctacta	tgaaaaataa	tgatgttaaa	1260
ggttatgaaa	acctaataga	aaatgcaagt	aaggatccta	atgttaacaa	aagctatcaa	1320
gatcacatgc	aaaaattagt	ggataattac	aataattaca	caataccact	agtatctgac	1380
gattacatga	aaaaatatag	taacaaaagc	ttaaatgaaa	taaaatcaga	tattgaaagt	1440
actatgaatt	taacaaattc	gcaaataact	aaagaaagt	ctcaatactt	tgatacttat	1500
actctaaaag	caaattacac	attagattcc	aacaaagggtg	aaattgataa	ttggaattgt	1560
atgaataata	aagttaatga	atctctagag	aaactaaaca	aattaggatg	gggcggatat	1620
aaaacagtta	ctgcttattt	ctcaaatcct	aaagtaaact	cacacaatca	ggtagaatat	1680
aatatagttt	tccatggatt	attaactcac	aacaaaaact	ttaacgaagc	accaacaatt	1740
aaattagatt	ttcctaagga	ggcaaataca	aacgaaaaaa	ttaaattttc	tagcgaaggc	1800
tcaactgatg	atggaaaaat	agtttcctat	gcttgggatc	ttggagatgg	tgaaactagc	1860
tcagaaaaaa	atcctactca	tgtttataaa	gctcctggta	cttacacagt	gaaacttaca	1920
gtaacagacg	acaaaggcat	taaatcagaa	aaaagtgc	ctataaacat	aaagaaagta	1980
cttacaggaa	atgcagtatc	agaaaaagaa	aataacaatg	attacgtaaa	tgctaaccga	2040
gtttattcta	aagatttagt	aagtggatct	gttagttcat	ccgacgatag	agatattttt	2100
tatttcaatg	ttactaagcc	ttcagatata	actataaatg	cggaaaaaat	taataaagat	2160
aaaagtgaat	ttacttggct	tttatttagc	gaagaagata	aatcaaaacta	tatagcctat	2220
ccaaataaaa	aactagaaaa	cttattttat	agcactgtaa	aaatagataa	acctggtaaa	2280
tactatttag	taatttataa	agttagtggg	gaaaaatcag	attatagatt	taatatagaa	2340
ggagatatat	cagcatctcc	aaaagatgat	actgataaag	atgaattagt	tatatctgaa	2400
aaggaagata	ataattcttt	tgacaaagct	aatagagttt	gtaaaaatca	atcagtaata	2460
gctacttttag	ataactaaca	tcctcgtagc	acatactatt	ttgatgcttt	aactgctggc	2520
aacatagaag	taactatgga	aaataccgat	aataattcta	atgaatttaa	ttggcttgct	2580
tacagttagcg	ataatactaa	taattatatt	ggatatgcta	caaaaagaga	aggtaataaa	2640
attataggaa	acttttaaagt	agataagcct	ggaagatact	atatagtggc	ttataagact	2700
tcttcaataa	aaatcaacta	caaattaaat	ataaaaagggtg	atattgataa	tgctccaaaa	2760
aatgatgaaa	tttatgaaaa	ggaaagtaat	gattcctttg	aaactgcaaa	taaaattatg	2820
cttaataacta	ccgtattagg	caacttaaat	gataaagatg	ttagagatat	ctattcattt	2880
gatataaaaa	aagctaaaga	tttagacata	aaactaaata	attttaaata	tttaggatta	2940
gcttgaatc	tttataaaga	atcagatttg	aataattata	ttgcttatgg	atcagtttca	3000
ggcaataacta	taaaagggaa	atgcaatgta	actcctggta	aatattactt	gtatgtatat	3060
aaatactctg	gtgacaatgg	caattattca	ttaacaataa	aataa		3105

&lt;210&gt; 136

&lt;211&gt; 1034

&lt;212&gt; PRT

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; Obtained from an environmental sample.

&lt;400&gt; 136

Met	Leu	Ala	Ile	Glu	Asn	Asn	Lys	Asn	Phe	Lys	Leu	Gly	Glu	Lys	Gly
1					5				10					15	
Gln	Asp	Thr	Val	Ile	Ser	Ala	Leu	Gly	Lys	Leu	Ile	Gly	Asn	Ala	Ser

## 10336256.txt

Cys Asn Ala Glu Val Val Asn Lys Thr Val Pro Ile Leu Glu Gln Tyr  
 Tyr Arg 35 Glu Met Asn Lys Tyr 40 Pro Lys Asp Lys Leu 45 Lys Ala Asp Ala  
 Val Tyr Asn Leu Met Lys 55 Glu Ile Asn Tyr Asp Ile Leu Gln Tyr Thr  
 65 Tyr Asp His Asn Ile Arg Asp Gly Lys Asn Thr Pro Trp Ser Ser Lys  
 Ile Asp Pro Phe 85 Ile Asn Thr Ile Ser Lys Phe Ala Gly Ile Ser Lys  
 Val Thr Glu Asp Asn Gly Trp Ile 105 Ile Asn Asn Gly Ile Tyr Tyr Thr  
 Ser Lys 115 Phe Ala Ile Tyr His 120 Ser Ser Pro Ser Ile 125 Pro His Ser Val  
 Ile 130 Asp Lys Cys Leu Glu 135 Ile Leu Pro Ala Tyr Ser Glu Gln Tyr Tyr  
 145 Ile Ala Val Glu Arg 150 Ile Lys Glu Asp Phe 155 Asn Cys Lys Asp Ser Lys  
 Gly Asn Val Ile Asp Ile Asp Lys Leu 170 Leu Glu Asp Gly Lys Lys His  
 Tyr Leu Pro 180 Lys Thr Tyr Thr Phe 185 Asn Gly Lys Met Ile Ile Lys  
 Ala Gly Asp Lys Val Glu Glu Ser Lys Ile Gln Arg Leu Tyr Trp Ala  
 Ser 210 Lys Glu Val Lys Ser Gln Phe His Arg Ile Ile Gly Asn Asp Lys  
 225 Pro Leu Glu Ala Gly Asn Ala Asp Asp Val Leu Thr Met Val Ile Tyr  
 Asn Ser Pro Glu Tyr Lys Leu Asn Arg Thr Leu Tyr Gly Tyr Ser  
 Val Asp Asn 260 Gly Gly Ile Tyr Ile Glu Gly Ile Gly Thr Phe Phe Thr  
 Tyr Glu Arg Thr Pro Glu Glu Ser Ile Tyr Ser Leu Glu Glu Leu Phe  
 Arg 290 His Glu Phe Thr His 310 Tyr Leu Gln Gly Arg Tyr Leu Val Pro Gly  
 305 Leu Phe Asn Glu Gly Asp Phe Tyr Lys Gly Asn Ser Gly Arg Ile Thr  
 Trp Phe Glu Glu Gly Ser Ala Glu Phe 345 Phe Ala Gly Ser Thr Arg Thr  
 Ser Val Leu Pro Arg Lys Ser Met Val Gly Gly Leu Ser Glu Asn Pro  
 Lys Glu Arg Phe Ser Ala Asp Lys Ile Leu His Ser Lys Tyr Asp Asp  
 Gly Trp Glu Phe Tyr Lys Tyr Gly Tyr Ala Phe Ser Asp Tyr Met Tyr  
 385 Asn Asn Asn Lys Lys 390 Leu Phe Ser Asp Leu Val Ser Thr Met Lys Asn  
 Asn Asp Val Lys Gly Tyr Glu Asn Leu Ile Glu Asn Ala Ser Lys Asp  
 Pro Asn Val 420 Asn Lys Ser Tyr Gln Asp His Met Gln Lys Leu Val Asp  
 Asn Tyr Asn Asn Tyr Thr Ile 440 Pro Leu Val Ser Asp Asp Tyr Met Lys  
 Lys Tyr Ser Asn Lys Ser Leu Asn Glu Ile Lys Ser Asp Ile Glu Ser  
 465 Thr Met Asn Leu Thr 470 Asn Ser Gln Ile Thr Lys Glu Ser Ser Gln Tyr  
 Phe Asp Thr Tyr Thr Leu Lys Ala Asn Tyr Thr Leu Asp Ser Asn Lys  
 Gly Glu Ile Asp Asn Trp Asn Cys 505 Met Asn Asn Lys Val Asn Glu Ser  
 Leu Glu Lys Leu Asn Lys Leu Gly Trp Gly Gly Tyr Lys Thr Val Thr  
 530 Ala Tyr Phe Ser Asn Pro Lys Val Asn Ser His Asn Gln Val Glu Tyr  
 545 Asn Ile Val Phe His Gly Leu Leu Thr His Asn Lys Asn Phe Asn Glu

## 10336256.txt

565  
 Ala Pro Thr Ile Lys Leu Asp Phe Pro Lys Glu Ala Asn Thr Asn Glu  
 570  
 Lys Ile Lys Phe Ser Ser Glu Gly Ser Thr Asp Asp Gly Lys Ile Val  
 585  
 Ser Tyr Ala Trp Asp Leu Gly Asp Gly Glu Thr Ser Ser Glu Lys Asn  
 590  
 Pro Thr His Val Tyr Lys Ala Pro Gly Thr Tyr Thr Val Lys Leu Thr  
 600  
 610  
 615  
 620  
 625  
 Val Thr Asp Asp Lys Gly Ile Lys Ser Glu Lys Ser Ala Ser Ile Asn  
 630  
 635  
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 675  
 680  
 685  
 690  
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 700  
 705  
 710  
 715  
 720  
 725  
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 950  
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 1020  
 1025  
 1030

<210> 137  
 <211> 705  
 <212> DNA  
 <213> Unknown

<220>  
 <223> Obtained from an environmental sample.

## 10336256.txt

```

<400> 137
ttgaaagctg taccacaggc agatatccct gctgggtttg aaaacacaca catgtgtaaa      60
gatgtttatc ttccgggaac tgatccaaga ggagctgtta ttaaaagcac aaaatggcca      120
aatggcagcg tcattactgt aagtctgaac ggtggaacag ccaaagttcg cagcaaagta      180
atgcaatatg ctaatgaatg gtctaagtat gctaacatta cttttaaat tttaccagc      240
ggaacagcac aaatccgggt tacctttaca caaggagcag gatcttattc ttatttagga      300
acacaagctc ttaatcgccc ttctaactct gaaacaatga acttcggttg gtttaatgat      360
tcaacaacag atacagagtt cagcagaaca acgattcatg aatttggaca tgctctaggt      420
atgatacagc agcaccagca tccttttagct aatatccctt gggataaaga aaaagtgtat      480
acctattatg gaggttatcc taactattgg tcaagagcac aggtagacag taacctgttt      540
gcaaaatatt ctactacaca aacgcaatat agtgcttatg atacacaatc tatcatgcat      600
tatagcatta gtagcagctt gacaacaaac ggattcagtg ttggcagcaa tactgttctt      660
tctactactg ataagcagtt tattgcatca gtatatccaa aataa      705

```

```

<210> 138
<211> 234
<212> PRT
<213> Unknown

```

```

<220>
<223> Obtained from an environmental sample.

```

```

<400> 138
Met Lys Ala Val Pro Gln Ala Asp Ile Pro Ala Gly Phe Glu Asn Thr
1      5      10      15
His Met Cys Lys Asp Val Tyr Leu Pro Gly Thr Asp Pro Arg Gly Ala
20      25      30
Val Ile Lys Ser Thr Lys Trp Pro Asn Gly Ser Val Ile Thr Val Ser
35      40      45
Leu Asn Gly Gly Thr Ala Lys Val Arg Ser Lys Val Met Gln Tyr Ala
50      55      60
Asn Glu Trp Ser Lys Tyr Ala Asn Ile Thr Phe Lys Phe Ile Thr Ser
65      70      75      80
Gly Thr Ala Gln Ile Arg Val Thr Phe Thr Gln Gly Ala Gly Ser Tyr
85      90      95
Ser Tyr Leu Gly Thr Gln Ala Leu Asn Arg Pro Ser Asn Ser Glu Thr
100      105      110
Met Asn Phe Gly Trp Phe Asn Asp Ser Thr Thr Asp Thr Glu Phe Ser
115      120      125
Arg Thr Thr Ile His Glu Phe Gly His Ala Leu Gly Met Ile His Glu
130      135      140
His Gln His Pro Leu Ala Asn Ile Pro Trp Asp Lys Glu Lys Val Tyr
145      150      155      160
Thr Tyr Tyr Gly Gly Tyr Pro Asn Tyr Trp Ser Arg Ala Gln Val Asp
165      170      175
Ser Asn Leu Phe Ala Lys Tyr Ser Thr Thr Gln Thr Gln Tyr Ser Ala
180      185      190
Tyr Asp Thr Gln Ser Ile Met His Tyr Ser Ile Ser Ser Ser Leu Thr
195      200      205
Thr Asn Gly Phe Ser Val Gly Ser Asn Thr Val Leu Ser Thr Thr Asp
210      215      220
Lys Gln Phe Ile Ala Ser Val Tyr Pro Lys
225      230

```

```

<210> 139
<211> 1428
<212> DNA
<213> Unknown

```

```

<220>
<223> Obtained from an environmental sample.

```

```

<400> 139
atggaaatgt caggaatgaa gcccgtcgac gcaaacaaga cccacaagcg catccggatc      60
gcagccggga ccgtggcgct cgccctgatg gcaacgggtt ccgtcgcgct ggctgccggc      120
ccgcaggccc gggcgggaa cgggacgtgg aaagtcagcc aggccttcgg caagcagcgc      180
accggccgca tcgtcggcgg catcggcgcg gtgggcgacc gttcggtcac ggtgcgcacc      240
tcgggctgcg gcggcacgat catcgccgac agctgggtgc tgaccgccgc gcattgcggc      300

```

## 10336256.txt

```

agccagagca ccgctctgggc aggctcgaac aacaccggca gccagacggc ctattccgtc 360
gcgcagtaca tccagcaccc caactacagc ccgaactcct ccgcaggcag ttacagcaac 420
gacttcgccc tgctccgcat caacggcacg ttcccggccc acctgatccg cgcgaaactg 480
cccgacgcgg cgatcatgca ggccatcgcc aagccaggcg atccggtgac cacgctgggc 540
tggggccgga cctcggaagg cggcagcagc accaccagcc tgcgcgaagt gaccgtcccg 600
gtcgtgtccg atgcaacctg cgccgcgtcc tacaacggca gttccgctgc cggcggcctc 660
aagctcaatc cggccgtgtc gatctgcgcc ggccctcgag cgggcggcca ggatgcctgc 720
cagggcgaca gcggcggccc gctgatcgcg ccctacaacg gctcgatcta cagcatcggc 780
gtcgtgagct acggactggg ctgcgcgcgg ccgaactatt acggcgtgta ttcggaaacg 840
gtcgccgtgc tggactggat caacggccac atcggcaacg gcggtggcag cggcaccgtc 900
atcaccgacg tcgttcttgt cgcgtcgaac ggctcgaccg cgccggccgg ccccgcgggc 960
tactcgctgg tcggttactg ggacgtcgac aagggcgggc cccagggcac gtacggcacc 1020
accggaagct tcatgaccgc gctgtacgtg cggcggcagc ttccttcgga aaccagcacc 1080
tgcgtcggcg ggatcggcct gtacacctcg gccggaagca ccgttcccgg cagcatcgcg 1140
cccaactgga cctatcgcgg catgtgggac atggacaagg gcggcggggg cggcaacctc 1200
aacagccagt ggcaggaata catgatgggc ctgtacacca ggccggcctc gactggccag 1260
ggcgccctgcc tcaccgatgt cgccctctac gcctcgaacg gctcgacgcc tgtcacgccc 1320
tcgggcttca gccaggtcgg ctgggtggac gtggacgcgg cgggcgcgtt cggcaccag 1380
ggttcacgcg gttcctacgt ggccacgctg tccacgaaga gcgagtga 1428

```

<210> 140  
 <211> 475  
 <212> PRT  
 <213> Unknown

<220>  
 <223> obtained from an environmental sample.

<221> SIGNAL  
 <222> (1)...(38)

<400> 140  
 Met Glu Met Ser Gly Met Lys Pro Val Asp Ala Asn Lys Thr His Lys  
 1 5 10 15  
 Arg Ile Arg Ile Ala Ala Gly Thr Val Ala Leu Ala Leu Met Ala Thr  
 20 25 30  
 Gly Ser Val Ala Leu Ala Ala Gly Pro Gln Ala Arg Ala Gly Asn Gly  
 35 40 45  
 Thr Trp Lys Val Ser Gln Ala Phe Gly Lys Gln Arg Thr Gly Arg Ile  
 50 55 60  
 Val Gly Gly Ile Gly Ala Val Gly Asp Arg Ser Phe Thr Val Arg Thr  
 65 70 75 80  
 Ser Gly Cys Gly Thr Ile Ile Ala Asp Ser Trp Val Leu Thr Ala  
 85 90 95  
 Ala His Cys Gly Ser Gln Ser Thr Val Trp Ala Gly Ser Asn Asn Thr  
 100 105 110  
 Gly Ser Gln Thr Ala Tyr Ser Val Ala Gln Tyr Ile Gln His Pro Asn  
 115 120 125  
 Tyr Ser Pro Asn Ser Ser Ala Gly Ser Tyr Ser Asn Asp Phe Ala Leu  
 130 135 140  
 Leu Arg Ile Asn Gly Thr Phe Pro Ala His Leu Ile Arg Ala Lys Leu  
 145 150 155 160  
 Pro Asp Ala Ala Ile Met Gln Ala Ile Ala Lys Pro Gly Asp Pro Val  
 165 170 175  
 Thr Thr Leu Gly Trp Gly Arg Thr Ser Glu Gly Gly Ser Ser Thr Thr  
 180 185 190  
 Ser Leu Arg Glu Val Thr Val Pro Val Val Ser Asp Ala Thr Cys Ala  
 195 200 205  
 Ala Ser Tyr Asn Gly Ser Ser Ala Ala Gly Gly Leu Lys Leu Asn Pro  
 210 215 220  
 Ala Val Ser Ile Cys Ala Gly Leu Ala Ala Gly Gly Gln Asp Ala Cys  
 225 230 235 240  
 Gln Gly Asp Ser Gly Gly Pro Leu Ile Ala Pro Tyr Asn Gly Ser Ile  
 245 250 255  
 Tyr Ser Ile Gly Val Val Ser Tyr Gly Leu Gly Cys Ala Arg Pro Asn  
 260 265 270  
 Tyr Tyr Gly Val Tyr Ser Glu Thr Val Ala Val Leu Asp Trp Ile Asn  
 275 280 285

10336256.txt

Gly His Ile Gly Asn Gly Gly Gly Ser Gly Thr Val Ile Thr Asp Val  
 290 295 300  
 Val Leu Val Ala Ser Asn Gly Ser Thr Ala Pro Ala Gly Pro Ala Gly  
 305 310 315 320  
 Tyr Ser Leu Val Gly Tyr Trp Asp Val Asp Lys Gly Gly Ala Gln Gly  
 325 330 335  
 Thr Tyr Gly Thr Thr Gly Ser Phe Met Thr Ala Leu Tyr Val Arg Arg  
 340 345 350  
 Gln Leu Pro Ser Glu Thr Ser Thr Cys Val Gly Gly Ile Gly Leu Tyr  
 355 360 365  
 Thr Ser Ala Gly Ser Thr Val Pro Gly Ser Ile Ala Pro Asn Trp Thr  
 370 375 380  
 Tyr Arg Gly Met Trp Asp Met Asp Lys Gly Gly Val Gly Asn Leu  
 385 390 395 400  
 Asn Ser Gln Trp Gln Glu Tyr Met Met Gly Leu Tyr Thr Arg Pro Ala  
 405 410 415  
 Ser Thr Gly Gln Gly Ala Cys Leu Thr Asp Val Ala Leu Tyr Ala Ser  
 420 425 430  
 Asn Gly Ser Thr Pro Val Thr Pro Ser Gly Phe Ser Gln Val Gly Trp  
 435 440 445  
 Trp Asp Val Asp Ala Gly Gly Ala Phe Gly Thr Gln Gly Ser Ser Gly  
 450 455 460  
 Ser Tyr Val Ala Thr Leu Ser Thr Lys Ser Glu  
 465 470 475

&lt;210&gt; 141

&lt;211&gt; 1755

&lt;212&gt; DNA

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; obtained from an environmental sample.

&lt;400&gt; 141

gtgaaaaaga	aagttgtatt	attggggctg	tctatgggtc	tattaagtaa	tcctgctatt	60
ggaacgggtat	gggcagaagg	agctgcgaat	cctgtatttt	ttcagaatga	gaatgaagaa	120
tcgaccacgt	ttacttcaac	tacctcggat	caattgcaaa	taaataaaaat	gaaggcatcc	180
ccittttgatg	tgatggcata	tgcaaagaga	tgaaaaagaa	agggtacaccg	taatcctgag	240
agcaacaaaag	tagaattcat	ttcagggcaa	tttaaacctt	aaaatcctta	taatttcaac	300
actgtttgttc	aggaattcgt	aggtgcaaac	tcggatgttt	ttaaagtaac	aacggaagac	360
accatacagg	taatgaaaga	agaaatgact	ccitttgggag	atttatgtaat	tcgtacccag	420
cagttcttca	gaggagtgcc	cgtatatggt	tcgacacaag	tattaaactt	aaatcaaaaa	480
ggagtggtaa	cagcatgggtc	cggagggatt	gtttcagaac	tgaacaagca	agaaaacctt	540
aataaagcaa	agaatccttag	tcaacaggca	gcgattcaaa	aagccgaaca	tgacctagggt	600
tttatccctg	agtattatat	tccaccggct	gtcgaactcg	taattttacat	gaaagaagag	660
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&lt;210&gt; 142

&lt;211&gt; 584

&lt;212&gt; PRT

10336256.txt

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; Obtained from an environmental sample.

&lt;221&gt; SIGNAL

&lt;222&gt; (1)...(25)

&lt;400&gt; 142

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Phe Phe Gln Asn Glu Asn Glu Glu Ser Thr Thr Phe Thr Ser Thr Thr
 35      40      45
Ser Asp Gln Leu Gln Ile Asn Lys Met Lys Ala Ser Pro Phe Asp Val
 50      55      60
Met Ala Tyr Ala Lys Arg Trp Lys Arg Lys Val His Arg Asn Pro Glu
 65      70      75      80
Ser Asn Lys Val Glu Phe Ile Ser Gly Gln Phe Lys Pro Lys Asn Pro
 85      90      95
Tyr Asn Phe Asn Thr Val Val Gln Glu Phe Val Gly Ala Asn Ser Asp
100      105      110
Val Phe Lys Val Thr Thr Glu Asp Thr Ile Gln Val Met Lys Glu Glu
115      120      125
Met Thr Pro Leu Gly Asp Tyr Val Ile Arg Thr Gln Gln Phe Phe Arg
130      135      140
Gly Val Pro Val Tyr Gly Ser Thr Gln Val Leu Asn Leu Asn Gln Lys
145      150      155      160
Gly Val Val Thr Ala Trp Ser Gly Gly Ile Val Ser Glu Leu Asn Lys
165      170      175
Gln Glu Asn Leu Asn Lys Ala Lys Asn Leu Ser Gln Gln Ala Ala Ile
180      185      190
Gln Lys Ala Glu His Asp Leu Gly Phe Ile Pro Glu Tyr Tyr Ile Pro
195      200      205
Pro Ala Val Glu Leu Val Ile Tyr Met Lys Glu Glu Ile Ala His Tyr
210      215      220
Ala Tyr His Val Asn Leu Asn Phe Leu Asn Pro Gln Pro Gly Asn Trp
225      230      235      240
Asp Tyr Phe Ile Asp Ala Asn Asp Gly Thr Ile Leu Asn Lys Val Asn
245      250      255
Arg Ile His Gln Val Gln Val Ala Arg Asn Met Val Asp Ser Asn Gln
260      265      270
Ile Gly Phe Gly Ile Gly Val His Gly Asp Lys Lys Gln Val Asn Thr
275      280      285
Val Phe Ser Asn Ser Tyr Tyr Tyr Leu Gln Asp Asn Thr Arg Gly Lys
290      295      300
Gly Ile Tyr Thr Tyr Asp Ala Lys Asn Ser Asn Arg Leu Pro Gly Thr
305      310      315      320
Leu Trp Arg Asn Ala Asp Asn Gln Phe Thr Ala Lys Tyr Asp Gly Pro
325      330      335
Ala Val Asp Ala His Tyr Tyr Ala Gly Val Val Tyr Asp Tyr Tyr Lys
340      345      350
Asn Lys Phe Asn Arg Asn Ser Tyr Asp Gly Ala Gly Ala Pro Ile Lys
355      360      365
Ser Thr Val His Tyr Gly Lys Ser Tyr Thr Asn Ala Phe Trp Asn Ser
370      375      380
Tyr Gln Met Val Tyr Gly Asp Gly Asp Gly Ser Thr Tyr Pro Phe Ser
385      390      395      400
Gly Ala Leu Asp Val Val Gly His Glu Leu Thr His Ala Val Thr Glu
405      410      415
Lys Thr Ala Asn Leu Ile Tyr Glu Asn Glu Ser Gly Ala Leu Asn Glu
420      425      430
Ala Met Ser Asp Ile Phe Gly Thr Leu Ile Glu Tyr Tyr Asn Asn Gln
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450      455      460
Phe Arg Ser Leu Ala Asp Pro Thr Lys Tyr Gly Asp Pro Asp His Tyr

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## 10336256.txt

465                      470                      475                      480  
 Ser Lys Arg Tyr Arg Gly Ser Asn Gln Ser Tyr Leu Val His Thr Asn  
                                  485                      490                      495  
 Ser Gly Ile Ile Asn Lys Ala Ala Tyr Leu Ile Ser Glu Gly Gly Thr  
                                  500                      505                      510  
 His Tyr Gly Val Thr Val Asn Gly Ile Gly Lys Glu Lys Leu Gly Asn  
                                  515                      520                      525  
 Ile Phe Tyr Arg Ala Leu Thr Gln Tyr Leu Thr Glu Ser Ala Thr Phe  
                                  530                      535                      540  
 Ser Gln Met Arg Ala Ala Ala Leu Gln Ala Ala Thr Asp Leu Tyr Gly  
 545                      550                      555                      560  
 Ala Ala Ser Ala Glu Val Ile Ser Val Gly Lys Ala Phe Asp Ala Val  
                                  565                      570                      575  
 Gly Val Asn Ser Ile Asp Leu Ser  
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&lt;210&gt; 143

&lt;211&gt; 2541

&lt;212&gt; DNA

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; obtained from an environmental sample.

&lt;400&gt; 143

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gtccccgtac	gcgaccggcc	cccgtaccc	gcctccacgg	acgcgtgcg	gcgtgactac	240
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accgtcacca	cgcagtactg	a				2541

10336256.txt

<210> 144  
 <211> 846  
 <212> PRT  
 <213> Unknown

<220>  
 <223> obtained from an environmental sample.

<221> SIGNAL  
 <222> (1)...(35)

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 Ala Ser Ala Thr Asp Pro Pro Pro Pro Ala Ala Gln Phe Leu  
 35 40 45  
 Ala Thr Arg Asp Pro Ala His Val Gln Lys Ser Arg Val Pro Val Arg  
 50 55 60  
 Asp Arg Pro Pro Leu Pro Ala Ser Thr Asp Ala Leu Arg Arg Asp Tyr  
 65 70 75 80  
 Asp Glu Ser Ala Gln Ala Gln Pro Arg Thr His Pro Arg Pro Ser Ala  
 85 90 95  
 Glu Arg Ala Ala Thr Ala Ala Ala Ala Cys Asp Val Thr Asp Phe  
 100 105 110  
 Thr Thr Arg Ser Gly Ser Glu Leu Val Arg Ala Ile Thr Ser Ser Thr  
 115 120 125  
 Thr Asp Cys Val Asn Thr Leu Phe Thr Leu Thr Gly Thr Asp Ala Asn  
 130 135 140  
 Ala Ala Phe Arg Glu Ser Gln Met Thr Thr Val Ala Tyr Ala Leu Arg  
 145 150 155 160  
 Asp Asn Ala Arg Ala Tyr Pro Gly Asp Asn Ser Thr Gly Thr Ala Gln  
 165 170 175  
 Leu Val Leu Tyr Leu Arg Ala Gly Tyr Val Gln Trp Tyr His Pro  
 180 185 190  
 Ser Asp Val Gly Ser Tyr Gly Pro Ala Leu Lys Thr Ala Ile Gln Ser  
 195 200 205  
 Gly Leu Asp Ala Phe Phe Gly Asn Ala Arg Ala Phe Thr Val Ala Asp  
 210 215 220  
 Ala Asn Gly Glu Val Leu Ser Glu Ala Val Thr Leu Ile Asp Ser Ala  
 225 230 235 240  
 Gln Glu Asn Asp Arg Tyr Leu Ser Val Val Lys Arg Leu Leu Asn Asp  
 245 250 255  
 Tyr Asn Ala Thr Tyr Asp Ala Ser Trp Trp Met Leu Asn Ala Val Asn  
 260 265 270  
 Asn Val Phe Thr Val Leu Phe Arg Ala His Gln Val Pro Ala Phe Val  
 275 280 285  
 Thr Ala Val Glu Ala Asp Arg Ser Val Leu Glu Thr Leu Arg Ser Phe  
 290 295 300  
 Ala Val Asn His Leu Asp Leu Leu Gly Thr Lys Asn Ala Phe Leu Thr  
 305 310 315 320  
 Ala Asn Ala Gly Arg Glu Leu Gly Arg Phe Leu Gln His Asp Ser Leu  
 325 330 335  
 Arg Gly Ala Val Arg Pro Leu Ala Lys Asp Leu Leu Gly Arg Ser Ser  
 340 345 350  
 Met Thr Gly Pro Thr Ala Arg Leu Trp Val Gly Val Ala Glu Met Ala  
 355 360 365  
 Asp Ala Tyr Asp Lys Ala Asn Cys Ser Tyr Tyr Gly Thr Cys Asp Leu  
 370 375 380  
 Ser Arg Arg Leu Gln Asp Val Val Leu Pro Val Ser His Thr Cys Ser  
 385 390 395 400  
 Ala ser Ile Lys Ile Arg Ala Gln Glu Met Thr Ala Glu Gln Leu Ala  
 405 410 415  
 Asp ser Cys Ala Ser Leu Ala Gly Gln Asp Ala Phe Phe His Asp Ile  
 420 425 430  
 Ala Lys Asp Gly Asp Arg Pro Val Ala Asp Asp Asn Asn Thr Thr Leu

## 10336256.txt

435 440 445  
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 450 455 460  
 Val Ile Phe Gly Ile Asp Thr Asn Asn Gly Gly Met Tyr Leu Glu Gly  
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 Asp Pro Ala Lys Ala Ser Asn Gln Pro Arg Phe Ile Ala Tyr Glu Ala  
 485 490 495  
 Glu Trp Val Arg Pro Arg Phe Glu Ile Trp Asn Leu Asn His Glu Tyr  
 500 505 510  
 Thr His Tyr Leu Asp Gly Arg Phe Asp Met Tyr Gly Asp Phe Glu Ala  
 515 520 525  
 Gly Met Thr Thr Pro Thr Val Trp Trp Val Glu Gly Phe Ala Glu Tyr  
 530 535 540  
 Val Ser Tyr Ser Tyr Arg Lys Leu Thr Tyr Glu Ala Ala Val Ala Glu  
 545 550 555 560  
 Ala Ala Lys Lys Thr Tyr Ala Leu Arg Thr Leu Phe Asp Thr Ala Tyr  
 565 570 575  
 Ser His Asp Thr Arg Ile Tyr Arg Trp Gly Tyr Leu Gly Val Arg  
 580 585 590  
 Tyr Met Leu Glu Arg His Pro Asp Asp Ile Ala Thr Leu Leu Gly His  
 595 600 605  
 Tyr Arg Thr Gly Ala Trp Asp Ala Ala Arg Thr Leu Leu Thr Gly Thr  
 610 615 620  
 Ile Gly Ser Arg Tyr Asp Ala Asp Trp Gln Thr Trp Leu Ala Ala Cys  
 625 630 635 640  
 Ala Ser Gly Ala Cys Ser Asp Gly Gly Ala Asn Lys Pro Pro Ala Ala  
 645 650 655 660  
 Ser Phe Thr Val Thr Ala Asn Ala Leu Ser Ala Gln Phe Thr Asp Thr  
 660 665 670  
 Ser Ala Asp Pro Asp Gly Arg Val Val Ser Arg Arg Trp Asp Phe Gly  
 675 680 685  
 Asp Gly Gly Ser Ser Thr Glu Ala Asn Pro Ser His Val Tyr Thr Ser  
 690 695 700  
 Gly Gly Thr Tyr Thr Val Thr Leu Thr Ala Thr Asp Asp Asp Gly Ala  
 705 710 715 720  
 Thr Gly Thr Ala Thr Arg Gln Val Thr Val Ser Ala Gly Gly Gly Ser  
 725 730 735  
 Leu Pro Glu Cys Ser Ser Ala Asp Thr Arg Gln Leu Asp Lys Asn Cys  
 740 745 750  
 Lys Arg Gly Asn Val Ser Ala Met Ser Gly Asn Tyr Ala Tyr Phe Tyr  
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 Ile Leu Ile Pro Glu Gly Val Arg Arg Leu Thr Val Thr Ser Ser Gly  
 770 775 780  
 Gly Thr Gly Asn Ala Asp Leu Tyr Tyr Tyr Trp Lys Gln Trp Ala Thr  
 785 790 795 800  
 Thr Thr Ala His Asn Tyr Arg Ser Thr Thr Ala Gly Asn Glu Glu Thr  
 805 810 815  
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 <211> 4772  
 <212> DNA  
 <213> Unknown

<220>  
 <223> obtained from an environmental sample.

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 ga t g g g g c t c ca g ac g ca ac c c c t c ag g ta c g g t t c t c t t c ga t ga ac t g c at t c t g at 180  
 g t c g c g t g g t c t g c g g c t c g c ag g ag c c t c g c c t c c c a c c g t c at t t c c g c g t g g g t 240  
 t g c c t t g c a c g a c g t c g t t a at c g t g c a a c t c g g a c a c g a t a a a t a at c g t g t c c c a c g 300  
 a ac g c c a ac t c a c c c t g a a t g c t t t c c a g ca at t c g c g c g g c g a c g a g g c g t t g g c c 360  
 g c g t t g t t c g t c a at t c t c c a g g g c g g c g a g ga t g t t c t t g c g g a c g g t g g t g c g g a c g t c 420

## 10336256.txt

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## 10336256.txt

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 <212> DNA  
 <213> Unknown

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 <212> PRT  
 <213> Unknown

<220>  
 <223> Obtained from an environmental sample.

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10336256.txt

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 50 55 60  
 Pro Val Leu Thr Ser Ile Ala Leu Gln Gly Ala Gly Gly Ser Asp Pro  
 65 70 75 80  
 Pro Ala Ala Trp Ser Ala Arg Glu Gln Thr Leu Val Asp Val Arg Ser  
 85 90 95  
 Ile Val Gly Thr Asp Gly Lys Pro Ala Asp Arg Phe Leu Cys Ala Pro  
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 Pro Gly Arg Asp Pro Asn Ser Ala Ala Thr Thr Leu Pro Glu Arg Ser  
 115 120 125  
 Leu Ala Gly Ala Val Val Leu Ala Trp Arg Gly Asn Cys Ser Phe Val  
 130 135 140  
 Ser Lys Ala Glu Arg Ala Lys Ser Ala Gly Ala Ala Gly Met Ile Leu  
 145 150 155 160  
 Val Asp Asn Arg Pro Gly Asp Thr Tyr Pro Ile Pro Val Ala Gly Leu  
 165 170 175  
 Ala Val Pro Ser Gly Met Val Gly Asp Val Asp Gly Ala His Leu Gly  
 180 185 190  
 Val Phe Leu Gln Ala Thr Gly Gly Arg Thr Thr Phe Arg Val Gly Arg  
 195 200 205  
 Ser Val Ser Glu Ile Val Thr Gly Arg Ser Gly Val Val Ala Ser Phe  
 210 215 220  
 Ser Ser Gly Gly Pro Thr Pro Phe Gly His Gln Leu Lys Pro Asp Val  
 225 230 235 240  
 Ala Ala Pro Gly Thr Gln Val Leu Ser Ser Thr Pro Pro Ala Ala Thr  
 245 250 255  
 Arg Thr Thr Phe Tyr Pro Leu Asp Gly Thr Ser Met Ala Thr Pro His  
 260 265 270  
 Val Ala Gly Ala Ala Ala Leu Leu Leu Gln Arg His Pro Ala Trp Ser  
 275 280 285  
 Pro Gln Glu Val Lys Ser Ala Leu Met Ser Thr Gly Val Pro Ala Trp  
 290 295 300  
 Ala Asp Ser Ala Arg Thr Gln Glu Ala Pro Val Leu Leu Glu Gly Gly  
 305 310 315 320  
 Gly Leu Val Asp Val Gly Arg Ala Asp Asp Pro Gly Ile Phe Thr Ser  
 325 330 335  
 Pro Ala Ser Leu Ser Phe Gly Asp Val Asn Val Ser His Gly Ala Gln  
 340 345 350  
 Thr Ala Pro Leu Leu Leu Ala Val Ser Asp Ala Gly Ala Gly  
 355 360 365  
 Thr Trp Asp Val Glu Leu Arg Pro Gln Ser Thr Ser Ala Gly Ala Ser  
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 385 390 395 400  
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 420 425 430  
 Tyr Phe Phe Ser Val Thr Arg Pro Gln Val Pro Leu Ala Pro Met Leu  
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 Gly Pro Leu Lys Lys Leu Gln Ala Gly Asp Thr Arg Ser Gly Ala Ser  
 450 455 460  
 Leu Val Arg Gln Tyr Arg Tyr Pro Thr Tyr Pro Phe Gly Pro Pro Pro  
 465 470 475 480  
 Gly Tyr Thr Gly Pro Met Asp Glu Ser Gly Gly Glu His Val Tyr  
 485 490 495  
 Thr Val Arg Val Thr Asp Pro Ala Val Asn Val Gly Val Ser Val Ile  
 500 505 510  
 Ala Ala Gly Pro Asn Ala Leu Val Asp Pro Trp Met Leu Ser Ala Leu  
 515 520 525  
 Asp Glu Asn Thr Val Val Gly Leu Ala Gly Thr Pro Val Ser Val Asn  
 530 535 540  
 Asn Leu Ala Ile Asp Trp Arg Phe Asp Val Gly Ala Ala Ala Val  
 545 550 555 560  
 Phe Pro Arg Arg Gln Gln Gln Leu Tyr Val Val Val Asp Ser Gly Ser

## 10336256.txt

Asp Glu Leu Thr Gly Glu Pro Leu Pro Gly Gln Tyr Val Leu Asn Ala  
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 595 600 605  
 Val Ser Ala Gly Arg Pro Leu Leu Ala Leu Arg Ala Leu Asp Ala Gly  
 610 615 620  
 Ala Gly Val Asp Pro Leu Ser Leu Val Ile Ala Tyr Gly Arg Val Leu  
 625 630 635 640  
 Val Gly Ala Ala Ala Tyr Asp Pro Val Ser Gly Leu Ala Leu Phe Pro  
 645 650 655  
 Leu Pro Pro Asp Val Pro Ala Leu Ser Thr Gly Thr Thr Ser Ala Glu  
 660 665 670  
 Leu Leu Ala Ser Asp Phe Gln Glu Ala Lys Asn Val Asp Thr Pro Gly  
 675 680 685  
 Gly Glu Ile Leu Pro Asn Thr Arg Phe Val Gln Ser Arg Ile Arg Val  
 690 695 700  
 Val Asp Gly Pro Ala Leu Thr Trp Leu Ala Pro Ala Gly Ser Cys  
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 Arg Thr Gly Pro Ile Gly Leu Tyr Ser Ala Thr Trp Arg Thr Ala Gly  
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 785 790 795

&lt;210&gt; 148

&lt;211&gt; 4437

&lt;212&gt; DNA

&lt;213&gt; Cochliobolus heterostrophus strain C4 (ATCC 48331)

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (203)...(1426)

&lt;223&gt; Exon

&lt;400&gt; 148

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tttttaaaca ccagtatcca tc atg gtg gga agc gtc aac aag ttt ctg gcc	232
Met Val Gly Ser Val Asn Lys Phe Leu Ala	
1 5 10	
att gcc ggc act gcc tcg gca gcc gtc ttc gac ctg ccc gtt gtc atc	280
Ile Ala Gly Thr Ala Ser Ala Ala Val Phe Asp Leu Pro Val Val Ile	
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Lys Ser Thr Tyr Ser Ser Val Lys Phe Asp Ile Gly Thr Pro Pro Lys	
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gaa cac cag cta ctg ttc gat acc ggc tcg tca acc ctc tgg acc gtt	376
Glu His Gln Leu Leu Phe Asp Thr Gly Ser Ser Thr Leu Trp Thr Val	
45 50 55	
agc act gac tgc aca caa gac tcg tgt cca gaa gga agc acg gag ctg	424
Ser Thr Asp Cys Thr Gln Asp Ser Cys Pro Glu Gly Ser Thr Glu Leu	
60 65 70	
tat aaa cga cgg tac tac aat gca tcg gca tca tcc acg gcc gtc gat	472
Tyr Lys Arg Arg Tyr Tyr Asn Ala Ser Ala Ser Ser Thr Ala Val Asp	
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aac cag tca ttc att gca gtc aat aag agc tca tgg ctt tgg atc act Asn Gln Ser Phe Ile Ala Val Asn Lys Ser Ser Trp Leu Trp Ile Thr 125 130 135	616
gca gac ggt ttt ctg ggc ctt ggc ttc tct acc atc gca gag cct aac Ala Asp Gly Phe Leu Gly Leu Gly Phe Ser Thr Ile Ala Glu Pro Asn 140 145 150	664
acg tcg aca ctg gtc gaa acg ctg cta tgg gat ggc aag cta gac aaa Thr Ser Thr Leu Val Glu Thr Leu Leu Trp Asp Gly Lys Leu Asp Lys 155 160 165 170	712
ccc cga ttc ggc cta tac tat ggc aca aac cta gga gac gag ggc cct Pro Arg Phe Gly Leu Tyr Tyr Gly Thr Asn Leu Gly Asp Glu Gly Pro 175 180 185	760
cag gac ggt gta ctg agc att ggc gac agt cac gag gac aag ttt gtt Gln Asp Gly Val Leu Ser Ile Gly Asp Ser His Glu Asp Lys Phe Val 190 195 200	808
gat ggc cag gtg gtt tat gct cct ctg cag aag gtc aac aac gag tat Asp Gly Gln Val Val Tyr Ala Pro Leu Gln Lys Val Asn Asn Glu Tyr 205 210 215	856
gat cta tgg cgc aca ccg ttg aag gct gtc aac cta ctg gtc gcc aag Asp Leu Trp Arg Thr Pro Leu Lys Ala Val Asn Leu Leu Val Ala Lys 220 225 230	904
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ccc acg acg cag ttt tct ggc aat gcc ata gag tca ccc aat gtg act Pro Thr Thr Gln Phe Ser Gly Asn Ala Ile Glu Ser Pro Asn Val Thr 255 260 265	1000
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gcg ccc gag aac gat gtc gta gtt agc att cgc ggc gat gaa tta ctc Ala Pro Glu Asn Asp Val Val Val Ser Ile Arg Gly Asp Glu Leu Leu 335 340 345	1240
aag cct gga gct caa tgt atg cca ccg ttt gac cct tcc aac gca cct Lys Pro Gly Ala Gln Cys Met Pro Pro Phe Asp Pro Ser Asn Ala Pro 350 355 360	1288

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Trp Asp Phe Gly Ala Asp Lys Val Ala Glu Tyr Lys Pro Arg Leu Gly	
380 385 390	
ttt ggt agg ctc aag aag cag ttt gac tgg aag tat cag tca	1426
Phe Gly Arg Leu Lys Lys Gln Phe Asp Trp Lys Tyr Gln Ser	
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catttacac c	4437

&lt;210&gt; 149

&lt;211&gt; 408

&lt;212&gt; PRT

&lt;213&gt; Cochliobolus heterostrophus strain C4 (ATCC 48331)

10336256.txt

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 35 40 45  
 Asp Thr Gly Ser Ser Thr Leu Trp Thr Val Ser Thr Asp Cys Thr Gln  
 50 55 60  
 Asp Ser Cys Pro Glu Gly Ser Thr Glu Leu Tyr Lys Arg Arg Tyr Tyr  
 65 70 75 80  
 Asn Ala Ser Ala Ser Thr Ala Val Asp Val Gly Ile Pro Ala Thr  
 85 90 95  
 Ile Pro Tyr Leu Gly Gly Asn Val Glu Gly Glu Ile Tyr Gln Asp Val  
 100 105 110  
 Phe Ser Ala Leu Asp Gly Ser Val Glu Trp Asn Gln Ser Phe Ile Ala  
 115 120 125  
 Val Asn Lys Ser Ser Trp Leu Trp Ile Thr Ala Asp Gly Phe Leu Gly  
 130 135 140  
 Leu Gly Phe Ser Thr Ile Ala Glu Pro Asn Thr Ser Thr Leu Val Glu  
 145 150 155 160  
 Thr Leu Leu Trp Asp Gly Lys Leu Asp Lys Pro Arg Phe Gly Leu Tyr  
 165 170 175  
 Tyr Gly Thr Asn Leu Gly Asp Glu Gly Pro Gln Asp Gly Val Leu Ser  
 180 185 190  
 Ile Gly Asp Ser His Glu Asp Lys Phe Val Asp Gly Gln Val Val Tyr  
 195 200 205  
 Ala Pro Leu Gln Lys Val Asn Asn Glu Tyr Asp Leu Trp Arg Thr Pro  
 210 215 220  
 Leu Lys Ala Val Asn Leu Val Ala Lys Asn Pro Ser Asn Pro Asn  
 225 230 235 240  
 His Thr Val Glu Thr His Ile Gly Lys Leu Pro Thr Thr Gln Phe Ser  
 245 250 255  
 Gly Asn Ala Ile Glu Ser Pro Asn Val Thr Leu Ser Thr Phe Gly Asp  
 260 265 270  
 Gly Thr Ala Ile Phe Asp Thr Gly Ala Gly Gly Leu Ser Leu Pro Glu  
 275 280 285  
 Asp Met Ile Asp Ser Ile Tyr Tyr Asn Leu Gly Trp Asp Tyr Gln Ser  
 290 295 300  
 Leu Leu Asn Gly Lys Gln Arg Phe Thr Cys Glu Ala Met Asn Ala Ser  
 305 310 315 320  
 Trp Ala Ile Ser Leu Ile Leu Gly Glu Gly Ala Pro Glu Asn Asp Val  
 325 330 335  
 Val Val Ser Ile Arg Gly Asp Glu Leu Leu Lys Pro Gly Ala Gln Cys  
 340 345 350  
 Met Pro Pro Phe Asp Pro Ser Asn Ala Pro Ser Phe Ala Leu Val Gly  
 355 360 365  
 Thr Thr Leu Leu Gln Arg Tyr Tyr Thr Ile Trp Asp Phe Gly Ala Asp  
 370 375 380  
 Lys Val Ala Glu Tyr Lys Pro Arg Leu Gly Phe Gly Arg Leu Lys Lys  
 385 390 395 400  
 Gln Phe Asp Trp Lys Tyr Gln Ser  
 405

&lt;210&gt; 150

&lt;211&gt; 1224

&lt;212&gt; DNA

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1224)

&lt;223&gt; Exon

&lt;400&gt; 150

atg gtg gga agc gtc aac aag ttt ctg gcc att gcc ggc act gcc tcg  
 Met Val Gly Ser Val Asn Lys Phe Leu Ala Ile Ala Gly Thr Ala Ser  
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1	5	10	15		
gca gcc gtc ttc gac ctg ccc gtt gtc atc aag agc aca tac agc agc	Ala Ala Val Phe Asp Leu Pro Val Val Ile Lys Ser Thr Tyr Ser Ser	20	25	30	96
gtc aag ttc gac atc ggc acg ccc ccg aaa gaa cac cag cta ctg ttc	Val Lys Phe Asp Ile Gly Thr Pro Pro Lys Glu His Gln Leu Leu Phe	35	40	45	144
gat acc ggc tcg tca acc ctc tgg acc gtt agc act gac tgc aca caa	Asp Thr Gly Ser Ser Thr Leu Trp Thr Val Ser Thr Asp Cys Thr Gln	50	55	60	192
gac tcg tgt cca gaa gga agc acg gag ctg tat aaa cga cgg tac tac	Asp Ser Cys Pro Glu Gly Ser Thr Glu Leu Tyr Lys Arg Arg Tyr Tyr	65	70	75	240
aat gca tcg gca tca tcc acg gcc gtc gat gtt ggc att ccc gcc aca	Asn Ala Ser Ala Ser Ser Thr Ala Val Asp Val Gly Ile Pro Ala Thr	85	90	95	288
att cct tac ttg ggc ggt aac gtt gag ggc gaa att tat cag gat gtc	Ile Pro Tyr Leu Gly Gly Asn Val Glu Gly Glu Ile Tyr Gln Asp Val	100	105	110	336
ttc agc gct cta gat ggg tcc gtg gaa tgg aac cag tca ttc att gca	Phe Ser Ala Leu Asp Gly Ser Val Glu Trp Asn Gln Ser Phe Ile Ala	115	120	125	384
gtc aat aag agc tca tgg ctt tgg atc act gca gac ggt ttt ctg ggc	Val Asn Lys Ser Ser Trp Leu Trp Ile Thr Ala Asp Gly Phe Leu Gly	130	135	140	432
ctt ggc ttc tct acc atc gca gag cct aac acg tcg aca ctg gtc gaa	Leu Gly Phe Ser Thr Ile Ala Glu Pro Asn Thr Ser Thr Leu Val Glu	145	150	155	480
acg ctg cta tgg gat ggc aag cta gac aaa ccc cga ttc ggc cta tac	Thr Leu Leu Trp Asp Gly Lys Leu Asp Lys Pro Arg Phe Gly Leu Tyr	165	170	175	528
tat ggc aca aac cta gga gac gag ggc cct cag gac ggt gta ctg agc	Tyr Gly Thr Asn Leu Gly Asp Glu Gly Pro Gln Asp Gly Val Leu Ser	180	185	190	576
att ggc gac agt cac gag gac aag ttt gtt gat ggc cag gtg gtt tat	Ile Gly Asp Ser His Glu Asp Lys Phe Val Asp Gly Gln Val Val Tyr	195	200	205	624
gct cct ctg cag aag gtc aac aac gag tat gat cta tgg cgc aca ccg	Ala Pro Leu Gln Lys Val Asn Asn Glu Tyr Asp Leu Trp Arg Thr Pro	210	215	220	672
ttg aag gct gtc aac cta ctg gtc gcc aag aac ccg tcc aac cca aac	Leu Lys Ala Val Asn Leu Leu Val Ala Lys Asn Pro Ser Asn Pro Asn	225	230	235	720
cac aca gtc gag acg cac att ggc aaa ctg ccc acg acg cag ttt tct	His Thr Val Glu Thr His Ile Gly Lys Leu Pro Thr Thr Gln Phe Ser	245	250	255	768
ggc aat gcc ata gag tca ccc aat gtg act ttg tca acg ttc ggc gac	Gly Asn Ala Ile Glu Ser Pro Asn Val Thr Leu Ser Thr Phe Gly Asp	260	265	270	816
ggc act gcc att ttc gac acg gga gct ggc ggc ctt tcc ctg cca gaa	Gly Thr Ala Ile Phe Asp Thr Gly Ala Gly Gly Leu Ser Leu Pro Glu				864

## 10336256.txt

275					280					285						
gat	atg	att	gat	tcc	ata	tac	tac	aat	ctc	ggc	tgg	gat	tac	caa	agt	912
Asp	Met	Ile	Asp	Ser	Ile	Tyr	Tyr	Asn	Leu	Gly	Trp	Asp	Tyr	Gln	Ser	
	290					295					300					
ctg	ctc	aac	ggc	aag	cag	cgc	ttt	aca	tgc	gag	gcc	atg	aac	gca	tcc	960
Leu	Leu	Asn	Gly	Lys	Gln	Arg	Phe	Thr	Cys	Glu	Ala	Met	Asn	Ala	Ser	
305					310					315					320	
tgg	gcc	att	tct	cta	atc	ctt	ggt	gaa	ggt	gcg	ccc	gag	aac	gat	gtc	1008
Trp	Ala	Ile	Ser	Leu	Ile	Leu	Gly	Glu	Gly	Ala	Pro	Glu	Asn	Asp	Val	
				325					330					335		
gta	gtt	agc	att	cgc	ggc	gat	gaa	tta	ctc	aag	cct	gga	gct	caa	tgt	1056
Val	Val	Ser	Ile	Arg	Gly	Asp	Glu	Leu	Leu	Lys	Pro	Gly	Ala	Gln	Cys	
			340					345					350			
atg	cca	ccg	ttt	gac	cct	tcc	aac	gca	cct	tca	ttt	gcg	ctt	gtt	ggc	1104
Met	Pro	Pro	Phe	Asp	Pro	Ser	Asn	Ala	Pro	Ser	Phe	Ala	Leu	Val	Gly	
		355					360					365				
act	acc	tta	ctc	cag	agg	tac	tac	act	ata	tgg	gac	ttt	ggt	gcg	gac	1152
Thr	Thr	Leu	Leu	Gln	Arg	Tyr	Tyr	Thr	Ile	Trp	Asp	Phe	Gly	Ala	Asp	
	370					375					380					
aag	gtg	gcc	gag	tac	aag	cct	cgg	ctt	gga	ttt	ggt	agg	ctc	aag	aag	1200
Lys	Val	Ala	Glu	Tyr	Lys	Pro	Arg	Leu	Gly	Phe	Gly	Arg	Leu	Lys	Lys	
385					390					395					400	
cag	ttt	gac	tgg	aag	tat	cag	tca									1224
Gln	Phe	Asp	Trp	Lys	Tyr	Gln	Ser									
				405												

&lt;210&gt; 151

&lt;211&gt; 408

&lt;212&gt; PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

&lt;220&gt;

&lt;221&gt; DOMAIN

&lt;222&gt; (5)...(389)

&lt;223&gt; Eukaryotic aspartyl protease

&lt;400&gt; 151

Met	Val	Gly	Ser	Val	Asn	Lys	Phe	Leu	Ala	Ile	Ala	Gly	Thr	Ala	Ser
1				5					10					15	
Ala	Ala	Val	Phe	Asp	Leu	Pro	Val	Val	Ile	Lys	Ser	Thr	Tyr	Ser	Ser
			20				25						30		
Val	Lys	Phe	Asp	Ile	Gly	Thr	Pro	Lys	Glu	His	Gln	Leu	Leu	Phe	
		35				40					45				
Asp	Thr	Gly	Ser	Ser	Thr	Leu	Trp	Thr	Val	Ser	Thr	Asp	Cys	Thr	Gln
	50				55						60				
Asp	Ser	Cys	Pro	Glu	Gly	Ser	Thr	Glu	Leu	Tyr	Lys	Arg	Arg	Tyr	Tyr
65				70					75					80	
Asn	Ala	Ser	Ala	Ser	Ser	Thr	Ala	Val	Asp	Val	Gly	Ile	Pro	Ala	Thr
			85						90				95		
Ile	Pro	Tyr	Leu	Gly	Gly	Asn	Val	Glu	Gly	Glu	Ile	Tyr	Gln	Asp	Val
		100					105					110			
Phe	Ser	Ala	Leu	Asp	Gly	Ser	Val	Glu	Trp	Asn	Gln	Ser	Phe	Ile	Ala
		115				120					125				
Val	Asn	Lys	Ser	Ser	Trp	Leu	Trp	Ile	Thr	Ala	Asp	Gly	Phe	Leu	Gly
	130				135					140					
Leu	Gly	Phe	Ser	Thr	Ile	Ala	Glu	Pro	Asn	Thr	Ser	Thr	Leu	Val	Glu
	145				150				155					160	
Thr	Leu	Leu	Trp	Asp	Gly	Lys	Leu	Asp	Lys	Pro	Arg	Phe	Gly	Leu	Tyr
				165					170					175	

10336256.txt

```

Tyr Gly Thr Asn Leu Gly Asp Glu Gly Pro Gln Asp Gly Val Leu Ser
180 185 190
Ile Gly Asp Ser His Glu Asp Lys Phe Val Asp Gly Gln Val Val Tyr
195 200 205
Ala Pro Leu Gln Lys Val Asn Asn Glu Tyr Asp Leu Trp Arg Thr Pro
210 215 220
Leu Lys Ala Val Asn Leu Val Ala Lys Asn Pro Ser Asn Pro Asn
225 230 235 240
His Thr Val Glu Thr His Ile Gly Lys Leu Pro Thr Thr Gln Phe Ser
245 250 255
Gly Asn Ala Ile Glu Ser Pro Asn Val Thr Leu Ser Thr Phe Gly Asp
260 265 270
Gly Thr Ala Ile Phe Asp Thr Gly Ala Gly Gly Leu Ser Leu Pro Glu
275 280 285
Asp Met Ile Asp Ser Ile Tyr Tyr Asn Leu Gly Trp Asp Tyr Gln Ser
290 295 300
Leu Leu Asn Gly Lys Gln Arg Phe Thr Cys Glu Ala Met Asn Ala Ser
305 310 315 320
Trp Ala Ile Ser Leu Ile Leu Gly Glu Gly Ala Pro Glu Asn Asp Val
325 330 335
Val Val Ser Ile Arg Gly Asp Glu Leu Lys Pro Gly Ala Gln Cys
340 345 350
Met Pro Pro Phe Asp Pro Ser Asn Ala Pro Ser Phe Ala Leu Val Gly
355 360 365
Thr Thr Leu Leu Gln Arg Tyr Tyr Thr Ile Trp Asp Phe Gly Ala Asp
370 375 380
Lys Val Ala Glu Tyr Lys Pro Arg Leu Gly Phe Gly Arg Leu Lys Lys
385 390 395 400
Gln Phe Asp Trp Lys Tyr Gln Ser
405

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&lt;210&gt; 152

&lt;211&gt; 3002

&lt;212&gt; DNA

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (257)...(304)

&lt;223&gt; Exon

&lt;221&gt; CDS

&lt;222&gt; (363)...(428)

&lt;223&gt; Exon

&lt;221&gt; CDS

&lt;222&gt; (588)...(725)

&lt;223&gt; Exon

&lt;221&gt; CDS

&lt;222&gt; (774)...(950)

&lt;223&gt; Exon

&lt;221&gt; CDS

&lt;222&gt; (1001)...(2290)

&lt;223&gt; Exon

&lt;400&gt; 152

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gcttggttgc cgtggcgggg cttgctgaac cttttgtcgt gctactacat ggtttggtcc 60
gttggtttgt ttgcggtgtt tatcacacaa gtgcaaacctt tggatacttc caccggtgcc 120
tgagcagtat gtagggagat tctgaaaccc tctagagggc atgttcgacc tacgtgatga 180
aagatcaagc tgagtagacg ttggcgggca ctttgcaaac ggccagttgc gcgtgttggt 240
tgctactagt caagca atg ggc cga gca agc cgt aac ttg cca tca tac cct 292
          Met Gly Arg Ala Ser Arg Asn Leu Pro Ser Tyr Pro
          1 5 10

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cgc ctt cct aac caggtataga gctgggttcc agttttccaa cctaatatcg
Arg Leu Pro Asn

```

344

15

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## 10336256.txt

aaa Lys	gtg Val 230	tac Tyr	atc Ile	acc Thr	ggc Gly	gag Glu 235	tca Ser	tac Tyr	gct Ala	ggg Gly	cgc Arg 240	tac Tyr	gtc Val	ccc Pro	tac Tyr	1303
att Ile 245	gcc Ala	gac Asp	gcc Ala	atg Met	ctg Leu 250	agc Ser	aag Lys	aac Asn	gac Asp	tca Ser 255	aca Thr	tac Tyr	tac Tyr	gac Asp	gtc Val 260	1351
aag Lys	ggc Gly	gtc Val	atg Met	ttt Phe 265	tac Tyr	gac Asp	ccc Pro	agc Ser	gta Val 270	gcc Ala	gaa Glu	gac Asp	ggc Gly	ctc Leu 275	cta Leu	1399
acc Thr	gac Asp	gtc Val	cct Pro 280	gcc Ala	gtc Val	gcc Ala	tac Tyr	gtc Val 285	gac Asp	gaa Glu	tgg Trp	gcc Ala	ggt Gly 290	ctc Leu	ttc Phe	1447
aac Asn	ttc Phe	aac Asn 295	cag Gln	agc Ser	ttc Phe	atg Met	gac Asp 300	gac Asp	atc Ile	cac His	gcc Ala	cgc Arg 305	gcc Ala	gac Asp	gcc Ala	1495
tgc Cys	ggc Gly 310	tac Tyr	acc Thr	gag Glu	tac Tyr	atg Met 315	gaa Glu	aaa Lys	tac Tyr	ctc Leu	act Thr 320	ttc Phe	ccc Pro	ccg Pro	acc Thr	1543
agc Ser 325	aaa Lys	ttc Phe	ccc Pro	acc Thr	ccg Pro 330	gcc Ala	aac Asn	aac Asn	tcc Ser	gac Asp 335	aca Thr	gaa Glu	ggc Gly	tgc Cys	tcc Ser 340	1591
ctt Leu	tgg Trp	caa Gln	gac Asp	att Ile 345	ttc Phe	gac Asp	gcc Ala	gtt Val	atc Ile 350	tac Tyr	aca Thr	aac Asn	ccc Pro	tgc Cys 355	ttc Phe	1639
gac Asp	gtc Val	tac Tyr	gca Ala 360	atc Ile	gca Ala	acc Thr	acc Thr	tgc Cys 365	cct Pro	ctc Leu	ctc Leu	tgg Trp	gac Asp 370	ccc Pro	ctc Leu	1687
ggc Gly	ttc Phe	ccc Pro 375	ggc Gly	tcc Ser	ttc Phe	gac Asp	tac Tyr 380	ctg Leu	cct Pro	cca Pro	cgc Arg	acc Thr 385	gaa Glu	atc Ile	tac Tyr	1735
ttt Phe 390	aac Asn	cgc Arg	agc Ser	gac Asp	gtt Val	cag Gln 395	gcc Ala	gcc Ala	atc Ile	aac Asn	gcg Ala 400	ccc Pro	atc Ile	cag Gln	ccc Pro	1783
tgg Trp 405	gcc Ala	gag Glu	tgc Cys	tcc Ser	aac Asn 410	ggc Gly	gtc Val	ctc Leu	gac Asp	aca Thr 415	gat Asp	acc Thr	tcg Ser	ccc Pro	ccg Pro 420	1831
tcg Ser	tcc Ser	tgg Trp	gaa Glu	gtc Val 425	atc Ile	ccc Pro	cgc Arg	atc Ile	atc Ile 430	gac Asp	gcc Ala	ctc Leu	gac Asp	cgc Arg 435	aca Thr	1879
atc Ile	att Ile	gcc Ala	cac His 440	ggc Gly	gaa Glu	ctc Leu	gac Asp	tac Tyr 445	gtc Val	ctg Leu	ctg Leu	cac His	aac Asn 450	ggc Gly	acc Thr	1927
ctg Leu	atg Met	gcc Ala 455	atc Ile	cag Gln	aac Asn	atg Met	acg Thr 460	tgg Trp	ggc Gly	ggc Gly	ctt Leu	cag Gln 465	ggc Gly	ttc Phe	cag Gln	1975
aac Asn	ccg Pro 470	ccc Pro	act Thr	gat Asp	gac Asp	ttc Phe 475	tac Tyr	gtc Val	ccc Pro	tac Tyr	cac His 480	gac Asp	gat Asp	ctg Leu	agc Ser	2023
ctg Leu 485	acg Thr	agt Ser	ctg Leu	agc Ser	gca Ala 490	aag Lys	gga Gly	ttg Leu	atg Met	ggc Gly 495	aag Lys	acg Thr	att Ile	acc Thr	gag Glu 500	2071

## 10336256.txt

cgc aag ctt acg ttt gtg cag cag gcg atg agt ggg cac atg gtg ccg 2119  
 Arg Lys Leu Thr Phe Val Gln Gln Ala Met Ser Gly His Met Val Pro  
 505 510 515

cag tac cag ccc agc agt gcg tac agg cag ttg gag ttt ttg ctc ggc 2167  
 Gln Tyr Gln Pro Ser Ser Ala Tyr Arg Gln Leu Glu Phe Leu Leu Gly  
 520 525 530

agg gtc gag agt ctg aca tcg aga gag ggt ttt acg acg ctg ccg aag 2215  
 Arg Val Glu Ser Leu Thr Ser Arg Glu Gly Phe Thr Thr Leu Pro Lys  
 535 540 545

agt gcg cag agt aat ggc acg agt att gga gag aag agg gat ttg ggt 2263  
 Ser Ala Gln Ser Asn Gly Thr Ser Ile Gly Glu Lys Arg Asp Leu Gly  
 550 555 560

gtt atg agg gag ttt aag agg tgg gtt tgagcgagct ttatctactt 2310  
 Val Met Arg Glu Phe Lys Arg Trp Val  
 565 570

ctttctctat agaaggaaaa gaaaaaaaaag aaggagattg agtaatgttg tcgtaatgtc 2370  
 gatattgtaag ataataaaaa aacaaaaacat acgtgcaaat catcccgccca cattctcgac 2430  
 ttcttttcttg ccatcccatcg ccaacatccc ctcttgccctc tccttcactg cctctggcac 2490  
 ctccgcaaac atcttgccga tagcctccac cgtcgtgttc cccccgctaa agacaacacc 2550  
 aacattccat ccctcctccc cagcctccct ctgcaccaat gccctaaact cctcgttaaa 2610  
 cagcacaacc gcgagcccaa cgaccgcaga gggctctaca aaacacttca tcctctcaag 2670  
 aaccaggcgc attgccttct taatctggtc ttcagtcacc gcaaacaagc ccgccacata 2730  
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 aatcgtaagc gtcttgacag atgtgacgcg ctacccgcg gcaacacccc tgcgtgcac 2850  
 gtcaccgccc tggaaactcg gttccgcgcc gaacacgcgg atgcccgtagc cgtgcagtgc 2910  
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<210> 153

<211> 16

<212> PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<400> 153

Met Gly Arg Ala Ser Arg Asn Leu Pro Ser Tyr Pro Arg Leu Pro Asn  
 1 5 10 15

<210> 154

<211> 22

<212> PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<400> 154

Gln Leu Asp Met Cys Arg Val Val Gly Arg Val Cys Leu Asn Asp Val  
 1 5 10 15  
 Ser Leu Ala Arg Cys Ala  
 20

<210> 155

<211> 46

<212> PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<400> 155

Ala Ser Val Ser Ala Arg Ser Ala Arg Ser Val Gly Arg Lys Val Glu  
 1 5 10 15  
 Phe Pro Arg Pro Arg Ile Gly Ile Pro Ala Gln Asn Val His Pro His  
 20 25 30  
 Lys Arg Gln Ala Thr Gln Ile Ile Asn Thr Glu Ala Ser Lys  
 35 40 45

<210> 156

<211> 59

10336256.txt

&lt;212&gt; PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

&lt;400&gt; 156

Ala Phe Ala Val Asn Gly Thr Ala Gly Ala Ile Pro Glu Val Tyr Phe  
 1 5 10 15  
 Asp Ile Gly Glu Ser Tyr Ala Gly Leu Leu Pro Ile Ser Lys Ala Ala  
 20 25 30  
 Asn Glu Thr Arg Glu Leu Tyr Phe Trp Phe Phe Pro Ser Glu Asn Pro  
 35 40 45  
 Asp Ala Ser Asp Glu Ile Thr Ile Trp Leu Asn  
 50 55

&lt;210&gt; 157

&lt;211&gt; 430

&lt;212&gt; PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

&lt;400&gt; 157

Gly Gly Pro Gly Cys Ser Ser Leu Glu Gly Phe Leu Gln Glu Asn Gly  
 1 5 10 15  
 Pro Ile Ser Trp Gln Tyr Gly Ser Gly Pro Gly Pro Val Tyr Asn Pro  
 20 25 30  
 Trp Asn Trp Ala Asn Leu Thr Asn Met Val Trp Val Glu Gln Pro Val  
 35 40 45  
 Gly Thr Gly Phe Ser Gln Gly Thr Pro Thr Ala Thr Asn Gln Glu Glu  
 50 55 60  
 Thr Ala Ala Glu Phe Leu Gly Phe Phe Lys Asn Phe Val Asp Thr Phe  
 65 70 75 80  
 Gly Leu Gln Asn Arg Lys Val Tyr Ile Thr Gly Glu Ser Tyr Ala Gly  
 85 90 95  
 Arg Tyr Val Pro Tyr Ile Ala Asp Ala Met Leu Ser Lys Asn Asp Ser  
 100 105 110  
 Thr Tyr Tyr Asp Val Lys Gly Val Met Phe Tyr Asp Pro Ser Val Ala  
 115 120 125  
 Glu Asp Gly Leu Leu Thr Asp Val Pro Ala Val Ala Tyr Val Asp Glu  
 130 135 140  
 Trp Ala Gly Leu Phe Asn Phe Asn Gln Ser Phe Met Asp Asp Ile His  
 145 150 155 160  
 Ala Arg Ala Asp Ala Cys Gly Tyr Thr Glu Tyr Met Glu Lys Tyr Leu  
 165 170 175  
 Thr Phe Pro Pro Thr Ser Lys Phe Pro Thr Pro Ala Asn Asn Ser Asp  
 180 185 190  
 Thr Glu Gly Cys Ser Leu Trp Gln Asp Ile Phe Asp Ala Val Ile Tyr  
 195 200 205  
 Thr Asn Pro Cys Phe Asp Val Tyr Ala Ile Ala Thr Thr Cys Pro Leu  
 210 215 220  
 Leu Trp Asp Pro Leu Gly Phe Pro Gly Ser Phe Asp Tyr Leu Pro Pro  
 225 230 235 240  
 Arg Thr Glu Ile Tyr Phe Asn Arg Ser Asp Val Gln Ala Ala Ile Asn  
 245 250 255  
 Ala Pro Ile Gln Pro Trp Ala Glu Cys Ser Asn Gly Val Leu Asp Thr  
 260 265 270  
 Asp Thr Ser Pro Pro Ser Ser Trp Glu Val Ile Pro Arg Ile Ile Asp  
 275 280 285  
 Ala Leu Asp Arg Thr Ile Ile Ala His Gly Glu Leu Asp Tyr Val Leu  
 290 295 300  
 Leu His Asn Gly Thr Leu Met Ala Ile Gln Asn Met Thr Trp Gly Gly  
 305 310 315 320  
 Leu Gln Gly Phe Gln Asn Pro Pro Thr Asp Asp Phe Tyr Val Pro Tyr  
 325 330 335  
 His Asp Asp Leu Ser Leu Thr Ser Leu Ala Lys Gly Leu Met Gly  
 340 345 350  
 Lys Thr Ile Thr Glu Arg Lys Leu Thr Phe Val Gln Gln Ala Met Ser  
 355 360 365  
 Gly His Met Val Pro Gln Tyr Gln Pro Ser Ser Ala Tyr Arg Gln Leu  
 370 375 380  
 Glu Phe Leu Leu Gly Arg Val Glu Ser Leu Thr Ser Arg Glu Gly Phe

10336256.txt

385 Thr Thr Leu Pro Lys 390 Ser Ala Gln Ser 395 Gly Thr Ser Ile Gly 400  
 Lys Arg Asp Leu 405 Val Met Arg Glu 410 Phe Lys Arg Trp Val 415  
 420 425 430

&lt;210&gt; 158

&lt;211&gt; 1719

&lt;212&gt; DNA

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1719)

&lt;400&gt; 158

atg ggc cga gca agc cgt aac ttg cca tca tac cct cgc ctt cct aac	48
Met Gly Arg Ala Ser 5 Arg Asn Leu Pro Ser 10 Tyr Pro Arg Leu 15 Asn	
cag tta gat atg tgc cgc gtc gtt ggc agg gta tgc ctg aat gat gtc	96
Gln Leu Asp Met 20 Cys Arg Val Val Gly 25 Arg Val Cys Leu 30 Asn Asp Val	
agc ctc gcg cgc tgc gcc gcc agt gtc tct gct cgg agc gct cgt tcc	144
Ser Leu Ala 35 Arg Cys Ala Ala Ser 40 Val Ser Ala Arg Ser 45 Ala Arg Ser	
gtt ggc agg aag gtg gaa ttc cct cgc cct cgc atc ggc ata ccg gcg	192
Val Gly 50 Arg Lys Val Glu 55 Phe 55 Pro Arg Pro Arg Ile 60 Gly Ile Pro Ala	
cag aat gtg cac cct cat aag cgc cag gct act cag atc ata aac act	240
Gln Asn Val His 70 His 70 Lys Arg Gln Ala Thr 75 Gln Ile Ile Asn Thr 80	
gaa gcc tcc aag gcc ttt gct gtg aac ggc act gct gga gct att ccc	288
Glu Ala Ser Lys 85 Phe Ala Val Asn Gly 90 Thr Ala Gly Ala 95 Ile Pro	
gaa gtc tac ttc gac att ggc gag tca tac gct ggt ctt ctc ccc att	336
Glu Val Tyr 100 Asp Ile Gly Glu Ser 105 Tyr Ala Gly Leu 110 Leu Pro Ile	
agc aaa gct gcc aat gag act cgg gag ctc tac ttt tgg ttc ttt cct	384
Ser Lys Ala 115 Ala Asn Glu Thr Arg Glu Leu Tyr Phe Trp 125 Phe Phe Pro	
tcg gag aac cca gat gct agc gac gaa atc acc atc tgg ttg aac ggt	432
Ser Glu Asn Pro Asp Ala Ser 135 Asp Glu Ile Thr Ile 140 Trp Leu Asn Gly	
ggt ccc ggc tgc tct tct ctc gaa gga ttt ctt cag gaa aac gga ccc	480
Gly Pro Gly Cys Ser 150 Leu Glu Gly Phe 155 Gln Glu Asn Gly Pro 160	
atc tca tgg caa tac ggc agc ggc cca ggt ccc gtc tac aac cca tgg	528
Ile Ser Trp Gln Tyr 165 Gly Ser Gly Pro 170 Pro Val Tyr Asn 175 Pro Trp	
aac tgg gcg aac ctc acc aac atg gtt tgg gtc gaa cag ccc gtc ggc	576
Asn Trp Ala 180 Leu Thr Asn Met Val 185 Trp Val Glu Gln Pro 190 Val Val Gly	
act ggc ttc tct cag gga acg ccg act gct act aat caa gaa gag act	624
Thr Gly Phe 195 Ser Gln Gly Thr Pro 200 Thr Ala Thr Asn 205 Gln Glu Glu Thr	

## 10336256.txt

gcc Ala 210	gcg Ala 210	gag Glu	ttc Phe	ctc Leu	ggt Gly	ttt Phe 215	ttc Phe	aag Lys	aac Asn	ttt Phe	gtt Val 220	gac Asp	act Thr	ttt Phe	ggt Gly	672
ctg Leu 225	cag Gln	aac Asn	cgc Arg	aaa Lys	gtg Val 230	tac Tyr	atc Ile	acc Thr	ggc Gly	gag Glu 235	tca Ser	tac Tyr	gct Ala	ggg Gly	cgc Arg 240	720
tac Tyr	gtc Val	ccc Pro	tac Tyr	att Ile 245	gcc Ala	gac Asp	gcc Ala	atg Met	ctg Leu 250	agc Ser	aag Lys	aac Asn	gac Asp	tca Ser 255	aca Thr	768
tac Tyr	tac Tyr	gac Asp	gtc Val 260	aag Lys	ggc Gly	gtc Val	atg Met	ttt Phe 265	tac Tyr	gac Asp	ccc Pro	agc Ser	gta Val 270	gcc Ala	gaa Glu	816
gac Asp	ggc Gly	ctc Leu 275	cta Leu	acc Thr	gac Asp	gtc Val	cct Pro 280	gcc Ala	gtc Val	gcc Ala	tac Tyr	gtc Val 285	gac Asp	gaa Glu	tgg Trp	864
gcc Ala 290	ggt Gly	ctc Leu	ttc Phe	aac Asn	ttc Phe 295	aac Asn	cag Gln	agc Ser	ttc Phe	atg Met	gac Asp 300	gac Asp	atc Ile	cac His	gcc Ala	912
cgc Arg 305	gcc Ala	gac Asp	gcc Ala	tgc Cys	ggc Gly 310	tac Tyr	acc Thr	gag Glu	tac Tyr	atg Met 315	gaa Glu	aaa Lys	tac Tyr	ctc Leu	act Thr 320	960
ttc Phe	ccc Pro	ccg Pro	acc Thr	agc Ser 325	aaa Lys	ttc Phe	ccc Pro	acc Thr	ccg Pro 330	gcc Ala	aac Asn	aac Asn	tcc Ser	gac Asp 335	aca Thr	1008
gaa Glu	ggc Gly	tgc Cys	tcc Ser 340	ctt Leu	tgg Trp	caa Gln	gac Asp	att Ile 345	ttc Phe	gac Asp	gcc Ala	gtt Val	atc Ile 350	tac Tyr	aca Thr	1056
aac Asn	ccc Pro	tgc Cys 355	ttc Phe	gac Asp	gtc Val	tac Tyr	gca Ala 360	atc Ile	gca Ala	acc Thr	acc Thr	tgc Cys 365	cct Pro	ctc Leu	ctc Leu	1104
tgg Trp 370	gac Asp	ccc Pro	ctc Leu	ggc Gly	ttc Phe	ccc Pro 375	ggc Gly	tcc Ser	ttc Phe	gac Asp	tac Tyr 380	ctg Leu	cct Pro	cca Pro	cgc Arg	1152
acc Thr 385	gaa Glu	atc Ile	tac Tyr	ttt Phe	aac Asn 390	cgc Arg	agc Ser	gac Asp	gtt Val	cag Gln 395	gcc Ala	gcc Ala	atc Ile	aac Asn	gcg Ala 400	1200
ccc Pro	atc Ile	cag Gln	ccc Pro	tgg Trp 405	gcc Ala	gag Glu	tgc Cys	tcc Ser	aac Asn 410	ggc Gly	gtc Val	ctc Leu	gac Asp	aca Thr 415	gat Asp	1248
acc Thr	tgc Ser	ccc Pro	ccg Pro	tgc Ser	tcc Ser	tgg Trp	gaa Glu	gtc Val 425	atc Ile	ccc Pro	cgc Arg	atc Ile	atc Ile 430	gac Asp	gcc Ala	1296
ctc Leu	gac Asp	cgc Arg 435	aca Thr	atc Ile	att Ile	gcc Ala	cac His 440	ggc Gly	gaa Glu	ctc Leu	gac Asp	tac Tyr 445	gtc Val	ctg Leu	ctg Leu	1344
cac His	aac Asn 450	ggc Gly	acc Thr	ctg Leu	atg Met	gcc Ala 455	atc Ile	cag Gln	aac Asn	atg Met	acg Thr 460	tgg Trp	ggc Gly	ggc Gly	ctt Leu	1392
cag Gln 465	ggc Gly	ttc Phe	cag Gln	aac Asn	ccg Pro 470	ccc Pro	act Thr	gat Asp	gac Asp	ttc Phe 475	tac Tyr	gtc Val	ccc Pro	tac Tyr	cac His 480	1440

## 10336256.txt

gac	gat	ctg	agc	ctg	acg	agt	ctg	agc	gca	aag	gga	ttg	atg	ggc	aag	1488
Asp	Asp	Leu	Ser	Leu	Thr	Ser	Leu	Ser	Ala	Lys	Gly	Leu	Met	Gly	Lys	
			485						490					495		
acg	att	acc	gag	cgc	aag	ctt	acg	ttt	gtg	cag	cag	gcg	atg	agt	ggg	1536
Thr	Ile	Thr	Glu	Arg	Lys	Leu	Thr	Phe	Val	Gln	Gln	Ala	Met	Ser	Gly	
			500					505					510			
cac	atg	gtg	ccg	cag	tac	cag	ccc	agc	agt	gcg	tac	agg	cag	ttg	gag	1584
His	Met	Val	Pro	Gln	Tyr	Gln	Pro	Ser	Ser	Ala	Tyr	Arg	Gln	Leu	Glu	
		515					520					525				
ttt	ttg	ctc	ggc	agg	gtc	gag	agt	ctg	aca	tcg	aga	gag	ggg	ttt	acg	1632
Phe	Leu	Leu	Gly	Arg	Val	Glu	Ser	Leu	Thr	Ser	Arg	Glu	Gly	Phe	Thr	
	530					535					540					
acg	ctg	ccg	aag	agt	gcg	cag	agt	aat	ggc	acg	agt	att	gga	gag	aag	1680
Thr	Leu	Pro	Lys	Ser	Ala	Gln	Ser	Asn	Gly	Thr	Ser	Ile	Gly	Glu	Lys	
	545				550					555					560	
agg	gat	ttg	ggg	gtt	atg	agg	gag	ttt	aag	agg	tgg	gtt				1719
Arg	Asp	Leu	Gly	Val	Met	Arg	Glu	Phe	Lys	Arg	Trp	Val				
				565					570							

&lt;210&gt; 159

&lt;211&gt; 573

&lt;212&gt; PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

&lt;220&gt;

&lt;221&gt; DOMAIN

&lt;222&gt; (96)...(532)

&lt;223&gt; Serine carboxypeptidase

&lt;400&gt; 159

Met	Gly	Arg	Ala	Ser	Arg	Asn	Leu	Pro	Ser	Tyr	Pro	Arg	Leu	Pro	Asn	
1				5					10					15		
Gln	Leu	Asp	Met	Cys	Arg	Val	Val	Gly	Arg	Val	Cys	Leu	Asn	Asp	Val	
			20					25					30			
Ser	Leu	Ala	Arg	Cys	Ala	Ala	Ser	Val	Ser	Ala	Arg	Ser	Ala	Arg	Ser	
		35					40					45				
Val	Gly	Arg	Lys	Val	Glu	Phe	Pro	Arg	Pro	Arg	Ile	Gly	Ile	Pro	Ala	
	50					55					60					
Gln	Asn	Val	His	Pro	His	Lys	Arg	Gln	Ala	Thr	Gln	Ile	Ile	Asn	Thr	
	65				70					75					80	
Glu	Ala	Ser	Lys	Ala	Phe	Ala	Val	Asn	Gly	Thr	Ala	Gly	Ala	Ile	Pro	
			85						90					95		
Glu	Val	Tyr	Phe	Asp	Ile	Gly	Glu	Ser	Tyr	Ala	Gly	Leu	Leu	Pro	Ile	
			100					105					110			
Ser	Lys	Ala	Ala	Asn	Glu	Thr	Arg	Glu	Leu	Tyr	Phe	Trp	Phe	Phe	Pro	
		115					120					125				
Ser	Glu	Asn	Pro	Asp	Ala	Ser	Asp	Glu	Ile	Thr	Ile	Trp	Leu	Asn	Gly	
	130					135					140					
Gly	Pro	Gly	Cys	Ser	Ser	Leu	Glu	Gly	Phe	Leu	Gln	Glu	Asn	Gly	Pro	
	145				150					155					160	
Ile	Ser	Trp	Gln	Tyr	Gly	Ser	Gly	Pro	Gly	Pro	Val	Tyr	Asn	Pro	Trp	
			165						170					175		
Asn	Trp	Ala	Asn	Leu	Thr	Asn	Met	Val	Trp	Val	Glu	Gln	Pro	Val	Gly	
		180						185					190			
Thr	Gly	Phe	Ser	Gln	Gly	Thr	Pro	Thr	Ala	Thr	Asn	Gln	Glu	Glu	Thr	
	195						200					205				
Ala	Ala	Glu	Phe	Leu	Gly	Phe	Phe	Lys	Asn	Phe	Val	Asp	Thr	Phe	Gly	
	210					215					220					
Leu	Gln	Asn	Arg	Lys	Val	Tyr	Ile	Thr	Gly	Glu	Ser	Tyr	Ala	Gly	Arg	
	225				230					235					240	
Tyr	Val	Pro	Tyr	Ile	Ala	Asp	Ala	Met	Leu	Ser	Lys	Asn	Asp	Ser	Thr	
				245					250					255		

## 10336256.txt

Tyr Tyr Asp Val Lys Gly Val Met Phe Tyr Asp Pro Ser Val Ala Glu  
 260 265 270  
 Asp Gly Leu Leu Thr Asp Val Pro Ala Val Ala Tyr Val Asp Glu Trp  
 275 280 285  
 Ala Gly Leu Phe Asn Phe Asn Gln Ser Phe Met Asp Asp Ile His Ala  
 290 295 300  
 Arg Ala Asp Ala Cys Gly Tyr Thr Glu Tyr Met Glu Lys Tyr Leu Thr  
 305 310 315 320  
 Phe Pro Pro Thr Ser Lys Phe Pro Thr Pro Ala Asn Asn Ser Asp Thr  
 325 330 335  
 Glu Gly Cys Ser Leu Trp Gln Asp Ile Phe Asp Ala Val Ile Tyr Thr  
 340 345 350  
 Asn Pro Cys Phe Asp Val Tyr Ala Ile Ala Thr Thr Cys Pro Leu Leu  
 355 360 365  
 Trp Asp Pro Leu Gly Phe Pro Gly Ser Phe Asp Tyr Leu Pro Pro Arg  
 370 375 380  
 Thr Glu Ile Tyr Phe Asn Arg Ser Asp Val Gln Ala Ala Ile Asn Ala  
 385 390 395 400  
 Pro Ile Gln Pro Trp Ala Glu Cys Ser Asn Gly Val Leu Asp Thr Asp  
 405 410 415  
 Thr Ser Pro Pro Ser Ser Trp Glu Val Ile Pro Arg Ile Ile Asp Ala  
 420 425 430  
 Leu Asp Arg Thr Ile Ile Ala His Gly Glu Leu Asp Tyr Val Leu Leu  
 435 440 445  
 His Asn Gly Thr Leu Met Ala Ile Gln Asn Met Thr Trp Gly Gly Leu  
 450 455 460  
 Gln Gly Phe Gln Asn Pro Thr Asp Asp Phe Tyr Val Pro Tyr His  
 465 470 475 480  
 Asp Asp Leu Ser Leu Thr Ser Leu Ser Ala Lys Gly Leu Met Gly Lys  
 485 490 495  
 Thr Ile Thr Glu Arg Lys Leu Thr Phe Val Gln Gln Ala Met Ser Gly  
 500 505 510  
 His Met Val Pro Gln Tyr Gln Pro Ser Ser Ala Tyr Arg Gln Leu Glu  
 515 520 525  
 Phe Leu Leu Gly Arg Val Glu Ser Leu Thr Ser Arg Glu Gly Phe Thr  
 530 535 540  
 Thr Leu Pro Lys Ser Ala Gln Ser Asn Gly Thr Ser Ile Gly Glu Lys  
 545 550 555 560  
 Arg Asp Leu Gly Val Met Arg Glu Phe Lys Arg Trp Val  
 565 570

&lt;210&gt; 160

&lt;211&gt; 3407

&lt;212&gt; DNA

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1001)...(1156)

&lt;223&gt; Exon

&lt;221&gt; CDS

&lt;222&gt; (1277)...(2023)

&lt;223&gt; Exon

&lt;221&gt; CDS

&lt;222&gt; (2177)...(2407)

&lt;223&gt; Exon

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(3407)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 160

actcgtatcg	tttctgttca	ttgttcacct	tgtcgggccc	cagaaccaag	tgtggttttag	60
catagcgcag	gtttggtggc	atttatattg	cgtcaagatg	tatagacgga	tagtcttttg	120
tcacttatac	ccacttttat	tcattttgcat	gtagcgcggg	agtttgctga	tgaaagagaa	180
agggtttttt	gtcttggtat	tttcttgctg	tgacgaaagt	tttttgttac	ctcactccaa	240

## 10336256.txt

aaagactatc atgtttgaaa ttatcatggt gagagaaaaa tcacatgttg caggtaggca 300  
 ggcataatggt ggcttacata ctatactaga gcacaaaaaa agaaggatag taagcgaaat 360  
 attcaagttg aaagggtcatg ttacgataac tcccccttg gacttattac ctattagtca 420  
 ctcagtcaag cttcttccct tttcctccac cttcttcttc ctcccccttc ccgtcagcaa 480  
 aacaatatga atgtactttg atttaccac tttcgggtcc tctcgcccg catcatcttt 540  
 tctttgtacg tcagacctgc ctcttggtggt acacatgcgt cacggtacac catgccggat 600  
 taggaaagcg acaagatgga tatgcggtac ccaagacttg cttggcgggg tatcctggat 660  
 ccccgcgag catgtttatt ggctaagatg gctggtgaag ctataatagg catgatgcgg 720  
 atgctgaaaa catgtgtgtt tatgtatctt ttttttgggt gagtggaccg ggtattgttg 780  
 gctttgtggg gattgtggac ggggatgggg tgggtaacgg tgagggtgagg ggggttacta 840  
 tagtataaat tggagttgat tttttgtct cttgtttgat ttcttttact tcaacttctt 900  
 ctatcctcgc tttttttct cgccttttgt aagaacaag gccgccgtgt tttttttctc 960  
 agtcaagatt tcaaaaggga caaaggaaag agaggacaag atg aag tcg ctt ggt 1015  
 Met Lys Ser Leu Gly  
 1 5

ctt ctc gca act gtt tgc gct act gct gcg ctg gcc aag gga ccc gag 1063  
 Leu Leu Ala Thr Val Cys Ala Thr Ala Ala Leu Ala Lys Gly Pro Glu  
 10 15 20

cga gtt agc aat gcg gcg agg agt att acg att gaa gtt gcg ccg ggg 1111  
 Arg Val Ser Asn Ala Ala Arg Ser Ile Thr Ile Glu Val Ala Pro Gly  
 25 30 35

gag acg cgc cag att act gag gat gag agg tgg gat att gct act 1156  
 Glu Thr Arg Gln Ile Thr Glu Asp Glu Arg Trp Asp Ile Ala Thr  
 40 45 50

gtgagtttgt ggtggttgtt gaaacacttg tctattatcc ctccctttct tccccacgga 1216  
 aacacctttt ttttaaaact acagctcctt tcgttttatt tttactaaact ataacaccag 1276  
 ggc ggc ggt tgt gga agc cac ttc ttc gac att acg gat tcg ttc gcc 1324  
 Gly Gly Gly Cys Gly Ser His Phe Phe Asp Ile Thr Asp Ser Phe Ala  
 55 60 65

gaa ccc ata gcc gtc acg cgc gcg gcc gcc tac cca tcc acc ttc caa 1372  
 Glu Pro Ile Ala Val Thr Arg Ala Ala Ala Tyr Pro Ser Thr Phe Gln  
 70 75 80

tac agc acc aac atc cgg cgc ctc ttc ccc tcg ctc agc tgg gcc aac 1420  
 Tyr Ser Thr Asn Ile Arg Arg Leu Phe Pro Ser Leu Ser Trp Ala Asn  
 85 90 95 100

atc aag aaa aac ctc gag caa tac tcg acc ttc cac acg cgc ttc tca 1468  
 Ile Lys Lys Asn Leu Glu Gln Tyr Ser Thr Phe His Thr Arg Phe Ser  
 105 110 115

gaa acc caa tct gcc gcc gac gct gcc cag tgg ctc ctc gcc caa gtc 1516  
 Glu Thr Gln Ser Gly Ala Asp Ala Ala Gln Trp Leu Leu Ala Gln Val  
 120 125 130

caa gcc gtg gtc aag caa gcc aac aaa tcg gcc gtc aca gcc tct gcc 1564  
 Gln Ala Val Val Lys Gln Ala Asn Lys Ser Gly Val Thr Ala Ser Ala  
 135 140 145

ttc ccc cac tcg ctc tgg ccg caa aac tca atc ata gcc cgc atc caa 1612  
 Phe Pro His Ser Leu Trp Pro Gln Asn Ser Ile Ile Ala Arg Ile Gln  
 150 155 160

ggc cgc tcc aac cgc act gtc gtc gta ggc gcc cac ctc gac tcc atc 1660  
 Gly Arg Ser Asn Arg Thr Val Val Val Gly Ala His Leu Asp Ser Ile  
 165 170 175 180

aac tcg gcc aac cgc ctc acc ggc cgc gcc ccg gcc gtc gac gac gac 1708  
 Asn Ser Ala Asn Arg Leu Thr Gly Arg Ala Pro Gly Val Asp Asp Asp  
 185 190 195

ggc agc gcc tcc atg ctt ctt ctc gag gcc ctg cgc gtg ctg ctc acc 1756  
 Gly Ser Gly Ser Met Leu Leu Leu Glu Ala Leu Arg Val Leu Leu Thr

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200	205	210	
gac tgc gcc ttt gca ggc tcc aac aac ctt ctc gag aac acg att gag	Asp Ser Ala Phe Ala Gly Ser Asn Asn Leu Leu Glu Asn Thr Ile Glu	1804	
ttc cac tgg tat gcc gct gaa gag ggc ggt ctc cgc ggg agc caa gac	Phe His Trp Tyr Ala Ala Glu Glu Gly Gly Leu Arg Gly Ser Gln Asp	1852	
atc ttc acg cag tac aag aac gca gga aga gag atc tgg gct atg ctg	Ile Phe Thr Gln Tyr Lys Asn Ala Gly Arg Glu Ile Trp Ala Met Leu	1900	
cag cag gat atg gtg ggg tac aca aag ggg acg ctg gat gcg ggc aag	Gln Gln Asp Met Val Gly Tyr Thr Lys Gly Thr Leu Asp Ala Gly Lys	1948	
ccc gag agt ttt ggg ctg att acg gat ttt acg gat gcc gtc ttg aat	Pro Glu Ser Phe Gly Leu Ile Thr Asp Phe Thr Asp Ala Val Leu Asn	1996	
cag tat ttg gta aaa gtg att ggt gag gtatgtaaat ttttttggtt	Gln Tyr Leu Val Lys Val Ile Gly Glu	2043	
ccttttcccc ttctctnnnn nnnnnnnnnn nnnnnnnccc ccccccccc cctccgtag	accttttccc ctctttttgc tgcaaaggga gggagacaag aaagaagaat acacaatgct	2103	
gatgttgatc cag tac acc gat atc acc tat gtc aac agc acg tgc ggt	Tyr Thr Asp Ile Thr Tyr Val Asn Ser Thr Cys Gly	2163	
	305 310	2212	
tat gca tgc tca gac cac ggt tcc gcc atg cgc agt gga tac cct gcc	Tyr Ala Cys Ser Asp His Gly Ser Ala Met Arg Ser Gly Tyr Pro Ala	2260	
tgc ttt gtc ttt gag tct gac ttc cgg tac cgc aat ccg tat atc cat	Ser Phe Val Phe Glu Ser Asp Phe Arg Tyr Arg Asn Pro Tyr Ile His	2308	
act ccg aac gat acc atg gag cac atg gac cct aac cac gtg ttg caa	Thr Pro Asn Asp Thr Met Glu His Met Asp Pro Asn His Val Leu Gln	2356	
cat gga cgc ttg gtg ctg ggc tat ttg tat gaa ctt ggg ttt agc aag	His Gly Arg Leu Val Leu Gly Tyr Leu Tyr Glu Leu Gly Phe Ser Lys	2404	
gcc taaggggggtt ctttacaat gggctctcac aatgtagttg tgcgcgggtt	Ala	2457	
gttggtgtaaa tgtgaatatg gatatgacat tttcttttga tgggttatgt acacatatat	gaaaaaattc agatatgatt ttgtctcttg tattgtttgc ctgtcatctc aaagaccacg	2517	
cctgttactt gttccagtgg ctgagcaaaa ggagtgaat tctacgtcgg gtgcgtcgtc	atactatgcc cctgcgtgtt cagccatacc aatccttatt ttagtaagag gacatgaaaa	2577	
gaaagtgtat gacgagaaaa cttgggtgaga caaggctcat ttgaattttg acatcgtgag	gcacgctgag caaatgaact tggataatgg attaacgtct gacacgaagc aagattaaca	2637	
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taagacttca acatactgca tttctcctcc atctacatac tatctgctca gtatattgat	ccaccatttc caacaaccgc tcgtactata ctatccccac cagataacat ccctagtact	2757	
cgccagttct caacctcttc ccaatgtttc tgcgaatcac gtcgcgctcg acgggttcga	cttgtgctcg gttggcattg agcgcctgac ggagcatacc cgcgtcgaag aagccatcta	2817	
tacacaagaa gagcaataat cagtataatg aaatctttga aaaaagaaat gtgagtatgt	gtggggaggg ggggaggggg gggtaaagaa aacgtgaggt aataaagtct tgggcacaaa	2877	
tcttgacagga tagatggaaa cgctaaattg cagcaaatctg gaaatgaaag agaaaacagga	tatcaagaag aatagaaaat tggcttcttt ttggctgcag atgctccctg	2937	
		2997	
		3057	
		3117	
		3177	
		3237	
		3297	
		3357	
		3407	

10336256.txt

<210> 161  
 <211> 52  
 <212> PRT  
 <213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<400> 161  
 Met Lys Ser Leu Gly Leu Leu Ala Thr Val Cys Ala Thr Ala Ala Leu  
 1 5 10 15  
 Ala Lys Gly Pro Glu Arg Val Ser Asn Ala Ala Arg Ser Ile Thr Ile  
 20 25 30  
 Glu Val Ala Pro Gly Glu Thr Arg Gln Ile Thr Glu Asp Glu Arg Trp  
 35 40 45  
 Asp Ile Ala Thr  
 50

<210> 162  
 <211> 249  
 <212> PRT  
 <213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<400> 162  
 Gly Gly Gly Cys Gly Ser His Phe Phe Asp Ile Thr Asp Ser Phe Ala  
 1 5 10 15  
 Glu Pro Ile Ala Val Thr Arg Ala Ala Tyr Pro Ser Thr Phe Gln  
 20 25 30  
 Tyr Ser Thr Asn Ile Arg Arg Leu Phe Pro Ser Leu Ser Trp Ala Asn  
 35 40 45  
 Ile Lys Lys Asn Leu Glu Gln Tyr Ser Thr Phe His Thr Arg Phe Ser  
 50 55 60  
 Glu Thr Gln Ser Gly Ala Asp Ala Ala Gln Trp Leu Leu Ala Gln Val  
 65 70 75 80  
 Gln Ala Val Val Lys Gln Ala Asn Lys Ser Gly Val Thr Ala Ser Ala  
 85 90 95  
 Phe Pro His Ser Leu Trp Pro Gln Asn Ser Ile Ile Ala Arg Ile Gln  
 100 105 110  
 Gly Arg Ser Asn Arg Thr Val Val Val Gly Ala His Leu Asp Ser Ile  
 115 120 125  
 Asn Ser Ala Asn Arg Leu Thr Gly Arg Ala Pro Gly Val Asp Asp Asp  
 130 135 140  
 Gly Ser Gly Ser Met Leu Leu Leu Glu Ala Leu Arg Val Leu Leu Thr  
 145 150 155 160  
 Asp Ser Ala Phe Ala Gly Ser Asn Asn Leu Leu Glu Asn Thr Ile Glu  
 165 170 175  
 Phe His Trp Tyr Ala Ala Glu Glu Gly Leu Arg Gly Ser Gln Asp  
 180 185 190  
 Ile Phe Thr Gln Tyr Lys Asn Ala Gly Arg Glu Ile Trp Ala Met Leu  
 195 200 205  
 Gln Gln Asp Met Val Gly Tyr Thr Lys Gly Thr Leu Asp Ala Gly Lys  
 210 215 220  
 Pro Glu Ser Phe Gly Leu Ile Thr Asp Phe Thr Asp Ala Val Leu Asn  
 225 230 235 240  
 Gln Tyr Leu Val Lys Val Ile Gly Glu  
 245

<210> 163  
 <211> 77  
 <212> PRT  
 <213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<400> 163  
 Tyr Thr Asp Ile Thr Tyr Val Asn Ser Thr Cys Gly Tyr Ala Cys Ser  
 1 5 10 15  
 Asp His Gly Ser Ala Met Arg Ser Gly Tyr Pro Ala Ser Phe Val Phe  
 20 25 30  
 Glu Ser Asp Phe Arg Tyr Arg Asn Pro Tyr Ile His Thr Pro Asn Asp  
 35 40 45  
 Thr Met Glu His Met Asp Pro Asn His Val Leu Gln His Gly Arg Leu

10336256.txt

50 55 60  
Val Leu Gly Tyr Leu Tyr Glu Leu Gly Phe Ser Lys Ala  
65 70 75

<210> 164  
<211> 1134  
<212> DNA  
<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<220>  
<221> CDS  
<222> (1)...(1134)

<400> 164

atg aag tcg ctt ggt ctt ctc gca act gtt tgc gct act gct gcg ctg	48
Met Lys Ser Leu Gly Leu Leu Ala Thr Val Cys Ala Thr Ala Ala Leu	
1 5 10 15	
gcc aag gga ccc gag cga gtt agc aat gcg gcg agg agt att acg att	96
Ala Lys Gly Pro Glu Arg Val Ser Asn Ala Ala Arg Ser Ile Thr Ile	
20 25 30	
gaa gtt gcg ccg ggg gag acg cgc cag att act gag gat gag agg tgg	144
Glu Val Ala Pro Gly Glu Thr Arg Gln Ile Thr Glu Asp Glu Arg Trp	
35 40 45	
gat att gct act ggc ggc ggt tgt gga agc cac ttc ttc gac att acg	192
Asp Ile Ala Thr Gly Gly Gly Cys Gly Ser His Phe Phe Asp Ile Thr	
50 55 60	
gat tcg ttc gcc gaa ccc ata gcc gtc acg cgc gcg gcc gcc tac cca	240
Asp Ser Phe Ala Glu Pro Ile Ala Val Thr Arg Ala Ala Ala Tyr Pro	
65 70 75 80	
tcc acc ttc caa tac agc acc aac atc cgg cgc ctc ttc ccc tcg ctc	288
Ser Thr Phe Gln Tyr Ser Thr Asn Ile Arg Arg Leu Phe Pro Ser Leu	
85 90 95	
agc tgg gcc aac atc aag aaa aac ctc gag caa tac tcg acc ttc cac	336
Ser Trp Ala Asn Ile Lys Lys Asn Leu Glu Gln Tyr Ser Thr Phe His	
100 105 110	
acg cgc ttc tca gaa acc caa tct ggc gcc gac gct gcc cag tgg ctc	384
Thr Arg Phe Ser Glu Thr Gln Ser Gly Ala Asp Ala Ala Gln Trp Leu	
115 120 125	
ctc gcc caa gtc caa gcc gtg gtc aag caa gcc aac aaa tcg ggc gtc	432
Leu Ala Gln Val Gln Ala Val Val Lys Gln Ala Asn Lys Ser Gly Val	
130 135 140	
aca gcc tct gcc ttc ccc cac tcg ctc tgg ccg caa aac tca atc ata	480
Thr Ala Ser Ala Phe Pro His Ser Leu Trp Pro Gln Asn Ser Ile Ile	
145 150 155 160	
gcc cgc atc caa ggc cgc tcc aac cgc act gtc gtc gta ggc gcc cac	528
Ala Arg Ile Gln Gly Arg Ser Asn Arg Thr Val Val Val Gly Ala His	
165 170 175	
ctc gac tcc atc aac tcg gcc aac cgc ctc acc ggc cgc gcc ccg ggc	576
Leu Asp Ser Ile Asn Ser Ala Asn Arg Leu Thr Gly Arg Ala Pro Gly	
180 185 190	
gtc gac gac gac ggc agc ggc tcc atg ctt ctt ctc gag gcc ctg cgc	624
Val Asp Asp Asp Gly Ser Gly Ser Met Leu Leu Leu Glu Ala Leu Arg	
195 200 205	
gtg ctg ctc acc gac tcg gcc ttt gca ggc tcc aac aac ctt ctc gag	672
Val Leu Leu Thr Asp Ser Ala Phe Ala Gly Ser Asn Asn Leu Leu Glu	

10336256.txt  
220

<p>210</p> <p>aac acg att gag ttc cac tgg tat gcc gct gaa gag ggc ggt ctc cgc Asn Thr Ile Glu Phe His Trp Tyr Ala Ala Glu Glu Gly Gly Leu Arg 225</p> <p>ggg agc caa gac atc ttc acg cag tac aag aac gca gga aga gag atc Gly Ser Gln Asp Ile Phe Thr Gln Tyr Lys Asn Ala Gly Arg Glu Ile 245</p> <p>tgg gct atg ctg cag cag gat atg gtg ggg tac aca aag ggg acg ctg Trp Ala Met Leu Gln Gln Asp Met Val Gly Tyr Thr Lys Gly Thr Leu 260</p> <p>gat gcg ggc aag ccc gag agt ttt ggg ctg att acg gat ttt acg gat Asp Ala Gly Lys Pro Glu Ser Phe Gly Leu Ile Thr Asp Phe Thr Asp 275</p> <p>gcc gtc ttg aat cag tat ttg gta aaa gtg att ggt gag tac acc gat Ala Val Leu Asn Gln Tyr Leu Val Lys Val Ile Gly Glu Tyr Thr Asp 290</p> <p>atc acc tat gtc aac agc acg tgc ggt tat gca tgc tca gac cac ggt Ile Thr Tyr Val Asn Ser Thr Cys Gly Tyr Ala Cys Ser Asp His Gly 305</p> <p>tcc gcc atg cgc agt gga tac cct gcc tcg ttt gtc ttt gag tct gac Ser Ala Met Arg Ser Gly Tyr Pro Ala Ser Phe Val Phe Glu Ser Asp 325</p> <p>ttc cgg tac cgc aat ccg tat atc cat act ccg aac gat acc atg gag Phe Arg Tyr Arg Asn Pro Tyr Ile His Thr Pro Asn Asp Thr Met Glu 340</p> <p>cac atg gac cct aac cac gtg ttg caa cat gga cgc ttg gtg ctg ggc His Met Asp Pro Asn His Val Leu Gln His Gly Arg Leu Val Leu Gly 355</p> <p>tat ttg tat gaa ctt ggg ttt agc aag gcc Tyr Leu Tyr Glu Leu Gly Phe Ser Lys Ala 370</p>	<p>215</p>	<p>720</p> <p>768</p> <p>816</p> <p>864</p> <p>912</p> <p>960</p> <p>1008</p> <p>1056</p> <p>1104</p> <p>1134</p>
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&lt;210&gt; 165

&lt;211&gt; 378

&lt;212&gt; PRT

&lt;213&gt; Cochliobolus heterostrophus strain C4 (ATCC 48331)

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; (1)...(17)

&lt;221&gt; DOMAIN

&lt;222&gt; (128)...(378)

&lt;223&gt; Peptidase family M28

&lt;400&gt; 165

Met	Lys	Ser	Leu	Gly	Leu	Leu	Ala	Thr	Val	Cys	Ala	Thr	Ala	Ala	Leu
1				5					10				15		
Ala	Lys	Gly	Pro	Glu	Arg	Val	Ser	Asn	Ala	Ala	Arg	Ser	Ile	Thr	Ile
			20					25					30		
Glu	Val	Ala	Pro	Gly	Glu	Thr	Arg	Gln	Ile	Thr	Glu	Asp	Glu	Arg	Trp
		35					40					45			
Asp	Ile	Ala	Thr	Gly	Gly	Gly	Cys	Gly	Ser	His	Phe	Phe	Asp	Ile	Thr
	50				55					60					
Asp	Ser	Phe	Ala	Glu	Pro	Ile	Ala	Val	Thr	Arg	Ala	Ala	Ala	Tyr	Pro
					70				75					80	
Ser	Thr	Phe	Gln	Tyr	Ser	Thr	Asn	Ile	Arg	Arg	Leu	Phe	Pro	Ser	Leu

## 10336256.txt

Ser Trp Ala Asn Ile Lys Lys Asn Leu Glu Gln Tyr Ser Thr Phe His  
 85 90 95  
 100 105 110  
 Thr Arg Phe Ser Glu Thr Gln Ser Gly Ala Asp Ala Ala Gln Trp Leu  
 115 120 125  
 Leu Ala Gln Val Gln Ala Val Val Lys Gln Ala Asn Lys Ser Gly Val  
 130 135 140  
 Thr Ala Ser Ala Phe Pro His Ser Leu Trp Pro Gln Asn Ser Ile Ile  
 145 150 155 160  
 Ala Arg Ile Gln Gly Arg Ser Asn Arg Thr Val Val Val Gly Ala His  
 165 170 175  
 Leu Asp Ser Ile Asn Ser Ala Asn Arg Leu Thr Gly Arg Ala Pro Gly  
 180 185 190  
 Val Asp Asp Gly Ser Gly Ser Met Leu Leu Leu Glu Ala Leu Arg  
 195 200 205  
 Val Leu Leu Thr Asp Ser Ala Phe Ala Gly Ser Asn Asn Leu Leu Glu  
 210 215 220  
 Asn Thr Ile Glu Phe His Trp Tyr Ala Ala Glu Glu Gly Gly Leu Arg  
 225 230 235 240  
 Gly Ser Gln Asp Ile Phe Thr Gln Tyr Lys Asn Ala Gly Arg Glu Ile  
 245 250 255  
 Trp Ala Met Leu Gln Gln Asp Met Val Gly Tyr Thr Lys Gly Thr Leu  
 260 265 270  
 Asp Ala Gly Lys Pro Glu Ser Phe Gly Leu Ile Thr Asp Phe Thr Asp  
 275 280 285  
 Ala Val Leu Asn Gln Tyr Leu Val Lys Val Ile Gly Glu Tyr Thr Asp  
 290 295 300  
 Ile Thr Tyr Val Asn Ser Thr Cys Gly Tyr Ala Cys Ser Asp His Gly  
 305 310 315 320  
 Ser Ala Met Arg Ser Gly Tyr Pro Ala Ser Phe Val Phe Glu Ser Asp  
 325 330 335  
 Phe Arg Tyr Arg Asn Pro Tyr Ile His Thr Pro Asn Asp Thr Met Glu  
 340 345 350  
 His Met Asp Pro Asn His Val Leu Gln His Gly Arg Leu Val Leu Gly  
 355 360 365  
 Tyr Leu Tyr Glu Leu Gly Phe Ser Lys Ala  
 370 375

&lt;210&gt; 166

&lt;211&gt; 4437

&lt;212&gt; DNA

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1834)...(1854)

&lt;223&gt; Exon

&lt;221&gt; CDS

&lt;222&gt; (1932)...(2114)

&lt;223&gt; Exon

&lt;221&gt; CDS

&lt;222&gt; (2190)...(3134)

&lt;223&gt; Exon

&lt;221&gt; CDS

&lt;222&gt; (3204)...(3437)

&lt;223&gt; Exon

&lt;400&gt; 166

actagcctcc	ttaatcaatt	agacctggcc	ggaactaccg	gcattataag	ttatacgatg	60
ttcatcattg	ccttaagaga	ccctatatag	tttgcgtctg	tacatacgca	gacttgtcac	120
ctcctggaat	tctgtctcat	attagcatct	ccgctgcgctg	gtactaataa	agccagtttt	180
tttttaaac	ccagtatcca	tcattggtggg	aagcgtcaac	aagtttctgg	ccattgccgg	240
caatgcctcg	gcagccgctc	tcgacctgcc	cgttgtcatc	aagagcacat	acagcagcgt	300
caagttcgac	atcggcacgc	ccccgaaaga	acaccagcta	ctgttcgata	ccggctcgtc	360
aaccctctgg	accgttagca	ctgactgcac	acaagactcg	tgtccagaag	gaagcacgga	420

## 10336256.txt

gctgtataaa cgacggtact acaatgcatc ggcatcatcc acggccgctcg atgttggcat 480  
 tcccgccaca attccttact tgggcggttaa cgttgagggc gaaatttatc aggatgtctt 540  
 cagcgcctcta gatgggtccg tggaatggaa ccagtcattc attgcagtca ataagagctc 600  
 atggcctttgg atcactgacg acgggttttct gggccttggc ttctctacca tcgcagagcc 660  
 taacacgtcg acactggctg aaacgctgct atgggatggc aagctagaca aaccccgatt 720  
 cggcctatac tatggcacaac acctaggaga cgagggccct caggacggtg tactgagcat 780  
 tggcgacagt cacgaggaca agtttgttga tggccagggt gtttatgctc ctctgcagaa 840  
 ggtcaacaac gagtatgatc tatggcgcac accgttgaag gctgtcaacc tactggtcgc 900  
 caagaacccg tccaacccaa accacacagt cgagacgcac attggcaaac tgcccacgac 960  
 gcagttttct ggcaatgccaa tagagtcacc caatgtgact ttgtcaacgt tcggcgacgg 1020  
 cactgccatt ttcgacacgg gagctggcgg cctttccctg ccagaagata tgattgattc 1080  
 catatactac aatctcggct gggattacca aagtctgctc aacggcaagc agcgctttac 1140  
 atgcgaggcc atgaacgcat cctgggcatc ttctctaact cttggtgaag gtgcgcccga 1200  
 gaacgatgtc gtagtttagca ttcgcggcga tgaattactc aagcctggag ctcaatgtat 1260  
 gccaccgttt gacccttcca acgcaccttc atttgcgctt gttggcacta cttactcca 1320  
 gaggtactac actatatggg actttggtgc ggacaagggt gccgagtaca agcctcggct 1380  
 tggatttggg aggtcaaga agcagtttga ctggaagtat cagtcataag ggtcacgtag 1440  
 aagggggagg ttttctcgcc aattgtgcat gtagtacgta aaatatcaag atgagatgca 1500  
 aacaaggcac ttggtgcagt ggtgaacatc gtggttcgag gcgcaaaagc gtcctgtgta 1560  
 acaacaatac gagcgatatg tagaccagct agtaatgcc aagcgaagtga gtgatatctt 1620  
 gcaaagtcgt cggagtgagc atgttgattg catgtgtatt tgtgtatgta catatctatg 1680  
 gtggtggtgg tgtcaaggcc aacacgagtc ttctaggtt acgtcaagga cctggtcgtc 1740  
 agttgctgac ggacgcgcgc aaccactgct ttctgtctc atctcgctg ctctgttctc 1800  
 tgacaaccaa acccaacaac ctctcatttc gcc atg atc cag gct ctt ctc cag 1854  
 Met Ile Gln Ala Leu Leu Gln  
 1 5

gtacgtctag ccttgcaatt gctgcctttg ctctaaaac tacctccctt ttcattcacc 1914  
 actaacgcat actacag cgc ctg gcc cgc tgg ctc gac cgg ccg caa ttc 1964  
 Arg Leu Ala Arg Trp Leu Asp Arg Pro Gln Phe  
 10 15

cca tgg aag cgc ctg gtt gtc ggc ttc tcc ctc gca gaa ttt gcc ctc 2012  
 Pro Trp Lys Arg Leu Val Val Gly Phe Ser Leu Ala Glu Phe Ala Leu  
 20 25 30

gaa aac tgg ctt ctc ttc cgc cag tat cgt gtc ctc caa cgc acc tct 2060  
 Glu Asn Trp Leu Leu Phe Arg Gln Tyr Arg Val Leu Gln Arg Thr Ser  
 35 40 45 50

atc ccc aag gct ctt gac aag gaa att gaa aag gaa acg ttt gac aag 2108  
 Ile Pro Lys Ala Leu Asp Lys Glu Ile Glu Lys Glu Thr Phe Asp Lys  
 55 60 65

tct cag gtgcgcctcc cctcgccgcc ccactgaggc cagacatggc gccaatcgtg 2164  
 Ser Gln

atattgaaac tgacaacggc tgcag caa tat ggt cgc gcc aaa gca agg ttc 2216  
 Gln Tyr Gly Arg Ala Lys Ala Arg Phe  
 70 75

agc ttc atc tcc ggt gtc ttc aac cag ctc aag cac cta gcc tct ctc 2264  
 Ser Phe Ile Ser Gly Val Phe Asn Gln Leu Lys His Leu Ala Ser Leu  
 80 85 90

tac ttc aac cta tac ccg ttt gtc tgg acc gcc gcc ggc act gtc ctc 2312  
 Tyr Phe Asn Leu Tyr Pro Phe Val Trp Thr Ala Ala Gly Thr Val Leu  
 95 100 105

gcc cgc tat gcg ccc gcc cgc ttt tcg ggc gag ata tcg cag tcg ctc 2360  
 Ala Arg Tyr Ala Pro Ala Arg Phe Ser Gly Glu Ile Ser Gln Ser Leu  
 110 115 120 125

ttg ttc atg tac atg ctc ggc tgg atc gac ttg gtc gcc agt ctc ggt 2408  
 Leu Phe Met Tyr Met Leu Gly Trp Ile Asp Leu Val Ala Ser Leu Gly  
 130 135 140

## 10336256.txt

ttc tgc tac tac cac agc ttc gtc ctg gaa gaa aag ttt ggc ttc aat	2456
Phe Ser Tyr Tyr His Ser Phe Val Leu Glu Glu Lys Phe Gly Phe Asn	
145 150 155	
aag atg acg gtc aag ctc tgg ctc acg gat atg gtc aag ggc cag gcg	2504
Lys Met Thr Val Lys Leu Trp Leu Thr Asp Met Val Lys Gly Gln Ala	
160 165 170	
ctc gcc att gca ttt ggt att ccg att gga agc gcc ttc ctg gcc att	2552
Leu Ala Ile Ala Phe Gly Ile Pro Ile Gly Ser Ala Phe Leu Ala Ile	
175 180 185	
atc aat aag acg ggg cag ggc ttt ttc tac tac ctg tgg atg ttc atg	2600
Ile Asn Lys Thr Gly Gln Gly Phe Phe Tyr Tyr Leu Trp Met Phe Met	
190 195 200 205	
cta gtt gtg cag att acc ggc atg act gtc tac ccg atc ctc att gtg	2648
Leu Val Val Gln Ile Thr Gly Met Thr Val Tyr Pro Ile Leu Ile Val	
210 215 220	
ccc ctg ttc aac aag ctg gag ccg ctc aag ccc ggc aaa ctc aag gag	2696
Pro Leu Phe Asn Lys Leu Glu Pro Leu Lys Pro Gly Lys Leu Lys Glu	
225 230 235	
tca gtc gag gca ctt gct tcc aag ctc aac ttt cct ctt tcg gag ctg	2744
Ser Val Glu Ala Leu Ala Ser Lys Leu Asn Phe Pro Leu Ser Glu Leu	
240 245 250	
cag gtc att gac ggc agc aag cgc agt gct cac agc aat gcc tac ttc	2792
Gln Val Ile Asp Gly Ser Lys Arg Ser Ala His Ser Asn Ala Tyr Phe	
255 260 265	
acg ggc cta ccc tgg att ggc aag aag aag att gtc atc tac gac aca	2840
Thr Gly Leu Pro Trp Ile Gly Lys Lys Lys Ile Val Ile Tyr Asp Thr	
270 275 280 285	
ctg ctg gaa aag agc acg gag aag gag gtc gag gct gta ctg gca cac	2888
Leu Leu Glu Lys Ser Thr Glu Lys Glu Val Glu Ala Val Leu Ala His	
290 295 300	
gag ctc ggt cac tgg aag atg aac cac acg tcg cga ctt ctc ttt att	2936
Glu Leu Gly His Trp Lys Met Asn His Thr Ser Arg Leu Leu Phe Ile	
305 310 315	
agc caa gcg cat cta ttc tac att ttt gcc ctt ttc tcc gtc ttc atc	2984
Ser Gln Ala His Leu Phe Tyr Ile Phe Ala Leu Phe Ser Val Phe Ile	
320 325 330	
aac aac cgg tcg ctg tac gca gac ttt ggc ttc cac cgg gag cag ccg	3032
Asn Asn Arg Ser Leu Tyr Ala Asp Phe Gly Phe His Arg Glu Gln Pro	
335 340 345	
acc att gtt ggt ttc atg ctc ttc aac gag att ctg tcg ccc acg gac	3080
Thr Ile Val Gly Phe Met Leu Phe Asn Glu Ile Leu Ser Pro Thr Asp	
350 355 360 365	
tcg atc gtc aag ctt ctc ctt aac atc tgg acc cgc agc atg gag tac	3128
Ser Ile Val Lys Leu Leu Leu Asn Ile Trp Thr Arg Ser Met Glu Tyr	
370 375 380	
gaa gca ggtacgtggc tcaaagtctt gcgtgtttgt gtatttgtgt gtgtgtatga	3184
Glu Ala	
tcaagactaa catgaaaca gat gct ttt gct gtc aaa ctt gga tat gcg cgc	3236
Asp Ala Phe Ala Val Lys Leu Gly Tyr Ala Arg	
385 390	

## 10336256.txt

gag cta ggc gca tcg tta atc aag ctg cag att cag aac cta tcg agc 3284  
 Glu Leu Gly Ala Ser Leu Ile Lys Leu Gln Ile Gln Asn Leu Ser Ser  
 395 400 405 410

atg gat gcc gac tgg ttc tac tcg agc ttc cac cac tcg cac ccc att 3332  
 Met Asp Ala Asp Trp Phe Tyr Ser Ser Phe His His Ser His Pro Ile  
 415 420 425

ttg acg gag cgt ctc aag gct atg aaa tgg act ggt gag aag aag att 3380  
 Leu Thr Glu Arg Leu Lys Ala Met Lys Trp Thr Gly Glu Lys Lys Ile  
 430 435 440

gtg gtt gac aag gcg gcc gac gag gac aag gct gta aag gca gcg gat 3428  
 Val Val Asp Lys Ala Ala Asp Glu Asp Lys Ala Val Lys Ala Ala Asp  
 445 450 455

cgg gag ctg taggcgctgg tgggtggtgg tgggtgcgtgt gagggtgcga 3477  
 Arg Glu Leu  
 460

tgtaggggcaa aaaaggccac gggcatgtgg aagcaagatt ggggtgcggac cattggtgta 3537  
 gtactagcat gtacttccaa tatgacggcg caaaagtggc agtgcctctc atctcgggtcg 3597  
 gtctgtggtg gcatgggcaag atggctaata cgactttttt gcctttgccc cattatccct 3657  
 cttcctctgc aggtctcgct ccttcttggc cttcttctctg gcatccttgt ccacctgtcc 3717  
 gtctggggggc gattgttggc tatggtcatg ggcctggtcc tgcttctctt tcttggtgcc 3777  
 gttgatctgc actggtggtt cctgctcacc ctcttgacag acgttgggtcc tgttgccac 3837  
 gtcgccaatc tcgatgccgc cttgctcggc ctggtagggt gccgcgtctt gccactcttg 3897  
 atctgcgcct gtatttttgc tgccctcgcc atcagcagca gcgtccaggg cctcgtcctg 3957  
 ggcctcgaga gtcgtgtcgg gctcaagata ctgcgcgcg aagcccgcag ctacacggcg 4017  
 cagatggtgc atgagcaggt tccccactgc gccgcccttt gcgttgaacg tcacgccatc 4077  
 gggagtata agggcgtcgg ggtgcaagtgc cgcattgtgc tcggagtgtt gcagggtactt 4137  
 ttccagcacg gcggatgcgt cgttgagaga cacgggcacg ctggatacct ggcggcgggg 4197  
 cgggggtgcc tcaagcagca tgggtgtgca attgtataaa agaatgagaa aagttagtta 4257  
 tggcgagac atcaatcttg ggttgagtgg tacattcaga aaagagtctt gggtagagc 4317  
 atgtgcatgg gcatgtaaag gtgcaacttt ttgcgcacgg acacccaacc catgttttac 4377  
 tattagtttt ggtctgcgga ctggagaatg gggcgctgca gtcgacgaac catttacacc 4437

<210> 167

<211> 7

<212> PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<400> 167

Met Ile Gln Ala Leu Leu Gln  
 1 5

<210> 168

<211> 61

<212> PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<400> 168

Arg Leu Ala Arg Trp Leu Asp Arg Pro Gln Phe Pro Trp Lys Arg Leu  
 1 5 10 15  
 Val Val Gly Phe Ser Leu Ala Glu Phe Ala Leu Glu Asn Trp Leu Leu  
 20 25 30  
 Phe Arg Gln Tyr Arg Val Leu Gln Arg Thr Ser Ile Pro Lys Ala Leu  
 35 40 45  
 Asp Lys Glu Ile Glu Lys Glu Thr Phe Asp Lys Ser Gln  
 50 55 60

<210> 169

<211> 315

<212> PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<400> 169

Gln Tyr Gly Arg Ala Lys Ala Arg Phe Ser Phe Ile Ser Gly Val Phe

## 10336256.txt

```

1      5      10      15
Asn Gln Leu Lys His Leu Ala Ser Leu Tyr Phe Asn Leu Tyr Pro Phe
20
Val Trp Thr Ala Ala Gly Thr Val Leu Ala Arg Tyr Ala Pro Ala Arg
35
Phe Ser Gly Glu Ile Ser Gln Ser Leu Leu Phe Met Tyr Met Leu Gly
50
Trp Ile Asp Leu Val Ala Ser Leu Gly Phe Ser Tyr Tyr His Ser Phe
65
Val Leu Glu Glu Lys Phe Gly Phe Asn Lys Met Thr Val Lys Leu Trp
85
Leu Thr Asp Met Val Lys Gly Gln Ala Leu Ala Ile Ala Phe Gly Ile
100
Pro Ile Gly Ser Ala Phe Leu Ala Ile Ile Asn Lys Thr Gly Gln Gly
115
Phe Phe Tyr Tyr Leu Trp Met Phe Met Leu Val Val Gln Ile Thr Gly
130
Met Thr Val Tyr Pro Ile Leu Ile Val Pro Leu Phe Asn Lys Leu Glu
145
Pro Leu Lys Pro Gly Lys Leu Lys Glu Ser Val Glu Ala Leu Ala Ser
165
Lys Leu Asn Phe Pro Leu Ser Glu Leu Gln Val Ile Asp Gly Ser Lys
180
Arg Ser Ala His Ser Asn Ala Tyr Phe Thr Gly Leu Pro Trp Ile Gly
195
Lys Lys Lys Ile Val Ile Tyr Asp Thr Leu Leu Glu Lys Ser Thr Glu
210
Lys Glu Val Glu Ala Val Leu Ala His Glu Leu Gly His Trp Lys Met
225
Asn His Thr Ser Arg Leu Leu Phe Ile Ser Gln Ala His Leu Phe Tyr
245
Ile Phe Ala Leu Phe Ser Val Phe Ile Asn Asn Arg Ser Leu Tyr Ala
260
Asp Phe Gly Phe His Arg Glu Gln Pro Thr Ile Val Gly Phe Met Leu
275
Phe Asn Glu Ile Leu Ser Pro Thr Asp Ser Ile Val Lys Leu Leu Leu
290
Asn Ile Trp Thr Arg Ser Met Glu Tyr Glu Ala
305
310
315

```

&lt;210&gt; 170

&lt;211&gt; 78

&lt;212&gt; PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

&lt;400&gt; 170

```

Asp Ala Phe Ala Val Lys Leu Gly Tyr Ala Arg Glu Leu Gly Ala Ser
1      5      10      15
Leu Ile Lys Leu Gln Ile Gln Asn Leu Ser Ser Met Asp Ala Asp Trp
20
Phe Tyr Ser Ser Phe His His Ser His Pro Ile Leu Thr Glu Arg Leu
35
Lys Ala Met Lys Trp Thr Gly Glu Lys Lys Ile Val Val Asp Lys Ala
50
Ala Asp Glu Asp Lys Ala Val Lys Ala Ala Asp Arg Glu Leu
65
70
75

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&lt;210&gt; 171

&lt;211&gt; 1383

&lt;212&gt; DNA

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1383)

&lt;400&gt; 171

atg atc cag gct ctt ctc cag cgc ctg gcc cgc tgg ctc gac cgg ccg

10336256.txt

Met	Ile	Gln	Ala	Leu	Leu	Gln	Arg	Leu	Ala	Arg	Trp	Leu	Asp	Arg	Pro		
1				5					10					15			
caa	ttc	cca	tgg	aag	cgc	ctg	gtt	gtc	ggc	ttc	tcc	ctc	gca	gaa	ttt		96
Gln	Phe	Pro	Trp	Lys	Arg	Leu	Val	Val	Gly	Phe	Ser	Leu	Ala	Glu	Phe		
			20					25					30				
gcc	ctc	gaa	aac	tgg	ctt	ctc	ttc	cgc	cag	tat	cgt	gtc	ctc	caa	cgc		144
Ala	Leu	Glu	Asn	Trp	Leu	Leu	Phe	Arg	Gln	Tyr	Arg	Val	Leu	Gln	Arg		
			35				40					45					
acc	tct	atc	ccc	aag	gct	ctt	gac	aag	gaa	att	gaa	aag	gaa	acg	ttt		192
Thr	Ser	Ile	Pro	Lys	Ala	Leu	Asp	Lys	Glu	Ile	Glu	Lys	Glu	Thr	Phe		
			50			55					60						
gac	aag	tct	cag	caa	tat	ggt	cgc	gcc	aaa	gca	agg	ttc	agc	ttc	atc		240
Asp	Lys	Ser	Gln	Gln	Tyr	Gly	Arg	Ala	Lys	Ala	Arg	Phe	Ser	Phe	Ile		
					70				75						80		
tcc	ggt	gtc	ttc	aac	cag	ctc	aag	cac	cta	gcc	tct	ctc	tac	ttc	aac		288
Ser	Gly	Val	Phe	Asn	Gln	Leu	Lys	His	Leu	Ala	Ser	Leu	Tyr	Phe	Asn		
				85					90					95			
cta	tac	ccg	ttt	gtc	tgg	acc	gcc	gcc	ggc	act	gtc	ctc	gcc	cgc	tat		336
Leu	Tyr	Pro	Phe	Val	Trp	Thr	Ala	Ala	Gly	Thr	Val	Leu	Ala	Arg	Tyr		
			100					105					110				
gcg	ccc	gcc	cgc	ttt	tcg	ggc	gag	ata	tcg	cag	tcg	ctc	ttg	ttc	atg		384
Ala	Pro	Ala	Arg	Phe	Ser	Gly	Glu	Ile	Ser	Gln	Ser	Leu	Leu	Phe	Met		
			115				120					125					
tac	atg	ctc	ggc	tgg	atc	gac	ttg	gtc	gcc	agt	ctc	ggt	ttc	tcg	tac		432
Tyr	Met	Leu	Gly	Trp	Ile	Asp	Leu	Val	Ala	Ser	Leu	Gly	Phe	Ser	Tyr		
						135					140						
tac	cac	agc	ttc	gtc	ctg	gaa	gaa	aag	ttt	ggc	ttc	aat	aag	atg	acg		480
Tyr	His	Ser	Phe	Val	Leu	Glu	Glu	Lys	Phe	Gly	Phe	Asn	Lys	Met	Thr		
					150				155						160		
gtc	aag	ctc	tgg	ctc	acg	gat	atg	gtc	aag	ggc	cag	gcg	ctc	gcc	att		528
Val	Lys	Leu	Trp	Leu	Thr	Asp	Met	Val	Lys	Gly	Gln	Ala	Leu	Ala	Ile		
				165					170					175			
gca	ttt	ggt	att	ccg	att	gga	agc	gcc	ttc	ctg	gcc	att	atc	aat	aag		576
Ala	Phe	Gly	Ile	Pro	Ile	Gly	Ser	Ala	Phe	Leu	Ala	Ile	Ile	Asn	Lys		
				180				185					190				
acg	ggg	cag	ggc	ttt	ttc	tac	tac	ctg	tgg	atg	ttc	atg	cta	gtt	gtg		624
Thr	Gly	Gln	Gly	Phe	Phe	Tyr	Tyr	Leu	Trp	Met	Phe	Met	Leu	Val	Val		
				195			200					205					
cag	att	acc	ggc	atg	act	gtc	tac	ccg	atc	ctc	att	gtg	ccc	ctg	ttc		672
Gln	Ile	Thr	Gly	Met	Thr	Val	Tyr	Pro	Ile	Leu	Ile	Val	Pro	Leu	Phe		
						215					220						
aac	aag	ctg	gag	ccg	ctc	aag	ccc	ggc	aaa	ctc	aag	gag	tca	gtc	gag		720
Asn	Lys	Leu	Glu	Pro	Leu	Lys	Pro	Gly	Lys	Leu	Lys	Glu	Ser	Val	Glu		
					230				235						240		
gca	ctt	gct	tcc	aag	ctc	aac	ttt	cct	ctt	tcg	gag	ctg	cag	gtc	att		768
Ala	Leu	Ala	Ser	Lys	Leu	Asn	Phe	Pro	Leu	Ser	Glu	Leu	Gln	Val	Ile		
				245				250						255			
gac	ggc	agc	aag	cgc	agt	gct	cac	agc	aat	gcc	tac	ttc	acg	ggc	cta		816
Asp	Gly	Ser	Lys	Arg	Ser	Ala	His	Ser	Asn	Ala	Tyr	Phe	Thr	Gly	Leu		
			260					265					270				
ccc	tgg	att	ggc	aag	aag	aag	att	gtc	atc	tac	gac	aca	ctg	ctg	gaa		864

10336256.txt

Pro Trp Ile Gly Lys Lys Lys Ile Val Ile Tyr Asp Thr Leu Leu Glu  
 275 280 285

aag agc acg gag aag gag gtc gag gct gta ctg gca cac gag ctc ggt 912  
 Lys Ser Thr Glu Lys Glu Val Glu Ala Val Leu Ala His Glu Leu Gly  
 290 295 300

cac tgg aag atg aac cac acg tcg cga ctt ctc ttt att agc caa gcg 960  
 His Trp Lys Met Asn His Thr Ser Arg Leu Leu Phe Ile Ser Gln Ala  
 305 310 315 320

cat cta ttc tac att ttt gcc ctt ttc tcc gtc ttc atc aac aac cgg 1008  
 His Leu Phe Tyr Ile Phe Ala Leu Phe Ser Val Phe Ile Asn Asn Arg  
 325 330 335

tcg ctg tac gca gac ttt ggc ttc cac cgg gag cag ccg acc att gtt 1056  
 Ser Leu Tyr Ala Asp Phe Phe His Arg Glu Gln Pro Thr Ile Val  
 340 345

ggt ttc atg ctc ttc aac gag att ctg tcg ccc acg gac tcg atc gtc 1104  
 Gly Phe Met Leu Phe Asn Glu Ile Leu Ser Pro Thr Asp Ser Ile Val  
 355 360 365

aag ctt ctc ctt aac atc tgg acc cgc agc atg gag tac gaa gca gat 1152  
 Lys Leu Leu Leu Asn Ile Trp Thr Arg Ser Met Glu Tyr Glu Ala Asp  
 370 375 380

gct ttt gct gtc aaa ctt gga tat gcg cgc gag cta ggc gca tcg tta 1200  
 Ala Phe Ala Val Lys Leu Gly Tyr Ala Arg Glu Leu Gly Ala Ser Leu  
 385 390 395 400

atc aag ctg cag att cag aac cta tcg agc atg gat gcc gac tgg ttc 1248  
 Ile Lys Leu Gln Ile Gln Asn Leu Ser Ser Met Asp Ala Asp Trp Phe  
 405 410 415

tac tcg agc ttc cac cac tcg cac ccc att ttg acg gag cgt ctc aag 1296  
 Tyr Ser Ser Phe His His Ser His Pro Ile Leu Thr Glu Arg Leu Lys  
 420 425 430

gct atg aaa tgg act ggt gag aag aag att gtg gtt gac aag gcg gcc 1344  
 Ala Met Lys Trp Thr Gly Glu Lys Lys Ile Val Val Asp Lys Ala Ala  
 435 440 445

gac gag gac aag gct gta aag gca gcg gat cgg gag ctg 1383  
 Asp Glu Asp Lys Ala Val Lys Ala Ala Asp Arg Glu Leu  
 450 455 460

&lt;210&gt; 172

&lt;211&gt; 461

&lt;212&gt; PRT

&lt;213&gt; Cochliobolus heterostrophus strain C4 (ATCC 48331)

&lt;220&gt;

&lt;221&gt; DOMAIN

&lt;222&gt; (239)...(439)

&lt;223&gt; Peptidase family M48

&lt;400&gt; 172

Met Ile Gln Ala Leu Leu Gln Arg Leu Ala Arg Trp Leu Asp Arg Pro  
 1 5 10 15  
 Gln Phe Pro Trp Lys Arg Leu Val Val Gly Phe Ser Leu Ala Glu Phe  
 20 25 30  
 Ala Leu Glu Asn Trp Leu Leu Phe Arg Gln Tyr Arg Val Leu Gln Arg  
 35 40 45  
 Thr Ser Ile Pro Lys Ala Leu Asp Lys Glu Ile Glu Lys Glu Thr Phe  
 50 55 60  
 Asp Lys Ser Gln Gln Tyr Gly Arg Ala Lys Ala Arg Phe Ser Phe Ile

10336256.txt

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65      70      75      80
Ser Gly Val Phe Asn Gln Leu Lys His Leu Ala Ser Leu Tyr Phe Asn
85      90      95
Leu Tyr Pro Phe Val Trp Thr Ala Ala Gly Thr Val Leu Ala Arg Tyr
100     105
Ala Pro Ala Arg Phe Ser Gly Glu Ile Ser Gln Ser Leu Leu Phe Met
115     120     125
Tyr Met Leu Gly Trp Ile Asp Leu Val Ala Ser Leu Gly Phe Ser Tyr
130     135     140
Tyr His Ser Phe Val Leu Glu Glu Lys Phe Gly Phe Asn Lys Met Thr
145     150     155     160
Val Lys Leu Trp Leu Thr Asp Met Val Lys Gly Gln Ala Leu Ala Ile
165     170     175
Ala Phe Gly Ile Pro Ile Gly Ser Ala Phe Leu Ala Ile Ile Asn Lys
180     185     190
Thr Gly Gln Gly Phe Phe Tyr Tyr Leu Trp Met Phe Met Leu Val Val
195     200     205
Gln Ile Thr Gly Met Thr Val Tyr Pro Ile Leu Ile Val Pro Leu Phe
210     215     220
Asn Lys Leu Glu Pro Leu Lys Pro Gly Lys Leu Lys Glu Ser Val Glu
225     230     235     240
Ala Leu Ala Ser Lys Leu Asn Phe Pro Leu Ser Glu Leu Gln Val Ile
245     250     255
Asp Gly Ser Lys Arg Ser Ala His Ser Asn Ala Tyr Phe Thr Gly Leu
260     265     270
Pro Trp Ile Gly Lys Lys Lys Ile Val Ile Tyr Asp Thr Leu Leu Glu
275     280     285
Lys Ser Thr Glu Lys Glu Val Glu Ala Val Leu Ala His Glu Leu Gly
290     295     300
His Trp Lys Met Asn His Thr Ser Arg Leu Leu Phe Ile Ser Gln Ala
305     310     315     320
His Leu Phe Tyr Ile Phe Ala Leu Phe Ser Val Phe Ile Asn Asn Arg
325     330     335
Ser Leu Tyr Ala Asp Phe Gly Phe His Arg Glu Gln Pro Thr Ile Val
340     345     350
Gly Phe Met Leu Phe Asn Glu Ile Leu Ser Pro Thr Asp Ser Ile Val
355     360     365
Lys Leu Leu Leu Asn Ile Trp Thr Arg Ser Met Glu Tyr Glu Ala Asp
370     375     380
Ala Phe Ala Val Lys Leu Gly Tyr Ala Arg Glu Leu Gly Ala Ser Leu
385     390     395     400
Ile Lys Leu Gln Ile Gln Asn Leu Ser Ser Met Asp Ala Asp Trp Phe
405     410     415
Tyr Ser Ser Phe His His Ser His Pro Ile Leu Thr Glu Arg Leu Lys
420     425     430
Ala Met Lys Trp Thr Gly Glu Lys Lys Ile Val Val Asp Lys Ala Ala
435     440     445
Asp Glu Asp Lys Ala Val Lys Ala Ala Asp Arg Glu Leu
450     455     460

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&lt;210&gt; 173

&lt;211&gt; 3237

&lt;212&gt; DNA

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1440)...(1808) .

&lt;223&gt; Exon

&lt;221&gt; CDS

&lt;222&gt; (1862)...(2044)

&lt;223&gt; Exon

&lt;221&gt; CDS

&lt;222&gt; (2096)...(2211)

&lt;223&gt; Exon

10336256.txt

<221> CDS  
 <222> (2263)...(2353)  
 <223> Exon

<221> CDS  
 <222> (2448)...(3011)  
 <223> Exon

<400> 173  
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 ttgggtcttag cttttgcgtca gccgattaat gaaataaacc taaacaaacg gccaggggata 120  
 tgctttattc gaatccgggg cgctcggcagc catgctcggc aataatccag aaaccctgtt 180  
 tcacaacgtg ctcttatcgg atagttgcgt ttaatatgag gaagaaattg aggaagaagg 240  
 acaagagggt ggatgatgaa gtatagttct tatcgtgact tggctgcgac aaagacggct 300  
 aggaactgtt cgattcagct gcgttttccc tctatatattc attcccgtct tggatttgaa 360  
 gcttcgatag ggagtgctag ctgcttactc ttatagccca gtctttccaa actgggtag 420  
 gaaatggaag ggttattcag ttggaggtct gttttatgtt aattcgagga tcacgtgat 480  
 agcaaagtca ccggatctga taacagaatt tagttttcag gtacaagtag atgtcgagcg 540  
 acctaaggct acattctcgt agcttttagat gcgcatataa ccgaacacgc tagtagcttc 600  
 atgagttccg tttccgaaac ggaacctgaa ttggggaaat agaacgcaga atgtagcttg 660  
 caattcgcgc aaccgaacaa gctttccagc cctgttttgt agatggagcg gacggaaaac 720  
 ggatacgtaa ccgaacaggg ccctagtagt cgtctaccgc atcaacgggt gcgcatgttt 780  
 tcgtgggttc ccgcatgtcc aaccaccaca gcctcaacaa tggctgcatt ggaaatccta 840  
 cttttatacct ttctcgctga aagcttatat taccatgctt gcagaatttg tcattactct 900  
 gggtgttgcc tttgtacaca agtcggcact tagtcccatt attagaccgt ggcaagttgc 960  
 cctaagcttc actattcagc ctcaataagc actcttattc agaatcacc aatgcaagaa 1020  
 caaagaagtt ggagacggac aaggagagtc tccgcacca atgtgcgggc ccatctgaca 1080  
 ttgcaagat gcacgggttg atgacgttgc cgctcttgcg ccagcaacg ccatgcaatg 1140  
 cctagaacac aactggcagg tcagaaggct aacgacttgg gatattaccg gattgcttct 1200  
 tatccacgac tatcccgtgt atccagcgga catgtataat gtcaccgtgc gcctgtagta 1260  
 cgtacggctg atgctggcat tggttgcctg aagacggcat gggttccttcc ccaccgggc 1320  
 ttccatggac tgcggtcttg ccaagcaaac gcatagtgaa agggatataa agtgaggttc 1380  
 gggcaagagt tataaacttc cctcttacac ccgcccgtt gggtgctcgt cagggtcatc 1439  
 atg aag ttt gta ttc aac ctt gcc tgg ctg tgc ctt gct gct ggc gcg 1487  
 Met Lys Phe Val Phe Asn Leu Ala Trp Leu Ser Leu Ala Ala Gly Ala  
 1 5 10 15  
 act att cgc agc tcg cag cca gtt acc tac gat ggc tac cag gtc cac 1535  
 Thr Ile Arg Ser Ser Gln Pro Val Thr Tyr Asp Gly Tyr Gln Val His  
 20 25 30  
 cgc atc cgg gcc att ggt caa cag ggc gtg atg gca aag cgt gca atg 1583  
 Arg Ile Arg Ala Ile Gly Gln Gln Gly Val Met Ala Lys Arg Ala Met  
 35 40 45  
 tcg tcc att cct cac gag acg ctc aat gaa gct cga ggt tcc tgg gac 1631  
 Ser Ser Ile Pro His Glu Thr Leu Asn Glu Ala Arg Gly Ser Trp Asp  
 50 55 60  
 gtg ctc att gca cca gac caa ctc gat gca ttc agc cgc ctc ggg ctg 1679  
 Val Leu Ile Ala Pro Asp Gln Leu Asp Ala Phe Ser Arg Leu Gly Leu  
 65 70 75 80  
 aag tcg cga acc ctg cac aag gac ttg gcc tac tcc att gct cgc gag 1727  
 Lys Ser Arg Thr Leu His Lys Asp Leu Ala Tyr Ser Ile Ala Arg Glu  
 85 90 95  
 cgt caa gtc agg aat gtt tgg aag agg caa tca aac ggc tct gat gat 1775  
 Arg Gln Val Arg Asn Val Trp Lys Arg Gln Ser Asn Gly Ser Asp Asp  
 100 105 110  
 gct tgg ttt gac agc tat cac ccc tat gaa gat gtaagtgcatt gtttatcagt 1828  
 Ala Trp Phe Asp Ser Tyr His Pro Tyr Glu Asp  
 115 120  
 ctcgaggaaa gaatcatgct aacatcattg aag cac atc act tgg tgg aag gat 1882  
 His Ile Thr Trp Trp Lys Asp  
 125 130

## 10336256.txt

ctc cag gcc act ttc ccc gag cag tca aac tgg acg agt agc gga acg 1930  
 Leu Gln Ala Thr Phe Pro Glu Gln Ser Asn Trp Thr Ser Ser Gly Thr  
 135 140 145

tcc tac gag gga cgc gac ctg ttc ggt gtg cat ctc tgg gga gca ggt 1978  
 Ser Tyr Glu Gly Arg Asp Leu Phe Gly Val His Leu Trp Gly Ala Gly  
 150 155 160

ggc cct gga aag cct gca gtc atc tac cac ggt act gta cat gcc cgt 2026  
 Gly Pro Gly Lys Pro Ala Val Ile Tyr His Gly Thr Val His Ala Arg  
 165 170 175

gaa tgg atc gtc gct ccc gtttagtaaac ccaaaaaggc agttctcctt 2074  
 Glu Trp Ile Val Ala Pro

atcataacta acactttata g acc att gag tac atc aca aaa cag ctc att 2125  
 Thr Ile Glu Tyr Ile Thr Lys Gln Leu Ile  
 185 190

gat gga tac aag gcc gga gac aac gac aca aag gca atc ttg gac aaa 2173  
 Asp Gly Tyr Lys Ala Gly Asp Asn Asp Thr Lys Ala Ile Leu Asp Lys  
 195 200 205 210

tac gac ttc tac atc ttt ccc ttt gtg aac ccg gat gg taagctgcga 2221  
 Tyr Asp Phe Tyr Ile Phe Pro Phe Val Asn Pro Asp Gly  
 215 220

ctccactgcat tgcgttgacc aattcactca cacgtgacag g t ttc gtc ttc tcc 2275  
 Phe Val Phe Ser  
 225

cag acc gac gac cgt ctc tgg cgc aag aac cgc cag ccc cca ccc gcc 2323  
 Gln Thr Asp Asp Arg Leu Trp Arg Lys Asn Arg Gln Pro Pro Ala  
 230 235 240

aac caa aac caa acc tgc ttc ggc cgc gat gtaagcactc cccaacttcc 2373  
 Asn Gln Asn Gln Thr Cys Phe Gly Arg Asp  
 245 250

cccaaacttc gtattccaat ttcaatctca attctcaatt ccaattccag tcccactaac 2433  
 catatcttgt aaag atc aac cgc aac tgg gaa aca aac tgg gac gcc gac 2483  
 Ile Asn Arg Asn Trp Glu Thr Asn Trp Asp Ala Asp  
 255 260 265

ccc cgc ggc gcc tcg cca gac gcc tgc tca caa gtg tac cgc ggc gag 2531  
 Pro Arg Gly Ala Ser Pro Asp Ala Cys Ser Gln Val Tyr Arg Gly Glu  
 270 275 280

aaa ccc cgc gac gcg ccc gaa aac gag agc atg gac aac ttc atc cgc 2579  
 Lys Pro Arg Asp Ala Pro Glu Asn Glu Ser Met Asp Asn Phe Ile Arg  
 285 290 295

aaa gtc cgc gac gag caa ggc att acg ctc tac att gac tgg cac agc 2627  
 Lys Val Arg Asp Glu Gln Gly Ile Thr Leu Tyr Ile Asp Trp His Ser  
 300 305 310

tac tcg cag ctc atc ctc ttc ccc ttt ggc cac aaa gaa acg ctc tac 2675  
 Tyr Ser Gln Leu Ile Leu Phe Pro Phe Gly His Lys Glu Thr Leu Tyr  
 315 320 325

gcc ccc gaa ctc ggc atg tgg acc aag acg gcc tcg ctg atg agc gag 2723  
 Ala Pro Glu Leu Gly Met Trp Thr Lys Thr Ala Ser Leu Met Ser Glu  
 330 335 340 345

tac att cgc gat tcg tca agg aac gat act acg tat ctg ttt ggt ccg 2771  
 Tyr Ile Arg Asp Ser Ser Arg Asn Asp Thr Thr Tyr Leu Phe Gly Pro

10336256.txt

350	355	360	
agc gga gcg acg ctg tac ccc acg acg ggt gcg tcg att gat cat gtt	370		2819
Ser Gly Ala Thr Leu Tyr Pro Thr Thr Gly Ala Ser Ile Asp His Val			
	375		
tat acg att ggt agg gcc aag ttc tcg ttt aca atc gag ttg ccg gat			2867
Tyr Thr Ile Gly Arg Ala Lys Phe Ser Phe Thr Ile Glu Leu Pro Asp	385		
	390		
acc ggt gac ttt ggg ttt gtg ctg ccg cca gag agg atc agg cct gcg			2915
Thr Gly Asp Phe Gly Phe Val Leu Pro Pro Glu Arg Ile Arg Pro Ala	400		
	405		
att gag gag cag tgg gtg gga cag cag gtc ctg ctg gcg ctc ttg gac			2963
Ile Glu Glu Gln Trp Val Gly Gln Gln Val Leu Leu Ala Leu Leu Asp	415	420	425
gag ccg ttt ttt gac ggt gtg ggc cct gcg att ggg act agt acg tgg			3011
Glu Pro Phe Phe Asp Gly Val Gly Pro Ala Ile Gly Thr Ser Thr Trp	430	435	440
taaggctgct attcgtttct aagatgattg atatgataca ctatgtatgt atgtagtaaa			3071
tagaaagata agaaagttga gcgagaaaag agtcaggcca tactgtgttg aaagttcatg			3131
cttggccttca agcgttgatg tgaaaagtcg gcttcacttg gccttgcattg aaactaacgt			3191
cagtgatatg agtgagagca gccgcgccat tctccatgcc ctcaat			3237

&lt;210&gt; 174

&lt;211&gt; 123

&lt;212&gt; PRT

&lt;213&gt; Cochliobolus heterostrophus strain C4 (ATCC 48331)

&lt;400&gt; 174

Met Lys Phe Val Phe Asn Leu Ala Trp Leu Ser Leu Ala Ala Gly Ala  
 1 5 10 15  
 Thr Ile Arg Ser Ser Gln Pro Val Thr Tyr Asp Gly Tyr Gln Val His  
 20 25 30  
 Arg Ile Arg Ala Ile Gly Gln Gln Gly Val Met Ala Lys Arg Ala Met  
 35 40 45  
 Ser Ser Ile Pro His Glu Thr Leu Asn Glu Ala Arg Gly Ser Trp Asp  
 50 55 60  
 Val Leu Ile Ala Pro Asp Gln Leu Asp Ala Phe Ser Arg Leu Gly Leu  
 65 70 75 80  
 Lys Ser Arg Thr Leu His Lys Asp Leu Ala Tyr Ser Ile Ala Arg Glu  
 85 90 95  
 Arg Gln Val Arg Asn Val Trp Lys Arg Gln Ser Asn Gly Ser Asp Asp  
 100 105 110  
 Ala Trp Phe Asp Ser Tyr His Pro Tyr Glu Asp  
 115 120

&lt;210&gt; 175

&lt;211&gt; 61

&lt;212&gt; PRT

&lt;213&gt; Cochliobolus heterostrophus strain C4 (ATCC 48331)

&lt;400&gt; 175

His Ile Thr Trp Trp Lys Asp Leu Gln Ala Thr Phe Pro Glu Gln Ser  
 1 5 10 15  
 Asn Trp Thr Ser Ser Gly Thr Ser Tyr Glu Gly Arg Asp Leu Phe Gly  
 20 25 30  
 Val His Leu Trp Gly Ala Gly Gly Pro Gly Lys Pro Ala Val Ile Tyr  
 35 40 45  
 His Gly Thr Val His Ala Arg Glu Trp Ile Val Ala Pro  
 50 55 60

&lt;210&gt; 176

&lt;211&gt; 39

&lt;212&gt; PRT

10336256.txt

&lt;213&gt; Cochliobolus heterostrophus strain C4 (ATCC 48331)

&lt;400&gt; 176

Thr Ile Glu Tyr Ile Thr Lys Gln Leu Ile Asp Gly Tyr Lys Ala Gly  
 1 5 10 15  
 Asp Asn Asp Thr Lys Ala Ile Leu Asp Lys Tyr Asp Phe Tyr Ile Phe  
 20 25 30  
 Pro Phe Val Asn Pro Asp Gly  
 35

&lt;210&gt; 177

&lt;211&gt; 30

&lt;212&gt; PRT

&lt;213&gt; Cochliobolus heterostrophus strain C4 (ATCC 48331)

&lt;400&gt; 177

Phe Val Phe Ser Gln Thr Asp Asp Arg Leu Trp Arg Lys Asn Arg Gln  
 1 5 10 15  
 Pro Pro Pro Ala Asn Gln Asn Gln Thr Cys Phe Gly Arg Asp  
 20 25 30

&lt;210&gt; 178

&lt;211&gt; 188

&lt;212&gt; PRT

&lt;213&gt; Cochliobolus heterostrophus strain C4 (ATCC 48331)

&lt;400&gt; 178

Ile Asn Arg Asn Trp Glu Thr Asn Trp Asp Ala Asp Pro Arg Gly Ala  
 1 5 10 15  
 Ser Pro Asp Ala Cys Ser Gln Val Tyr Arg Gly Glu Lys Pro Arg Asp  
 20 25 30  
 Ala Pro Glu Asn Glu Ser Met Asp Asn Phe Ile Arg Lys Val Arg Asp  
 35 40 45  
 Glu Gln Gly Ile Thr Leu Tyr Ile Asp Trp His Ser Tyr Ser Gln Leu  
 50 55 60  
 Ile Leu Phe Pro Phe Gly His Lys Glu Thr Leu Tyr Ala Pro Glu Leu  
 65 70 75 80  
 Gly Met Trp Thr Lys Thr Ala Ser Leu Met Ser Glu Tyr Ile Arg Asp  
 85 90 95  
 Ser Ser Arg Asn Asp Thr Thr Tyr Leu Phe Gly Pro Ser Gly Ala Thr  
 100 105 110  
 Leu Tyr Pro Thr Thr Gly Ala Ser Ile Asp His Val Tyr Thr Ile Gly  
 115 120 125  
 Arg Ala Lys Phe Ser Phe Thr Ile Glu Leu Pro Asp Thr Gly Asp Phe  
 130 135 140  
 Gly Phe Val Leu Pro Pro Glu Arg Ile Arg Pro Ala Ile Glu Glu Gln  
 145 150 155 160  
 Trp Val Gly Gln Gln Val Leu Leu Ala Leu Leu Asp Glu Pro Phe Phe  
 165 170 175  
 Asp Gly Val Gly Pro Ala Ile Gly Thr Ser Thr Trp  
 180 185

&lt;210&gt; 179

&lt;211&gt; 1323

&lt;212&gt; DNA

&lt;213&gt; Cochliobolus heterostrophus strain C4 (ATCC 48331)

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1323)

&lt;400&gt; 179

atg aag ttt gta ttc aac ctt gcc tgg ctg tcg ctt gct gct ggc gcg  
 Met Lys Phe Val Phe Asn Leu Ala Trp Leu Ser Leu Ala Ala Gly Ala  
 1 5 10 15

48

act att cgc agc tcg cag cca gtt acc tac gat ggc tac cag gtc cac  
 Thr Ile Arg Ser Ser Gln Pro Val Thr Tyr Asp Gly Tyr Gln Val His  
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10336256.txt

20	25	30	
cgc atc cgg gcc att ggt caa cag ggc gtg atg gca aag cgt gca atg Arg Ile Arg Ala Ile Gly Gln Gln Gly Val Met Ala Lys Arg Ala Met 35 40 45			144
tcg tcc att cct cac gag acg ctc aat gaa gct cga ggt tcc tgg gac Ser Ser Ile Pro His Glu Thr 55 Leu Asn Glu Ala Arg 60 Gly Ser Trp Asp			192
gtg ctc att gca cca gac caa ctc gat gca ttc agc cgc ctc ggg ctg Val Leu Ile Ala Pro Asp 70 Gln Leu Asp Ala Phe 75 Ser Arg Leu Gly Leu 80			240
aag tcg cga acc ctg cac aag gac ttg gcc tac tcc att gct cgc gag Lys Ser Arg Thr Leu 85 His Lys Asp Leu Ala Tyr Ser Ile Ala Arg 95 Glu			288
cgt caa gtc agg aat gtt tgg aag agg caa tca aac ggc tct gat gat Arg Gln Val Arg 100 Asn Val Trp Lys Arg 105 Gln Ser Asn Gly Ser 110 Asp Asp			336
gct tgg ttt gac agc tat cac ccc tat gaa gat cac atc act tgg tgg Ala Trp Phe 115 Asp Ser Tyr His Pro Tyr Glu Asp His Ile Thr Trp Trp 125			384
aag gat ctc cag gcc act ttc ccc gag cag tca aac tgg acg agt agc Lys Asp Leu Gln Ala Thr 135 Phe Pro Glu Gln Ser Asn Trp Thr Ser Ser 140			432
gga acg tcc tac gag gga cgc gac ctg ttc ggt gtg cat ctc tgg gga Gly Thr Ser Tyr Glu Gly 150 Arg Asp Leu Phe Gly Val His Leu Trp Gly 160			480
gca ggt ggc cct gga aag cct gca gtc atc tac cac ggt act gta cat Ala Gly Gly Pro Gly 165 Lys Pro Ala Val Ile Tyr His Gly Thr Val His 175			528
gcc cgt gaa tgg atc gtc gct ccc acc att gag tac atc aca aaa cag Ala Arg Glu Trp 180 Ile Val Ala Pro Thr Ile Ile Tyr Ile Thr Lys Gln 190			576
ctc att gat gga tac aag gcc gga gac aac gac aca aag gca atc ttg Leu Ile Asp Gly Tyr Lys Ala Gly 200 Asp Asn Asp Thr Lys 205 Ala Ile Leu			624
gac aaa tac gac ttc tac atc ttt ccc ttt gtg aac ccg gat ggt ttc Asp Lys Tyr Asp Phe Tyr 215 Phe Pro Phe Val Asn 220 Pro Asp Gly Phe			672
gtc ttc tcc cag acc gac gac cgt ctc tgg cgc aag aac cgc cag ccc Val Phe Ser Gln Thr 230 Asp Asp Arg Leu Trp Arg Lys Asn Arg Gln Pro 240			720
cca ccc gcc aac caa aac caa acc tgc ttc ggc cgc gat atc aac cgc Pro Pro Ala Asn Gln Asn Gln Thr Cys Phe Gly Arg Asp Ile Asn Arg 255			768
aac tgg gaa aca aac tgg gac gcc gac ccc cgc ggc gcc tcg cca gac Asn Trp Glu Thr 260 Asn Trp Asp Ala Asp Pro Arg Gly Ala Ser Pro Asp 270			816
gcc tgc tca caa gtg tac cgc ggc gag aaa ccc cgc gac gcg ccc gaa Ala Cys Ser Gln Val Tyr Arg Gly Glu Lys Pro Arg Asp 285 Ala Pro Glu			864
aac gag agc atg gac aac ttc atc cgc aaa gtc cgc gac gag caa ggc Asn Glu Ser Met Asp Asn Phe Ile Arg Lys Val Arg Asp 290 Glu Gln Gly			912

10336256.txt  
300

290	295																	
att acg ctc tac att gac tgg cac agc tac tcg cag ctc atc ctc ttc	ile thr leu tyr ile asp trp his ser tyr ser gln leu ile leu phe																	960
305	310																	
ccc ttt ggc cac aaa gaa acg ctc tac gcc ccc gaa ctc ggc atg tgg	pro phe gly his lys glt thr leu tyr ala pro glu leu gly met trp																	1008
325	330																	
acc aag acg gcc tcg ctg atg agc gag tac att cgc gat tcg tca agg	thr lys thr ala ser leu met ser glu tyr ile arg asp ser ser arg																	1056
340	345																	
aac gat act acg tat ctg ttt ggt ccg agc gga gcg acg ctg tac ccc	asn asp thr thr tyr leu phe gly pro ser gly ala thr leu tyr pro																	1104
355	360																	
acg acg ggt gcg tcg att gat cat gtt tat acg att ggt agg gcc aag	thr thr gly ala ser ile asp his val tyr thr ile gly arg ala lys																	1152
370	375																	
ttc tcg ttt aca atc gag ttg ccg gat acc ggt gac ttt ggg ttt gtg	phe ser phe thr ile glu leu pro asp thr gly asp phe gly phe val																	1200
385	390																	
ctg ccg cca gag agg atc agg cct gcg att gag gag cag tgg gtg gga	leu pro pro glu arg ile arg pro ala ile glu glu gln trp val gly																	1248
405	410																	
cag cag gtc ctg ctg gcg ctc ttg gac gag ccg ttt ttt gac ggt gtg	gln gln val leu leu ala leu leu asp glu pro phe phe asp gly val																	1296
420	425																	
ggc cct gcg att ggg act agt acg tgg	gly pro ala ile gly thr ser thr trp																	1323
435	440																	

&lt;210&gt; 180

&lt;211&gt; 441

&lt;212&gt; PRT

&lt;213&gt; Cochliobolus heterostrophus strain C4 (ATCC 48331)

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; (1)...(21)

&lt;221&gt; DOMAIN

&lt;222&gt; (116)...(325)

&lt;223&gt; Zinc carboxypeptidase

&lt;400&gt; 180

Met	Lys	Phe	Val	Phe	Asn	Leu	Ala	Trp	Leu	Ser	Leu	Ala	Ala	Gly	Ala	1	5	10	15
Thr	Ile	Arg	Ser	Gln	Pro	Val	Thr	Tyr	Asp	Gly	Tyr	Gln	Val	His		20	25	30	
Arg	Ile	Arg	Ala	Ile	Gly	Gln	Gln	Gly	Val	Met	Ala	Lys	Arg	Ala	Met	35	40	45	
Ser	Ser	Ile	Pro	His	Glu	Thr	Leu	Asn	Glu	Ala	Arg	Gly	Ser	Trp	Asp	50	55	60	
Val	Leu	Ile	Ala	Pro	Asp	Gln	Leu	Asp	Ala	Phe	Ser	Arg	Leu	Gly	Leu	65	70	75	80
Lys	Ser	Arg	Thr	Leu	His	Lys	Asp	Leu	Ala	Tyr	Ser	Ile	Ala	Arg	Glu	85	90	95	
Arg	Gln	Val	Arg	Asn	Val	Trp	Lys	Arg	Gln	Ser	Asn	Gly	Ser	Asp	Asp	100	105	110	
Ala	Trp	Phe	Asp	Ser	Tyr	His	Pro	Tyr	Glu	Asp	His	Ile	Thr	Trp	Trp				

## 10336256.txt

```

115      120      125
Lys Asp Leu Gln Ala Thr Phe Pro Glu Gln Ser Asn Trp Thr Ser Ser
130      135      140
Gly Thr Ser Tyr Glu Gly Arg Asp Leu Phe Gly Val His Leu Trp Gly
145      150      155
Ala Gly Gly Pro Gly Lys Pro Ala Val Ile Tyr His Gly Thr Val His
160      165      170
Ala Arg Glu Trp Ile Val Ala Pro Thr Ile Glu Tyr Ile Thr Lys Gln
175      180      185
Leu Ile Asp Gly Tyr Lys Ala Gly Asp Asn Asp Thr Lys Ala Ile Leu
190      195      200
Asp Lys Tyr Asp Phe Tyr Ile Phe Pro Phe Val Asn Pro Asp Gly Phe
205      210      215
Val Phe Ser Gln Thr Asp Asp Arg Leu Trp Arg Lys Asn Arg Gln Pro
220      225      230
Pro Pro Ala Asn Gln Asn Gln Thr Cys Phe Gly Arg Asp Ile Asn Arg
235      240      245
Asn Trp Glu Thr Asn Trp Asp Ala Asp Pro Arg Gly Ala Ser Pro Asp
250      255      260
Ala Cys Ser Gln Val Tyr Arg Gly Glu Lys Pro Arg Asp Ala Pro Glu
265      270      275
Asn Glu Ser Met Asp Asn Phe Ile Arg Lys Val Arg Asp Glu Gln Gly
280      285      290
Ile Thr Leu Tyr Ile Asp Trp His Ser Tyr Ser Gln Leu Ile Leu Phe
295      300      305
Pro Phe Gly His Lys Glu Thr Leu Tyr Ala Pro Glu Leu Gly Met Trp
310      315      320
Thr Lys Thr Ala Ser Leu Met Ser Glu Tyr Ile Arg Asp Ser Ser Arg
325      330      335
Asn Asp Thr Thr Tyr Leu Phe Gly Pro Ser Gly Ala Thr Leu Tyr Pro
340      345      350
Thr Thr Gly Ala Ser Ile Asp His Val Tyr Thr Ile Gly Arg Ala Lys
355      360      365
Phe Ser Phe Thr Ile Glu Leu Pro Asp Thr Gly Asp Phe Gly Phe Val
370      375      380
Leu Pro Pro Glu Arg Ile Arg Pro Ala Ile Glu Glu Gln Trp Val Gly
385      390      395
Gln Gln Val Leu Ala Leu Leu Asp Glu Pro Phe Phe Asp Gly Val
400      405      410
Gly Pro Ala Ile Gly Thr Ser Thr Trp
415      420      425
430      435      440

```

&lt;210&gt; 181

&lt;211&gt; 3266

&lt;212&gt; DNA

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (7)...(114)

&lt;223&gt; Exon

&lt;221&gt; CDS

&lt;222&gt; (856)...(1134)

&lt;223&gt; Exon

&lt;221&gt; CDS

&lt;222&gt; (1185)...(1337)

&lt;223&gt; Exon

&lt;221&gt; CDS

&lt;222&gt; (1442)...(1786)

&lt;223&gt; Exon

&lt;221&gt; CDS

&lt;222&gt; (1838)...(2266)

&lt;223&gt; Exon

## 10336256.txt

<400> 181  
gtgtgc atg tgg cac gcg gcg gtt gtg tct gcg aat gga ggc gca gag 48  
Met Trp His Ala Ala Val Val Ser Ala Asn Gly Gly Ala Glu  
1 5 10

ggc ttg ggt ggt ggg gga cga ggc acg gtc agg gat gtt ttt ttg gag 96  
Gly Leu Gly Gly Gly Gly Arg Gly Thr Val Arg Asp Val Phe Leu Glu  
15 20 25 30

gtg gca gct gct gtc ggg taagttgcac agcgtgaggt ttcaggggtgg 144  
Val Ala Ala Ala Val Gly  
35

gactgggtggg attgacgggt cttttaggaa caaaggaaaa tcgtggctgg attgatttgt 204  
cgagttgatt ttcgatgggt ggggggaacg atgttctgga ttattctttg ttccttctat 264  
gatacgtata ttgggaagca atgatacgggt atttgtgtag cgggtcaggc ggttttactc 324  
tgccgcagcc acagataggt tgtgccgcat ctgcacgtgt ccgttgaact tgccaatcga 384  
tatcacttgt ttgtggtcat ggtttacccc cttttcgtgc actgtagata cctcacatgt 444  
tggaagatag cttttgccgc tctatctaaa gcttcggact attttaatga tatcaagtct 504  
tttgcaaccc aagaaggatt aagagcaciaa ggcggtaacta tgaagtctta ttccagcagt 564  
cccactgtca ccaacatgcc acgccgtttt ggtccgcctt gaaagaaaca ctgcagcaga 624  
tacggcttaa gacattggcc caagtaaggt tgcactgcac acgtacgac ctaatacttg 684  
actctcacgg actacgtgct tgagtgccag agaaactgtc cccctttagt caacagcgac 744  
ccgtacaaca tgtatattta tcagtagcgc tgccttccaa ggaggtaaatt cagagcttgc 804  
aatattgttc actcccttac tttgctaaaa ctcaacgtac tgtcattcag c aaa cct 861  
Lys Pro

cga aag att ctt act gca ata atg tac ttc att ctg cta tcc ttg ctt 909  
Arg Lys Ile Leu Thr Ala Ile Met Tyr Phe Ile Leu Leu Ser Leu Leu  
40 45 50

gct tca ctt gta acc gct aca cca tta gtc aaa gca ccc ggt agc aag 957  
Ala Ser Leu Val Thr Ala Thr Pro Leu Val Lys Ala Pro Gly Ser Lys  
55 60 65 70

gcc att gcc aac aag tgg att gtc aaa ctc aag gac aac gtc gcc acg 1005  
Ala Ile Ala Asn Lys Trp Ile Val Lys Leu Lys Asp Asn Val Ala Thr  
75 80 85

atg gcc gct gat ggc gtg aaa gca gct att tcc aca aag ccc gat tac 1053  
Met Ala Ala Asp Gly Val Lys Ala Ala Ile Ser Thr Lys Pro Asp Tyr  
90 95 100

cag tat tcg atg cct ggc ttc cga ggc ttc gca gga act cta tcc gac 1101  
Gln Tyr Ser Met Pro Gly Phe Arg Gly Phe Ala Gly Thr Leu Ser Asp  
105 110 115

gat gag gta gca ctg ttg caa gct tca gat caa gtaaggcatt tgcagcacaa 1154  
Asp Glu Val Ala Leu Leu Gln Ala Ser Asp Gln  
120 125

gtccgaaagc ccctttgttg atttgtgtag att gag tat atc cag caa gat gct 1208  
Ile Glu Tyr Ile Gln Gln Asp Ala  
130 135

gaa gtt tac acg acg gca att atc gaa cag tcg aat gcc acg tgg gga 1256  
Glu Val Tyr Thr Thr Ala Ile Ile Glu Gln Ser Asn Ala Thr Trp Gly  
140 145 150

ata tcc cgt atc tcg cat aca aag cca agt gaa acg gcg tat ctc tat 1304  
Ile Ser Arg Ile Ser His Thr Lys Pro Ser Glu Thr Ala Tyr Leu Tyr  
155 160 165

gat tcc agt gca gga gag gga acg tgt gcg tat gtttttatct gccgccagac 1357  
Asp Ser Ser Ala Gly Glu Gly Thr Cys Ala Tyr  
170 175 180

## 10336256.txt

gttctctgtg tatcactgac gaaatgtgaa gctatgtgat tgatacagga gtcgatgtta 1417  
 cgcacccccga gtttcaagga cgta agt aat gac gct caa atg caa gac ttg 1468  
 Ser Asn Asp Ala Gln Met Gln Asp Leu  
 185

cag act gac cca gta aca ggc gct tta ttc ctg gca gac ctc act cat 1516  
 Gln Thr Asp Pro Val Thr Gly Ala Leu Phe Leu Ala Asp Leu Thr His  
 190 195 200 205

gaa ggt aat ttt ata gac ggg tat ggt cat gga acg cac gtc gct gga 1564  
 Glu Gly Asn Phe Ile Asp Gly Tyr Gly His Gly Thr His Val Ala Gly  
 210 215 220

aca att ggg tct gcc act tgg gga gta gca aag aaa act acc atc ttt 1612  
 Thr Ile Gly Ser Ala Thr Trp Gly Val Ala Lys Lys Thr Thr Ile Phe  
 225 230 235

gct gtg cga gta ctc gac tcc aat ggc tgg ggt aca aac gct gat gtg 1660  
 Ala Val Arg Val Leu Asp Ser Asn Gly Trp Gly Thr Asn Ala Asp Val  
 240 245 250

att gcg ggc ctg gag ttg atc ttg cga gat gca aga gag cgt agg ggg 1708  
 Ile Ala Gly Leu Glu Leu Ile Leu Arg Asp Ala Arg Glu Arg Arg Gly  
 255 260 265

acg gat cag tgt cgc aat ggc ttt gtt gtc aat atc agc ctg gga agt 1756  
 Thr Asp Gln Cys Arg Asn Gly Phe Val Val Asn Ile Ser Leu Gly Ser  
 270 275 280 285

gaa aag ctt cca gct ttg aat gat gct gta agtagctctt gtcaagtttt 1806  
 Glu Lys Leu Pro Ala Leu Asn Asp Ala Val  
 290 295

cttgtctgaa cgctgattta gatgtaaggt c gca gct atg gtt gca gag gat 1858  
 Ala Ala Met Val Ala Glu Asp  
 300

atc ttt cta gga gtt gca gca ggt aac gat ggt gtg cca gct gat gac 1906  
 Ile Phe Leu Gly Val Ala Ala Gly Asn Asp Gly Val Pro Ala Asp Asp  
 305 310 315

ttc tct ccg gga tcc gag cct tcg gtc tgc act gta gga gca acg gca 1954  
 Phe Ser Pro Gly Ser Glu Pro Ser Val Cys Thr Val Gly Ala Thr Ala  
 320 325 330

gcg aat gat aca ctt gcc caa tgg tcc aat cat ggt tct cgg atc gac 2002  
 Ala Asn Asp Thr Leu Ala Gln Trp Ser Asn His Gly Ser Arg Ile Asp  
 335 340 345 350

att cta gct ccc ggc cta gac atc act agc act ctt ccc aat ggt gtg 2050  
 Ile Leu Ala Pro Gly Leu Asp Ile Thr Ser Thr Leu Pro Asn Gly Val  
 355 360 365

gtt gcc tcg ttt tcg ggt aca agt atg gca gct ccg cat gtt gtt ggc 2098  
 Val Ala Ser Phe Ser Gly Thr Ser Met Ala Ala Pro His Val Val Gly  
 370 375 380

ctt gca gcg tat ttg ctt gga ctc ggg tca cca gca aag gat ctc tgt 2146  
 Leu Ala Ala Tyr Leu Leu Gly Leu Gly Ser Pro Ala Lys Asp Leu Cys  
 385 390 395

ggt aca atc gct gcc ttg gcg atc aaa aat gcg atc gat caa gat acg 2194  
 Gly Thr Ile Ala Ala Leu Ala Ile Lys Asn Ala Ile Asp Gln Asp Thr  
 400 405 410

ctt cca aaa gga aca cca aac cta ttg gcg ttc aat ggc gca gac gcc 2242  
 Leu Pro Lys Gly Thr Pro Asn Leu Leu Ala Phe Asn Gly Ala Asp Ala  
 415 420 425 430

## 10336256.txt

agc cag aag cgt atg agg cat tca tgaagtgttt gggagacgtg aagaagtaca 2296  
 Ser Gln Lys Arg Met Arg His Ser  
 435

agggtatttcg gaattcgcca cggcgatttg ggatattcct tgtgtatgta tgcaggtgtc 2356  
 aatatcatcg ccattgccat gagcatccct ccaatacgca tccctgtccg atggataatt 2416  
 ctggaagaca ctgactcac agccacaatg ctatattgcc gatggccgct tggccataaa 2476  
 atacaacaca ggataagtaa tcagcttgca ggcccgtttt tgccggtctg tctcacgtca 2536  
 gggcctgtca gcgacaaacg gcctatcaca gtccagcaat aaattctccg aactccatgg 2596  
 ctgtaccaac actcatgcat acaaaccgta actttgagac ccgagccttg tcacggtgat 2656  
 gtcgcccag cgattatcgc cgatcgggac ttccccaatc ctgctggtat agcccgatcg 2716  
 accaaccagc gacaatcaga caaggaatt gcgggtagg ggtatgcaat aacaggctag 2776  
 tccaacctac acacgcgact tttctccaag acccaagcat cccagcttga ttgcctctca 2836  
 tacttgatcc cgctatctgt taatcattac aggcgcgtag tagctctcct tcaatcacac 2896  
 agcactcgtc actgcggaac caaaagtcac ggcgctcatic tttgatctcc cgccacagaa 2956  
 agtggcacca tcagcgtgta tagaccagat gcctcaagaa caacggaaac agttgggccc 3016  
 cactagcagc ctgatgtccc cagccgtcgc tcagatcctt gaaggactag gagatgacca 3076  
 ctcgagtagc agcgacgaag actctgacct atcagacgat caagagaagg gacatcccaa 3136  
 gtcgcagtct aagaaggatg tcagcgccca gaagatacag cagaagaaac aaaagctcaa 3196  
 ctgagctcaa gcacctcggc catcctctct ctccccgaac agaagcagaa gtcgctccag 3256  
 gtcagcaacc 3266

&lt;210&gt; 182

&lt;211&gt; 36

&lt;212&gt; PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

&lt;400&gt; 182

Met Trp His Ala Ala Val Val Ser Ala Asn Gly Gly Ala Glu Gly Leu  
 1 5 10 15  
 Gly Gly Gly Gly Arg Gly Thr Val Arg Asp Val Phe Leu Glu Val Ala  
 20 25 30  
 Ala Ala Val Gly  
 35

&lt;210&gt; 183

&lt;211&gt; 93

&lt;212&gt; PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

&lt;400&gt; 183

Lys Pro Arg Lys Ile Leu Thr Ala Ile Met Tyr Phe Ile Leu Leu Ser  
 1 5 10 15  
 Leu Leu Ala Ser Leu Val Thr Ala Thr Pro Leu Val Lys Ala Pro Gly  
 20 25 30  
 Ser Lys Ala Ile Ala Asn Lys Trp Ile Val Lys Leu Lys Asp Asn Val  
 35 40 45  
 Ala Thr Met Ala Ala Asp Gly Val Lys Ala Ala Ile Ser Thr Lys Pro  
 50 55 60  
 Asp Tyr Gln Tyr Ser Met Pro Gly Phe Arg Gly Phe Ala Gly Thr Leu  
 65 70 75 80  
 Ser Asp Asp Glu Val Ala Leu Leu Gln Ala Ser Asp Gln  
 85 90

&lt;210&gt; 184

&lt;211&gt; 51

&lt;212&gt; PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

&lt;400&gt; 184

Ile Glu Tyr Ile Gln Gln Asp Ala Glu Val Tyr Thr Thr Ala Ile Ile  
 1 5 10 15  
 Glu Gln Ser Asn Ala Thr Trp Gly Ile Ser Arg Ile Ser His Thr Lys  
 20 25 30  
 Pro ser Glu Thr Ala Tyr Leu Tyr Asp Ser Ser Ala Gly Glu Gly Thr  
 35 40 45  
 Cys Ala Tyr

10336256.txt

50

&lt;210&gt; 185

&lt;211&gt; 115

&lt;212&gt; PRT

&lt;213&gt; Cochliobolus heterostrophus strain C4 (ATCC 48331)

&lt;400&gt; 185

```

Ser Asn Asp Ala Gln Met Gln Asp Leu Gln Thr Asp Pro Val Thr Gly
 1      5      10      15
Ala Leu Phe Leu Ala Asp Leu Thr His Glu Gly Asn Phe Ile Asp Gly
 20      25      30
Tyr Gly His Gly Thr His Val Ala Gly Thr Ile Gly Ser Ala Thr Trp
 35      40      45
Gly Val Ala Lys Lys Thr Thr Ile Phe Ala Val Arg Val Leu Asp Ser
 50      55      60
Asn Gly Trp Gly Thr Asn Ala Asp Val Ile Ala Gly Leu Glu Leu Ile
 65      70      75      80
Leu Arg Asp Ala Arg Glu Arg Arg Gly Thr Asp Gln Cys Arg Asn Gly
 85      90      95
Phe Val Val Asn Ile Ser Leu Gly Ser Glu Lys Leu Pro Ala Leu Asn
100      105      110
Asp Ala Val
115

```

&lt;210&gt; 186

&lt;211&gt; 143

&lt;212&gt; PRT

&lt;213&gt; Cochliobolus heterostrophus strain C4 (ATCC 48331)

&lt;400&gt; 186

```

Ala Ala Met Val Ala Glu Asp Ile Phe Leu Gly Val Ala Ala Gly Asn
 1      5      10      15
Asp Gly Val Pro Ala Asp Asp Phe Ser Pro Gly Ser Glu Pro Ser Val
 20      25      30
Cys Thr Val Gly Ala Thr Ala Ala Asn Asp Thr Leu Ala Gln Trp Ser
 35      40      45
Asn His Gly Ser Arg Ile Asp Ile Leu Ala Pro Gly Leu Asp Ile Thr
 50      55      60
Ser Thr Leu Pro Asn Gly Val Val Ala Ser Phe Ser Gly Thr Ser Met
 65      70      75      80
Ala Ala Pro His Val Val Gly Leu Ala Ala Tyr Leu Leu Gly Leu Gly
 85      90      95
Ser Pro Ala Lys Asp Leu Cys Gly Thr Ile Ala Ala Leu Ala Ile Lys
100      105      110
Asn Ala Ile Asp Gln Asp Thr Leu Pro Lys Gly Thr Pro Asn Leu Leu
115      120      125
Ala Phe Asn Gly Ala Asp Ala Ser Gln Lys Arg Met Arg His Ser
130      135      140

```

&lt;210&gt; 187

&lt;211&gt; 1314

&lt;212&gt; DNA

&lt;213&gt; Cochliobolus heterostrophus strain C4 (ATCC 48331)

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1314)

&lt;400&gt; 187

```

atg tgg cac gcg gcg gtt gtg tct gcg aat gga ggc gca gag ggc ttg
Met Trp His Ala Ala Val Val Ser Ala Asn Gly Gly Ala Glu Gly Leu
 1      5      10      15

ggt ggt ggg gga cga ggc acg gtc agg gat gtt ttt ttg gag gtg gca
Gly Gly Gly Gly Arg Gly Thr Val Arg Asp Val Phe Leu Glu Val Ala
 20      25      30

```

48

96

## 10336256.txt

gct Ala	gct Ala	gtc Val 35	ggg Gly	aaa Lys	cct Pro	cga Arg	aag Lys 40	att Ile	ctt Leu	act Thr	gca Ala	ata Ile 45	atg Met	tac Tyr	ttc Phe	144
att Ile	ctg Leu 50	cta Leu	tcc Ser	ttg Leu	ctt Leu	gct Ala 55	tca Ser	ctt Leu	gta Val	acc Thr	gct Ala 60	aca Thr	cca Pro	tta Leu	gtc Val	192
aaa Lys 65	gca Ala	ccc Pro	ggt Gly	agc Ser	aag Lys 70	gcc Ala	att Ile	gcc Ala	aac Asn	aag Lys 75	tgg Trp	att Ile	gtc Val	aaa Lys	ctc Leu 80	240
aag Lys	gac Asp	aac Asn	gtc Val	gcc Ala 85	acg Thr	atg Met	gcc Ala	gct Ala	gat Asp 90	ggc Gly	gtg Val	aaa Lys	gca Ala	gct Ala 95	att Ile	288
tcc Ser	aca Thr	aag Lys	ccc Pro 100	gat Asp	tac Tyr	cag Gln	tat Tyr	tcg Ser 105	atg Met	cct Pro	ggc Gly	ttc Phe	cga Arg 110	ggc Gly	ttc Phe	336
gca Ala	gga Gly	act Thr 115	cta Leu	tcc Ser	gac Asp	gat Asp	gag Glu 120	gta Val	gca Ala	ctg Leu	ttg Leu	caa Gln 125	gct Ala	tca Ser	gat Asp	384
caa Gln 130	att Ile	gag Glu	tat Tyr	atc Ile	cag Gln	caa Gln 135	gat Asp	gct Ala	gaa Glu	gtt Val	tac Tyr 140	acg Thr	acg Thr	gca Ala	att Ile	432
atc Ile 145	gaa Glu	cag Gln	tcg Ser	aat Asn	gcc Ala 150	acg Thr	tgg Trp	gga Gly	ata Ile	tcc Ser 155	cg Arg	atc Ile	tcg Ser	cat His	aca Thr 160	480
aag Lys	cca Pro	agt Ser	gaa Glu	acg Thr 165	gcg Ala	tat Tyr	ctc Leu	tat Tyr	gat Asp 170	tcc Ser	agt Ser	gca Ala	gga Gly	gag Glu 175	gga Gly	528
acg Thr	tgt Cys	gcg Ala	tat Tyr 180	agt Ser	aat Asn	gac Asp	gct Ala	caa Gln 185	atg Met	caa Gln	gac Asp	ttg Leu	cag Gln 190	act Thr	gac Asp	576
cca Pro	gta Val	aca Thr 195	ggc Gly	gct Ala	tta Leu	ttc Phe	ctg Leu 200	gca Ala	gac Asp	ctc Leu	act Thr	cat His 205	gaa Glu	ggt Gly	aat Asn	624
ttt Phe 210	ata Ile	gac Asp	ggg Gly	tat Tyr	ggt Gly	cat His 215	gga Gly	acg Thr	cac His	gtc Val	gct Ala 220	gga Gly	aca Thr	att Ile	ggg Gly	672
tct Ser 225	gcc Ala	act Thr	tgg Trp	gga Gly	gta Val 230	gca Ala	aag Lys	aaa Lys	act Thr	acc Thr 235	atc Ile	ttt Phe	gct Ala	gtg Val	cga Arg 240	720
gta Val	ctc Leu	gac Asp	tcc Ser	aat Asn 245	ggc Gly	tgg Trp	ggt Gly	aca Thr	aac Asn 250	gct Ala	gat Asp	gtg Val	att Ile	gcg Ala 255	ggc Gly	768
ctg Leu	gag Glu	ttg Leu	atc Ile 260	ttg Leu	cga Arg	gat Asp	gca Ala	aga Arg 265	gag Glu	cg Arg	agg Arg	ggg Gly	acg Thr 270	gat Asp	cag Gln	816
tgt Cys	cg Arg	aat Asn 275	ggc Gly	ttt Phe	ggt Val	gtc Val	aat Asn 280	atc Ile	agc Ser	ctg Leu	gga Gly	agt Ser 285	gaa Glu	aag Lys	ctt Leu	864
cca Pro	gct Ala 290	ttg Leu	aat Asn	gat Asp	gct Ala	gta Val 295	gca Ala	gct Ala	atg Met	gtt Val	gca Ala 300	gag Glu	gat Asp	atc Ile	ttt Phe	912

## 10336256.txt

cta gga gtt gca gca ggt aac gat ggt gtg cca gct gat gac ttc tct 960  
 Leu Gly Val Ala Ala Gly Asn Asp Gly Val Pro Ala Asp Asp Phe Ser  
 305 310 315 320

ccg gga tcc gag cct tcg gtc tgc act gta gga gca acg gca gcg aat 1008  
 Pro Gly Ser Glu Pro Ser Val Cys Thr Val Gly Ala Thr Ala Ala Asn  
 325 330 335

gat aca ctt gcc caa tgg tcc aat cat ggt tct cgg atc gac att cta 1056  
 Asp Thr Leu Ala Gln Trp Ser Asn His Gly Ser Arg Ile Asp Ile Leu  
 340 345 350

gct ccc ggc cta gac atc act agc act ctt ccc aat ggt gtg gtt gcc 1104  
 Ala Pro Gly Leu Asp Ile Thr Ser Thr Leu Pro Asn Gly Val Val Ala  
 355 360 365

tcg ttt tcg ggt aca agt atg gca gct ccg cat gtt gtt ggc ctt gca 1152  
 Ser Phe Ser Gly Thr Ser Met Ala Ala Pro His Val Val Gly Leu Ala  
 370 375 380

gcg tat ttg ctt gga ctc ggg tca cca gca aag gat ctc tgt ggt aca 1200  
 Ala Tyr Leu Leu Gly Leu Gly Ser Pro Ala Lys Asp Leu Cys Gly Thr  
 385 390 395 400

atc gct gcc ttg gcg atc aaa aat gcg atc gat caa gat acg ctt cca 1248  
 Ile Ala Ala Leu Ala Ile Lys Asn Ala Ile Asp Gln Asp Thr Leu Pro  
 405 410 415

aaa gga aca cca aac cta ttg gcg ttc aat ggc gca gac gcc agc cag 1296  
 Lys Gly Thr Pro Asn Leu Leu Ala Phe Asn Gly Ala Asp Ala Ser Gln  
 420 425 430

aag cgt atg agg cat tca 1314  
 Lys Arg Met Arg His Ser  
 435

<210> 188  
 <211> 438  
 <212> PRT  
 <213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<220>  
 <221> DOMAIN  
 <222> (156)...(426)  
 <223> Subtilase family

<221> DOMAIN  
 <222> (74)...(142)  
 <223> Subtilisin N-terminal region

<400> 188  
 Met Trp His Ala Ala Val Val Ser Ala Asn Gly Gly Ala Glu Gly Leu  
 1 5 10 15  
 Gly Gly Gly Gly Arg Gly Thr Val Arg Asp Val Phe Leu Glu Val Ala  
 20 25 30  
 Ala Ala Val Gly Lys Pro Arg Lys Ile Leu Thr Ala Ile Met Tyr Phe  
 35 40 45  
 Ile Leu Leu Ser Leu Leu Ala Ser Leu Val Thr Ala Thr Pro Leu Val  
 50 55 60  
 Lys Ala Pro Gly Ser Lys Ala Ile Ala Asn Lys Trp Ile Val Lys Leu  
 65 70 75 80  
 Lys Asp Asn Val Ala Thr Met Ala Ala Asp Gly Val Lys Ala Ala Ile  
 85 90 95  
 Ser Thr Lys Pro Asp Tyr Gln Tyr Ser Met Pro Gly Phe Arg Gly Phe  
 100 105 110  
 Ala Gly Thr Leu Ser Asp Asp Glu Val Ala Leu Leu Gln Ala Ser Asp  
 115 120 125

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Gln Ile Glu Tyr Ile Gln Gln Asp Ala Glu Val Tyr Thr Thr Ala Ile  
 130 135 140  
 Ile Glu Gln Ser Asn Ala Thr Trp Gly Ile Ser Arg Ile Ser His Thr  
 145 150 155 160  
 Lys Pro Ser Glu Thr Ala Tyr Leu Tyr Asp Ser Ser Ala Gly Glu Gly  
 165 170 175  
 Thr Cys Ala Tyr Ser Asn Asp Ala Gln Met Gln Asp Leu Gln Thr Asp  
 180 185 190  
 Pro Val Thr Gly Ala Leu Phe Leu Ala Asp Leu Thr His Glu Gly Asn  
 195 200 205  
 Phe Ile Asp Gly Tyr Gly His Gly Thr His Val Ala Gly Thr Ile Gly  
 210 215 220  
 Ser Ala Thr Trp Gly Val Ala Lys Lys Thr Thr Ile Phe Ala Val Arg  
 225 230 235 240  
 Val Leu Asp Ser Asn Gly Trp Gly Thr Asn Ala Asp Val Ile Ala Gly  
 245 250 255  
 Leu Glu Leu Ile Leu Arg Asp Ala Arg Glu Arg Arg Gly Thr Asp Gln  
 260 265 270  
 Cys Arg Asn Gly Phe Val Val Asn Ile Ser Leu Gly Ser Glu Lys Leu  
 275 280 285  
 Pro Ala Leu Asn Asp Ala Val Ala Ala Met Val Ala Glu Asp Ile Phe  
 290 295 300  
 Leu Gly Val Ala Ala Gly Asn Asp Gly Val Pro Ala Asp Asp Phe Ser  
 305 310 315 320  
 Pro Gly Ser Glu Pro Ser Val Cys Thr Val Gly Ala Thr Ala Ala Asn  
 325 330 335  
 Asp Thr Leu Ala Gln Trp Ser Asn His Gly Ser Arg Ile Asp Ile Leu  
 340 345 350  
 Ala Pro Gly Leu Asp Ile Thr Ser Thr Leu Pro Asn Gly Val Val Ala  
 355 360 365  
 Ser Phe Ser Gly Thr Ser Met Ala Ala Pro His Val Val Gly Leu Ala  
 370 375 380  
 Ala Tyr Leu Leu Gly Leu Gly Ser Pro Ala Lys Asp Leu Cys Gly Thr  
 385 390 395 400  
 Ile Ala Ala Leu Ala Ile Lys Asn Ala Ile Asp Gln Asp Thr Leu Pro  
 405 410 415  
 Lys Gly Thr Pro Asn Leu Leu Ala Phe Asn Gly Ala Asp Ala Ser Gln  
 420 425 430  
 Lys Arg Met Arg His Ser  
 435

&lt;210&gt; 189

&lt;211&gt; 4101

&lt;212&gt; DNA

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1499)...(1597)

&lt;223&gt; Exon

&lt;221&gt; CDS

&lt;222&gt; (1649)...(1967)

&lt;223&gt; Exon

&lt;221&gt; CDS

&lt;222&gt; (2005)...(3104)

&lt;223&gt; Exon

&lt;400&gt; 189

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tcgcagtact	gatttttcgt	agctttttcta	gtcatatcat	tgcatgtctc	tcgagatata	120
gatgggatcg	taaacaaaac	cctattttgag	cactttgaat	caatctctac	ttcaaaggag	180
tggcgaaaaa	agagtgatgt	tatgataccc	aacgcaagct	cgcaaagggtg	gagaaacagc	240
agttaatgag	ctcacttagc	gatgtcccat	tgcccagaca	acggcccaaa	agaaaccagg	300
tttttctttc	ttctcgaccg	agctggaatc	atatgggtatt	gagaatttcc	aagggccggc	360
cagtgtcact	agctaccgac	cgatttcgag	ttagaagcgt	tatccgtact	tgaagtcaaa	420
ggtctcaatt	caatactcag	atgtaccagg	agagggaacg	ccgaccggtg	gacgacaatg	480

## 10336256.txt

```

tcggcgacta cattctagat ccacggaaac tgatggaagt tatcatgaaa attacgctcc 540
tcgagacatt tcctgttcct acatgcacgg tcagaactcg tgggtgcagc tgtgaagaaa 600
gcaaacatat tcacgtggat cgactgggca acgcatgcat aaagactccg cggaaggaag 660
aagagattct ctaccaacgc ctgacttcgc gatttcgcaa ttgcctatta gtattaggca 720
tacgacacgg tgcccagatt gcgatcggag ggtatacccg atgtgtgcag ccatgaccga 780
cggaattga caataacaga ggatgttggg aggggagagg gctccacaca aaacaaccct 840
gcatgttttc ggggcgtgca accggaccag gaacagtatg actatgcacc tggttttgca 900
gcagcgcgca tccacgtcaa gcagccctca ggtacacatg atgatgtgta tcagtcacaa 960
aagcttggtc agctcaaac tggcattgca cctgtaccac acacggcgat gaaaacacag 1020
ctccagcccc agcaccacac acgcgctaag atgtacaaat acgtcttcca gccatgaatc 1080
agccccatat tgccaccagg acaaccacca agcggcactt ggcaagcttg gcagtccgcc 1140
gcgctgaagc ttaccaaggc ctcttatcac gtcttgacac ggctcgtgtg cttgtttact 1200
gggtccgctc acagcggcta ttggtggatg aagggtcagc ctggtgtgcg gatgcgcca 1260
cttggtgga tgtagcagg cgcaaagagc tttgtatgtg ggtttgattg taagctgcat 1320
ttcaggcata cagtgtgtt ggtaggagcg atatttccgg tctctgggcc catttgcagc 1380
tactacgagc tgcaggtggt atggatttag gtaagctagt aaatagcata aattgcacag 1440
catgccctgc caatttgaa acgacactcc ctttgcacaa aagcaggcaa tagtcgca 1498
atg gca tat ctg aag tca atc gca gca ctt gct gca tgt gct gta gcg 1546
Met Ala Tyr Leu Lys Ser Ile Ala Ala Leu Ala Ala Cys Ala Val Ala
1 5 10 15

ggt gag gca gca gcc ctt cat cct cgc act aac aag acg ctg gtt gat 1594
Val Glu Ala Ala Ala Leu His Pro Arg Thr Asn Lys Thr Leu Val Asp
20 25 30

tcg gtacgagtat acatacattc atttcccagag ttgctctaac acgcattata 1647
Ser

g caa tcg ctc cgt gat acg att gac att gac aac ttg tat gcc aaa gcg 1696
Gln Ser Leu Arg Asp Thr Ile Asp Ile Asp Asn Leu Tyr Ala Lys Ala
35 40 45

gag atc ctt cag gag att gca tac aac aca ccg gga aag aac cgt gtg 1744
Glu Ile Leu Gln Glu Ile Ala Tyr Asn Thr Pro Gly Lys Asn Arg Val
50 55 60 65

att ggt agc cag ggc cat gag gat act gta gaa tac atc aag ggc cag 1792
Ile Gly Ser Gln Gly His Glu Asp Thr Val Glu Tyr Ile Lys Gly Gln
70 75 80

ctc gag gca ttc ccc gac tac tac gat gtg tac act cag gat gtg cct 1840
Leu Glu Ala Phe Pro Asp Tyr Tyr Asp Val Tyr Thr Gln Asp Val Pro
85 90 95

ctc tca atc gga acc act gcc acg ctc cgt gca aac aac aag acg att 1888
Leu Ser Ile Gly Thr Thr Ala Thr Leu Arg Ala Asn Asn Lys Thr Ile
100 105 110

gag gct ttt gca gta act ctg gct ccg ggt ggc aat gta act gga ccg 1936
Glu Ala Phe Ala Val Thr Leu Ala Pro Gly Gly Asn Val Thr Gly Pro
115 120 125

ctc gtt gct att ccc aac ttg ggt tgt gaa g aggtaggttc atgttttcga 1987
Leu Val Ala Ile Pro Asn Leu Gly Cys Glu
130 135

ctatatatac ccaaaga ag ata tca gga agc aag act aac atg gaa aag gcg 2039
Glu Ile Ser Gly Ser Lys Thr Asn Met Glu Lys Ala
140 145 150

gat ttc cca gaa tct ctc gag ggc tct gta gct ctg atc aag cgt ggt 2087
Asp Phe Pro Glu Ser Leu Glu Gly Ser Val Ala Leu Ile Lys Arg Gly
155 160 165

acg tgc tcg tac ggc gag aag gtg cag att gct gct gcc aaa gga gcc 2135
Thr Cys Ser Tyr Gly Glu Lys Val Gln Ile Ala Ala Ala Lys Gly Ala
170 175 180

```

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ttg ggt gta gtg gca tgg aac aat gcc gag ggc act ctt gag ggc tac	2183
Leu Gly Val Val Ala Trp Asn Asn Ala Glu Gly Thr 195	
tcg ctc caa gtc ttg tat ccc aag ggc aag ttt gtc cct gta gcc ggc	2231
Ser Leu Gln Val Leu Tyr Pro Lys Gly Lys Phe Val Pro Val Ala Gly 215	
atc acc atg ggc caa gga gaa gcg ctt ctt gcg cag ctc aac gct ggt	2279
Ile Thr Met Gly Gln Gly Glu Ala Leu Leu 225 Ala Gln Leu Asn Ala Gly 230	
gtc aag atc aat gtc gac atg tca aca gac gcc aag gtg ttc aac act	2327
Val Lys Ile Asn Val Asp Met Ser Thr 240 Asp Ala Lys Val Phe Asn Thr 245	
cgc aac gtg att gcg gag aca aag gct ggc gac cac gac aac gtg atc	2375
Arg Asn Val Ile Ala Glu Thr Lys 255 Ala Gly Asp His Asp Asn Val Ile 260	
cac gtc agc ggc cat tct gac tcg gtc act gct ggc cca ggc atc aac	2423
His Val Ser Gly His Ser Asp Ser Val Thr Ala Gly 275 Pro Gly Ile Asn 265	
gac aat gga tcg ggc act att tcc att ctc gag att gct att caa ctg	2471
Asp Asn Gly Ser Gly Thr 285 Ile Ser Ile Leu Glu Ile Ala Ile Gln Leu 295	
acc aac ttt acc gtc aac aac gcc gtg cgc ttc agc tgg tgg aca gca	2519
Thr Asn Phe Thr Val 300 Asn Asn Ala Val Arg 305 Phe Ser Trp Trp Thr Ala 310	
gag gag gcc ggt ctt ctc gga gcc gag tac tac gtg cac gag ctg ccc	2567
Glu Glu Ala Gly 315 Leu Leu Gly Ala Glu Tyr Tyr Val His Glu Leu Pro 325	
caa gct gag aag gac aag atc cgt ctt ttg ctc gac ttt gac atg atg	2615
Gln Ala Glu Lys Asp Lys Ile Arg 335 Leu Leu Leu Asp Phe Asp Met Met 340	
gcc tca ccc aac ttt gcc tac caa atc tat gac ggt gat ggt tcg gca	2663
Ala Ser Pro Asn Phe Ala Tyr 350 Gln Ile Tyr Asp Gly Asp Gly Ser Ala 345	
ttc aac ctg act ggg ccg gtt ggc tca gcc gag gct gag cac gag ttt	2711
Phe Asn Leu Thr Gly Pro Val Gly Ser Ala Glu Ala Glu His Glu Phe 375	
gcc gcc tac ttt gac agc att ggc ctc aac cac act gag att gaa ttc	2759
Ala Ala Tyr Phe Asp Ser Ile Gly Leu Asn His Thr Glu Ile Glu Phe 390	
gac ggc cgg tca gac tac ggc ccg ttc ctt gag gct ggc atc gct tct	2807
Asp Gly Arg Ser 395 Asp Tyr Gly Pro Phe Leu Glu Ala Gly Ile Ala Ser 405	
ggt ggc att gcc ggt gga gcc gag ggt atc aag aca gaa gag gag gcg	2855
Gly Gly Ile Ala Gly Gly Ala Glu Gly Ile Lys Thr Glu Glu Glu Ala 420	
gcc atg ttt ggc gga ggc gcc ggt gtt cct tac gac gtc aac tac cac	2903
Ala Met Phe Gly Gly Gly Ala Gly Val Pro Tyr Asp Val Asn Tyr His 435	
gag gat ggc gat acc gtc aac aac ttg aac ctc gag gcg tgg atc gag	2951
Glu Asp Gly Asp Thr Val Asn Asn Leu Asn Leu Glu Ala Trp Ile Glu 455	

## 10336256.txt

```

ttc aca agg gct att gcg cac atg acg gcc aag tat gct gtg tcg tgg      2999
Phe Thr Arg Ala Ile Ala His Met Thr Ala Lys Tyr Ala Val Ser Trp
                               460                               465                               470

gac agc atc ccg cca agg aac gcg acg gct gcg cag aag cgg tca gag      3047
Asp Ser Ile Pro Pro Arg Asn Ala Thr Ala Ala Gln Lys Arg Ser Glu
                               475                               480                               485

agg tat gcc gag ttt aag cag gcg ttc cag aag acc aag agg tac cag      3095
Arg Tyr Ala Glu Phe Lys Gln Ala Phe Gln Lys Thr Lys Arg Tyr Gln
                               490                               495                               500

agg tgg gta tagattgggc tcgatcccgga ggcttttgag tggatgtgag      3144
Arg Trp Val
                               505

cttagacacg actttaatgg tgaatatcaa agaaatcttc aaggcaatgt ttgtgcaagc      3204
aaaagtggat gaatgtgaga aaacgagttt gtggaattgc acgcatgtca tttgccgttt      3264
tacaagatgg acggtggcct tactcttcgt cgtcatcgtc aactacgggt acaggctcgt      3324
ccttgccggt cttgttgact ttgcggtcct tgtcagcacc agcaggcttg gcgtcctttg      3384
ctttcttctt gtcgtcctcg tcctcgtcgt cctcatcgtc gacgtcgtca gaagcggcat      3444
cctcgtcgtc ttccggcgctc agctcggcct cttcctcctc gctctcatcc ccgtcctcgt      3504
ctttgctttt ggctttggta gtgcgcttgg cttttttctt tggcgctatg aaaaagcaaa      3564
aaaagtaaga gagagtggcg gagaagggga tagggaccac caagggttta ctcaagatga      3624
cttacgtggc tcttcctcgt ccgagtcgtc tgaatcaaag tttgagcctt cagactctgc      3684
gtatctggat ggccgggtca gtcttgctgc aggtgtcgca tgcgcgcgca aagggcattg      3744
tttgatgaa tggggccaga ggcgccatgg tagctatgtc aggtgtagag gtagagtgga      3804
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actgcctttg gaggcattgc cagcgaccag acggcgtagc ggtacaaact caaaacatca      3924
attcaaggat gcgcacacag gcgatggcaa tgaagccaaa accaccgggt tgcgacgtgg      3984
tgggtagagg catgacgtca agaaagcgtc gacttactct tcttcttcgt cgctctcgtc      4044
gctggggagg gccacgagct cctcgtcgtc gttcttcctc ttcttgtag tcatggc      4101

```

&lt;210&gt; 190

&lt;211&gt; 33

&lt;212&gt; PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

&lt;400&gt; 190

```

Met Ala Tyr Leu Lys Ser Ile Ala Ala Leu Ala Ala Cys Ala Val Ala
 1           5           10           15
Val Glu Ala Ala Ala Leu His Pro Arg Thr Asn Lys Thr Leu Val Asp
 20           25           30
Ser

```

&lt;210&gt; 191

&lt;211&gt; 106

&lt;212&gt; PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

&lt;400&gt; 191

```

Gln Ser Leu Arg Asp Thr Ile Asp Ile Asp Asn Leu Tyr Ala Lys Ala
 1           5           10           15
Glu Ile Leu Gln Glu Ile Ala Tyr Asn Thr Pro Gly Lys Asn Arg Val
 20           25           30
Ile Gly Ser Gln Gly His Glu Asp Thr Val Glu Tyr Ile Lys Gly Gln
 35           40           45
Leu Glu Ala Phe Pro Asp Tyr Tyr Asp Val Tyr Thr Gln Asp Val Pro
 50           55           60
Leu Ser Ile Gly Thr Thr Ala Thr Leu Arg Ala Asn Asn Lys Thr Ile
 65           70           75           80
Glu Ala Phe Ala Val Thr Leu Ala Pro Gly Gly Asn Val Thr Gly Pro
 85           90           95
Leu Val Ala Ile Pro Asn Leu Gly Cys Glu
100           105

```

10336256.txt

&lt;210&gt; 192

&lt;211&gt; 367

&lt;212&gt; PRT

&lt;213&gt; Cochliobolus heterostrophus strain C4 (ATCC 48331)

&lt;400&gt; 192

```

Glu Ile Ser Gly Ser Lys Thr Asn Met Glu Lys Ala Asp Phe Pro Glu
1      5      10      15
Ser Leu Glu Gly Ser Val Ala Leu Ile Lys Arg Gly Thr Cys Ser Tyr
20     25     30
Gly Glu Lys Val Gln Ile Ala Ala Lys Gly Ala Leu Gly Val Val
35     40     45
Ala Trp Asn Asn Ala Glu Gly Thr Leu Glu Gly Tyr Ser Leu Gln Val
50     55     60
Leu Tyr Pro Lys Gly Lys Phe Val Pro Val Ala Gly Ile Thr Met Gly
65     70     75     80
Gln Gly Glu Ala Leu Leu Ala Gln Leu Asn Ala Gly Val Lys Ile Asn
85     90     95
Val Asp Met Ser Thr Asp Ala Lys Val Phe Asn Thr Arg Asn Val Ile
100    105    110
Ala Glu Thr Lys Ala Gly Asp His Asp Asn Val Ile His Val Ser Gly
115    120    125
His Ser Asp Ser Val Thr Ala Gly Pro Gly Ile Asn Asp Asn Gly Ser
130    135    140
Gly Thr Ile Ser Ile Leu Glu Ile Ala Ile Gln Leu Thr Asn Phe Thr
145    150    155    160
Val Asn Asn Ala Val Arg Phe Ser Trp Trp Thr Ala Glu Glu Ala Gly
165    170    175
Leu Leu Gly Ala Glu Tyr Tyr Val His Glu Leu Pro Gln Ala Glu Lys
180    185    190
Asp Lys Ile Arg Leu Leu Leu Asp Phe Asp Met Met Ala Ser Pro Asn
195    200    205
Phe Ala Tyr Gln Ile Tyr Asp Gly Asp Gly Ser Ala Phe Asn Leu Thr
210    215    220
Gly Pro Val Gly Ser Ala Glu Ala Glu His Glu Phe Ala Ala Tyr Phe
225    230    235    240
Asp Ser Ile Gly Leu Asn His Thr Glu Ile Glu Phe Asp Gly Arg Ser
245    250    255
Asp Tyr Gly Pro Phe Leu Glu Ala Gly Ile Ala Ser Gly Gly Ile Ala
260    265    270
Gly Gly Ala Glu Gly Ile Lys Thr Glu Glu Glu Ala Ala Met Phe Gly
275    280    285
Gly Gly Ala Gly Val Pro Tyr Asp Val Asn Tyr His Glu Asp Gly Asp
290    295    300
Thr Val Asn Asn Leu Asn Leu Glu Ala Trp Ile Glu Phe Thr Arg Ala
305    310    315    320
Ile Ala His Met Thr Ala Lys Tyr Ala Val Ser Trp Asp Ser Ile Pro
325    330    335
Pro Arg Asn Ala Thr Ala Ala Gln Lys Arg Ser Glu Arg Tyr Ala Glu
340    345    350
Phe Lys Gln Ala Phe Gln Lys Thr Lys Arg Tyr Gln Arg Trp Val
355    360    365

```

&lt;210&gt; 193

&lt;211&gt; 1518

&lt;212&gt; DNA

&lt;213&gt; Cochliobolus heterostrophus strain C4 (ATCC 48331)

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1518)

&lt;400&gt; 193

```

atg gca tat ctg aag tca atc gca gca ctt gct gca tgt gct gta gcg
Met Ala Tyr Leu Lys Ser Ile Ala Ala Leu Ala Ala Cys Ala Val Ala
1      5      10      15

```

48

```

gtt gag gca gca gcc ctt cat cct cgc act aac aag acg ctg gtt gat

```

96

10336256.txt

Val	Glu	Ala	Ala	Ala	Leu	His	Pro	Arg	Thr	Asn	Lys	Thr	Leu	Val	Asp		
			20					25					30				
tcg	caa	tcg	ctc	cgt	gat	acg	att	gac	att	gac	aac	ttg	tat	gcc	aaa	144	
Ser	Gln	Ser	Leu	Arg	Asp	Thr	Ile	Asp	Ile	Asp	Asn	Leu	Tyr	Ala	Lys		
		35					40					45					
gcg	gag	atc	ctt	cag	gag	att	gca	tac	aac	aca	ccg	gga	aag	aac	cgt	192	
Ala	Glu	Ile	Leu	Gln	Glu	Ile	Ala	Tyr	Asn	Thr	Pro	Gly	Lys	Asn	Arg		
	50					55					60						
gtg	att	ggt	agc	cag	ggc	cat	gag	gat	act	gta	gaa	tac	atc	aag	ggc	240	
Val	Ile	Gly	Ser	Gln	Gly	His	Glu	Asp	Thr	Val	Glu	Tyr	Ile	Lys	Gly		
65					70					75					80		
cag	ctc	gag	gca	ttc	ccc	gac	tac	tac	gat	gtg	tac	act	cag	gat	gtg	288	
Gln	Leu	Glu	Ala	Phe	Pro	Asp	Tyr	Tyr	Asp	Val	Tyr	Thr	Gln	Asp	Val		
				85					90					95			
cct	ctc	tca	atc	gga	acc	act	gcc	acg	ctc	cgt	gca	aac	aac	aag	acg	336	
Pro	Leu	Ser	Ile	Gly	Thr	Thr	Ala	Thr	Leu	Arg	Ala	Asn	Asn	Lys	Thr		
			100					105					110				
att	gag	gct	ttt	gca	gta	act	ctg	gct	ccg	ggt	ggc	aat	gta	act	gga	384	
Ile	Glu	Ala	Phe	Ala	Val	Thr	Leu	Ala	Pro	Gly	Gly	Asn	Val	Thr	Gly		
		115					120					125					
ccg	ctc	gtt	gct	att	ccc	aac	ttg	ggt	tgt	gaa	gag	ata	tca	gga	agc	432	
Pro	Leu	Val	Ala	Ile	Pro	Asn	Leu	Gly	Cys	Glu	Glu	Ile	Ser	Gly	Ser		
		130				135					140						
aag	act	aac	atg	gaa	aag	gcg	gat	ttc	cca	gaa	tct	ctc	gag	ggc	tct	480	
Lys	Thr	Asn	Met	Glu	Lys	Ala	Asp	Phe	Pro	Glu	Ser	Leu	Glu	Gly	Ser		
145					150					155					160		
gta	gct	ctg	atc	aag	cgt	ggt	acg	tgc	tcg	tac	ggc	gag	aag	gtg	cag	528	
Val	Ala	Leu	Ile	Lys	Arg	Gly	Thr	Cys	Ser	Tyr	Gly	Glu	Lys	Val	Gln		
				165					170					175			
att	gct	gct	gcc	aaa	gga	gcc	ttg	ggt	gta	gtg	gca	tgg	aac	aat	gcc	576	
Ile	Ala	Ala	Ala	Lys	Gly	Ala	Leu	Gly	Val	Val	Ala	Trp	Asn	Asn	Ala		
			180					185					190				
gag	ggc	act	ctt	gag	ggc	tac	tcg	ctc	caa	gtc	ttg	tat	ccc	aag	ggc	624	
Glu	Gly	Thr	Leu	Glu	Gly	Tyr	Ser	Leu	Gln	Val	Leu	Tyr	Pro	Lys	Gly		
		195					200					205					
aag	ttt	gtc	cct	gta	gcc	ggc	atc	acc	atg	ggc	caa	gga	gaa	gcg	ctt	672	
Lys	Phe	Val	Pro	Val	Ala	Gly	Ile	Thr	Met	Gly	Gln	Gly	Glu	Ala	Leu		
	210					215					220						
ctt	gcg	cag	ctc	aac	gct	ggt	gtc	aag	atc	aat	gtc	gac	atg	tca	aca	720	
Leu	Ala	Gln	Leu	Asn	Ala	Gly	Val	Lys	Ile	Asn	Val	Asp	Met	Ser	Thr		
225					230					235					240		
gac	gcc	aag	gtg	ttc	aac	act	cgc	aac	gtg	att	gcg	gag	aca	aag	gct	768	
Asp	Ala	Lys	Val	Phe	Asn	Thr	Arg	Asn	Val	Ile	Ala	Glu	Thr	Lys	Ala		
				245					250					255			
ggc	gac	cac	gac	aac	gtg	atc	cac	gtc	agc	ggc	cat	tct	gac	tcg	gtc	816	
Gly	Asp	His	Asp	Asn	Val	Ile	His	Val	Ser	Gly	His	Ser	Asp	Ser	Val		
			260					265					270				
act	gct	ggc	cca	ggc	atc	aac	gac	aat	gga	tcg	ggc	act	att	tcc	att	864	
Thr	Ala	Gly	Pro	Gly	Ile	Asn	Asp	Asn	Gly	Ser	Gly	Thr	Ile	Ser	Ile		
		275					280					285					
ctc	gag	att	gct	att	caa	ctg	acc	aac	ttt	acc	gtc	aac	aac	gcc	gtg	912	

10336256.txt

Leu	Glu	Ile	Ala	Ile	Gln	Leu	Thr	Asn	Phe	Thr	Val	Asn	Asn	Ala	Val		
290						295					300						
cgc	ttc	agc	tgg	tgg	aca	gca	gag	gag	gcc	ggt	ctt	ctc	gga	gcc	gag	960	
Arg	Phe	Ser	Trp	Trp	Thr	Ala	Glu	Glu	Ala	Gly	Leu	Leu	Gly	Ala	Glu	320	
305					310					315							
tac	tac	gtg	cac	gag	ctg	ccc	caa	gct	gag	aag	gac	aag	atc	cgt	ctt	1008	
Tyr	Tyr	Val	His	Glu	Leu	Pro	Gln	Ala	Glu	Lys	Asp	Lys	Ile	Arg	Leu	335	
				325					330								
ttg	ctc	gac	ttt	gac	atg	atg	gcc	tca	ccc	aac	ttt	gcc	tac	caa	atc	1056	
Leu	Leu	Asp	Phe	Asp	Met	Met	Ala	Ser	Pro	Asn	Phe	Ala	Tyr	Gln	Ile	350	
			340					345									
tat	gac	ggt	gat	ggt	tcg	gca	ttc	aac	ctg	act	ggg	ccg	ggt	ggc	tca	1104	
Tyr	Asp	Gly	Asp	Gly	Ser	Ala	Phe	Asn	Leu	Thr	Gly	Pro	Val	Gly	Ser	365	
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gcc	gag	gct	gag	cac	gag	ttt	gcc	gcc	tac	ttt	gac	agc	att	ggc	ctc	1152	
Ala	Glu	Ala	Glu	His	Glu	Phe	Ala	Ala	Tyr	Phe	Asp	Ser	Ile	Gly	Leu	370	
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aac	cac	act	gag	att	gaa	ttc	gac	ggc	cgg	tca	gac	tac	ggc	ccg	ttc	1200	
Asn	His	Thr	Glu	Ile	Glu	Phe	Asp	Gly	Arg	Ser	Asp	Tyr	Gly	Pro	Phe	385	
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ctt	gag	gct	ggc	atc	gct	tct	ggt	ggc	att	gcc	ggt	gga	gcc	gag	ggt	1248	
Leu	Glu	Ala	Gly	Ile	Ala	Ser	Gly	Gly	Ile	Ala	Gly	Gly	Ala	Glu	Gly	405	
				410					415					415			
atc	aag	aca	gaa	gag	gag	gcg	gcc	atg	ttt	ggc	gga	ggc	gcc	ggt	gtt	1296	
Ile	Lys	Thr	Glu	Glu	Glu	Ala	Ala	Met	Phe	Gly	Gly	Gly	Ala	Gly	Val	420	
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cct	tac	gac	gtc	aac	tac	cac	gag	gat	ggc	gat	acc	gtc	aac	aac	ttg	1344	
Pro	Tyr	Asp	Val	Asn	Tyr	His	Glu	Asp	Gly	Asp	Thr	Val	Asn	Asn	Leu	435	
		435					440					445					
aac	ctc	gag	gcg	tgg	atc	gag	ttc	aca	agg	gct	att	gcg	cac	atg	acg	1392	
Asn	Leu	Glu	Ala	Trp	Ile	Glu	Phe	Thr	Arg	Ala	Ile	Ala	His	Met	Thr	450	
						455					460						
gcc	aag	tat	gct	gtg	tcg	tgg	gac	agc	atc	ccg	cca	agg	aac	gcg	acg	1440	
Ala	Lys	Tyr	Ala	Val	Ser	Trp	Asp	Ser	Ile	Pro	Pro	Arg	Asn	Ala	Thr	465	
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gct	gcg	cag	aag	cgg	tca	gag	agg	tat	gcc	gag	ttt	aag	cag	gcg	ttc	1488	
Ala	Ala	Gln	Lys	Arg	Ser	Glu	Arg	Tyr	Ala	Glu	Phe	Lys	Gln	Ala	Phe	485	
				485					490					495			
cag	aag	acc	aag	agg	tac	cag	agg	tgg	gta							1518	
Gln	Lys	Thr	Lys	Arg	Tyr	Gln	Arg	Trp	Val							500	
			500					505									

&lt;210&gt; 194

&lt;211&gt; 506

&lt;212&gt; PRT

&lt;213&gt; Cochliobolus heterostrophus strain C4 (ATCC 48331)

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; (1)...(19)

&lt;221&gt; DOMAIN

&lt;222&gt; (121)...(228)

&lt;223&gt; PA (protease associated) domain

10336256.txt

&lt;221&gt; DOMAIN

&lt;222&gt; (234)...(468)

&lt;223&gt; Peptidase family M28

&lt;400&gt; 194

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Ser Gln Ser Leu Arg Asp Thr Ile Asp Ile Asp Asn Leu Tyr Ala Lys
35      40      45
Ala Glu Ile Leu Gln Glu Ile Ala Tyr Asn Thr Pro Gly Lys Asn Arg
50      55      60
Val Ile Gly Ser Gln Gly His Glu Asp Thr Val Glu Tyr Ile Lys Gly
65      70      75      80
Gln Leu Glu Ala Phe Pro Asp Tyr Tyr Asp Val Tyr Thr Gln Asp Val
85      90      95
Pro Leu Ser Ile Gly Thr Thr Ala Thr Leu Arg Ala Asn Asn Lys Thr
100      105      110
Ile Glu Ala Phe Ala Val Thr Leu Ala Pro Gly Gly Asn Val Thr Gly
115      120      125
Pro Leu Val Ala Ile Pro Asn Leu Gly Cys Glu Glu Ile Ser Gly Ser
130      135      140
Lys Thr Asn Met Glu Lys Ala Asp Phe Pro Glu Ser Leu Glu Gly Ser
145      150      155      160
Val Ala Leu Ile Lys Arg Gly Thr Cys Ser Tyr Gly Glu Lys Val Gln
165      170      175
Ile Ala Ala Ala Lys Gly Ala Leu Gly Val Val Ala Trp Asn Asn Ala
180      185      190
Glu Gly Thr Leu Glu Gly Tyr Ser Leu Gln Val Leu Tyr Pro Lys Gly
195      200      205
Lys Phe Val Pro Val Ala Gly Ile Thr Met Gly Gln Gly Glu Ala Leu
210      215      220
Leu Ala Gln Leu Asn Ala Gly Val Lys Ile Asn Val Asp Met Ser Thr
225      230      235      240
Asp Ala Lys Val Phe Asn Thr Arg Asn Val Ile Ala Glu Thr Lys Ala
245      250      255
Gly Asp His Asp Asn Val Ile His Val Ser Gly His Ser Asp Ser Val
260      265      270
Thr Ala Gly Pro Gly Ile Asn Asp Asn Gly Ser Gly Thr Ile Ser Ile
275      280      285
Leu Glu Ile Ala Ile Gln Leu Thr Asn Phe Thr Val Asn Asn Ala Val
290      295      300
Arg Phe Ser Trp Trp Thr Ala Glu Glu Ala Gly Leu Leu Gly Ala Glu
305      310      315      320
Tyr Tyr Val His Glu Leu Pro Gln Ala Glu Lys Asp Lys Ile Arg Leu
325      330      335
Leu Leu Asp Phe Asp Met Met Ala Ser Pro Asn Phe Ala Tyr Gln Ile
340      345      350
Tyr Asp Gly Asp Gly Ser Ala Phe Asn Leu Thr Gly Pro Val Gly Ser
355      360      365
Ala Glu Ala Glu His Glu Phe Ala Ala Tyr Phe Asp Ser Ile Gly Leu
370      375      380
Asn His Thr Glu Ile Glu Phe Asp Gly Arg Ser Asp Tyr Gly Pro Phe
385      390      395      400
Leu Glu Ala Gly Ile Ala Ser Gly Gly Ile Ala Gly Gly Ala Glu Gly
405      410      415
Ile Lys Thr Glu Glu Glu Ala Ala Met Phe Gly Gly Gly Ala Gly Val
420      425      430
Pro Tyr Asp Val Asn Tyr His Glu Asp Gly Asp Thr Val Asn Asn Leu
435      440      445
Asn Leu Glu Ala Trp Ile Glu Phe Thr Arg Ala Ile Ala His Met Thr
450      455      460
Ala Lys Tyr Ala Val Ser Trp Asp Ser Ile Pro Arg Asn Ala Thr
465      470      475      480
Ala Ala Gln Lys Arg Ser Glu Arg Tyr Ala Glu Phe Lys Gln Ala Phe
485      490      495

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10336256.txt

Gln Lys Thr Lys Arg Tyr Gln Arg Trp Val  
500 505

<210> 195  
 <211> 4182  
 <212> DNA  
 <213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<220>  
 <221> CDS  
 <222> (1001)...(2182)  
 <223> Exon

<221> CDS  
 <222> (2238)...(2367)  
 <223> Exon

<221> CDS  
 <222> (2425)...(2549)  
 <223> Exon

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 tccgagtcac gatgttatga gttgcatgta tgtacatatt gaataaatga tgttgcatgt 180  
 ccaatgcagt ctttgcacgt tgcctctttg cgaagggtgtg agcacgacga gcggtagccc 240  
 ggcgggggttc tccgctgcta ctgagcacgt gagcagtcctt ggcagcttgg cagtccgaca 300  
 cgtccgagcc tgcgtcactg aagaagaaga aaagaaagga atcgagggtc ggacgcgccg 360  
 gtacccctga ggctgcccag ctggagacac cttccgttca catgggctgc tccgcagttc 420  
 cttttcttgg ttccggcgta tcttagacag cgaaatatca tgaataccat tcgggcagct 480  
 tctttgcatt aacctataaa ggctgctcga cgatggcgct actcgattgg aacgccaaagt 540  
 cgcagacaac gcgcctatgc gtttagcagct gcgcatcacc attcaagctt tgccccgaaa 600  
 catttgcttt tgtgtcgccc tccaatctat cttatcaaac aaagcagctc atacgggcag 660  
 gccagccctg gtcacgatgc acagcacgat ctacttgatc ctcccgggca ggtgcataag 720  
 ggaaggacta cggaggattg accaaagaag aaggagatgt tgctagcgcc cccagccaat 780  
 tcgcaagacc gcccaatcac ggacttgcca acccatcccc acgccgacgc aactaggctt 840  
 aacgatgtat tatcacagcc gttagaagaa ggctcgctcat catgccatgg ggccgcacag 900  
 aatgtataag gcctcttccg tgctgcaata accagtcgcg cagagttact tcgtgctttc 960  
 gctttcacat ccctcattct ttttccaaat ccatctcaag atg aag tac tct ctc 1015  
 Met Lys Tyr Ser Leu  
 1 5

gcc gca gcc ctg att ctc cag ggt aca act gta ctt ggc agc ctt ctc 1063  
 Ala Ala Ala Leu Ile Leu Gln Gly Thr Thr Val Leu Gly Ser Leu Leu  
 10 15 20

ccc gtt cac ttc aag gca ccc agc cct tcc cac ttc ctc gac att gtc 1111  
 Pro Val His Phe Lys Ala Pro Ser Pro Ser His Phe Leu Asp Ile Val  
 25 30 35

aac aat ggc aca tac gat ctg ggc tgc cga cca aag gct gta cca cat 1159  
 Asn Asn Gly Thr Tyr Asp Leu Gly Cys Arg Pro Lys Ala Val Pro His  
 40 45 50

gag gac ggc cac ttt gag ctt cat gct ctc ctg acc gag gag caa att 1207  
 Glu Asp Gly His Phe Glu Leu His Ala Leu Leu Thr Glu Glu Gln Ile  
 55 60 65

gcc cac ctc gaa agg gaa tat gag cac tct ggc gag atc tct ctc cac 1255  
 Ala His Leu Glu Arg Glu Tyr Glu His Ser Gly Glu Ile Ser Leu His  
 70 75 80 85

cga cgc gac ctc agc aag agg gct gcc gac gca cca atc ggc act ggt 1303  
 Arg Arg Asp Leu Ser Lys Arg Ala Ala Asp Ala Pro Ile Gly Thr Gly  
 90 95 100

gac agg tgg caa ggt ggt gcc gtc aca cct tca ggt ctt gga acc aaa 1351  
 Asp Arg Trp Gln Gly Gly Ala Val Thr Pro Ser Gly Leu Gly Thr Lys

10336256.txt

105	110	115	
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tcg gca atc aag ggt ctc gtt aac ggt tat ggt atc aac acc att act Ser Ala Ile Lys Gly Leu Val Asn Gly Tyr Gly Ile Asn Thr Ile Thr 135 140 145			1447
ctg cca tac aag act ttc cag ggt gct acg cag acc gct gga tac gtc Leu Pro Tyr Lys Thr Phe Gln Gly Ala Thr Gln Thr Ala Gly Tyr Val 150 155 160 165			1495
ggt gct ggt acg gac aag tcg cag tac aag ctc tac ctc agt gct ggc Gly Ala Gly Thr Asp Lys Ser Gln Tyr Lys Leu Tyr Leu Ser Ala Gly 170 175 180			1543
atg cac gcc cgt gag cga ggt ggt ccc gat cag ctc att tac tgg atc Met His Ala Arg Glu Arg Gly Gly Pro Asp Gln Leu Ile Tyr Trp Ile 185 190 195			1591
tcc gac ttg ctt gct gcc aac aag gct gga acc ggt ctc aca tac ggc Ser Asp Leu Leu Ala Ala Asn Lys Ala Gly Thr Gly Leu Thr Tyr Gly 200 205 210			1639
agg aag acc tac acc aac gcc cag gtc aag agc gtt ctc gct gcc ggt Arg Lys Thr Tyr Thr Asn Ala Gln Val Lys Ser Val Leu Ala Ala Gly 215 220 225			1687
att gtc ttc ttc ccc ctt gtc aac cct gac gga gtt gcc tac gat caa Ile Val Phe Phe Pro Leu Val Asn Pro Asp Gly Val Ala Tyr Asp Gln 230 235 240 245			1735
tcc tct ggc tcc ctc tgg cgc aag aac cga aac act cgc tcc ggc aca Ser Ser Gly Ser Leu Trp Arg Lys Asn Arg Asn Thr Arg Ser Gly Thr 250 255 260			1783
agc ggc gca tcc gtc ggt gtc gat atc aac cgc aac ttt gat ttc ctc Ser Gly Ala Ser Val Gly Val Asp Ile Asn Arg Asn Phe Asp Phe Leu 265 270 275			1831
tgg aac ttc aag aag ttc ttc gac cca tcc acc tcg cct gct tcc acc Trp Asn Phe Lys Lys Phe Phe Asp Pro Ser Thr Ser Pro Ala Ser Thr 280 285 290			1879
tcg ccc agt tcg gag gct ttt tac ggc act gcc gcc gca tct gag ccc Ser Pro Ser Ser Glu Ala Phe Tyr Gly Thr Ala Ala Ser Glu Pro 295 300 305			1927
gag acc aag aac cac atc agc atc tac gac agc ttc ccc aag atc agg Glu Thr Lys Asn His Ile Ser Ile Tyr Asp Ser Phe Pro Lys Ile Arg 310 315 320 325			1975
tgg ttc atg gat atc cac tct gct act ggt gac atc cta tac aac tgg Trp Phe Met Asp Ile His Ser Ala Thr Gly Asp Ile Leu Tyr Asn Trp 330 335 340			2023
ggt gac gac gag aca cag tcc aca aac agc gct atg aac ttc ctt aac Gly Asp Asp Glu Thr Gln Ser Thr Asn Ser Ala Met Asn Phe Leu Asn 345 350 355			2071
act gct tat gac gga aag aga ggt cgt atc ggc gac agc aca tac aag Thr Ala Tyr Asp Gly Lys Arg Gly Arg Ile Gly Asp Ser Thr Tyr Lys 360 365 370			2119
gag tac atg ccc tct gcc gat gtc acc ggc atc aag agc gtt gcc tcc Glu Tyr Met Pro Ser Ala Asp Val Thr Gly Ile Lys Ser Val Ala Ser 375 380 385			2167

10336256.txt  
385

375

380

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aag acg gct gct gct agtaagttga cccttcagaa gttttgtata atatctgaac 2222
Lys Thr Ala Ala Ala
390

tgacattcgt atttta gtg gcc gct gta ggt gga cgt tca tac aca tcc atg 2273
Val Ala Ala Val Gly Gly Arg Ser Tyr Thr Ser Met
395 400 405

caa tcc gtt ggt ctc tac gcc act tcc ggt gcc tcg gat gac tac gcc 2321
Gln Ser Val Gly Leu Tyr Ala Thr Ser Gly Ala Ser Asp Asp Tyr Ala
410 415 420

gcc agc cgc gtg tac gcc aaa tcc ggt gct aac aag gtc ttt ggc t 2367
Ala Ser Arg Val Tyr Ala Lys Ser Gly Ala Asn Lys Val Phe Gly
425 430 435

gtaagtcttg attcttctac cttgtggtgt atgtatactg actttgcacg cctgtag tc 2426
Phe

acc atg gag ttt gga tac gca acc aac ttt tac ccc act ctc acc gag 2474
Thr Met Glu Phe Gly Tyr Ala Thr Asn Phe Tyr Pro Thr Leu Thr Glu
440 445 450

ttc aac cag aac atc ctt gac acc aat gct ggt ttc atg gat tgg gca 2522
Phe Asn Gln Asn Ile Leu Asp Thr Asn Ala Gly Phe Met Asp Trp Ala
455 460 465 470

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Leu Ala Ala Ile Ala Val Gly Val Asn
475

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&lt;210&gt; 196

&lt;211&gt; 394

&lt;212&gt; PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

&lt;400&gt; 196

10336256.txt

Met Lys Tyr Ser Leu Ala Ala Ala Leu Ile Leu Gln Gly Thr Thr Val  
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 20 25 30  
 Phe Leu Asp Ile Val Asn Asn Gly Thr Tyr Asp Leu Gly Cys Arg Pro  
 35 40 45  
 Lys Ala Val Pro His Glu Asp Gly His Phe Glu Leu His Ala Leu Leu  
 50 55 60  
 Thr Glu Glu Gln Ile Ala His Leu Glu Arg Glu Tyr Glu His Ser Gly  
 65 70 75 80  
 Glu Ile Ser Leu His Arg Arg Asp Leu Ser Lys Arg Ala Ala Asp Ala  
 85 90 95  
 Pro Ile Gly Thr Gly Asp Arg Trp Gln Gly Gly Ala Val Thr Pro Ser  
 100 105 110  
 Gly Leu Gly Thr Lys Ala Ala Gly Ser Thr Val Ser Ser Ile Met Asn  
 115 120 125  
 Pro Thr Glu Ile Asn Ser Ala Ile Lys Gly Leu Val Asn Gly Tyr Gly  
 130 135 140  
 Ile Asn Thr Ile Thr Leu Pro Tyr Lys Thr Phe Gln Gly Ala Thr Gln  
 145 150 155 160  
 Thr Ala Gly Tyr Val Gly Ala Gly Thr Asp Lys Ser Gln Tyr Lys Leu  
 165 170 175  
 Tyr Leu Ser Ala Gly Met His Ala Arg Glu Arg Gly Gly Pro Asp Gln  
 180 185 190  
 Leu Ile Tyr Trp Ile Ser Asp Leu Leu Ala Ala Asn Lys Ala Gly Thr  
 195 200 205  
 Gly Leu Thr Tyr Gly Arg Lys Thr Tyr Thr Asn Ala Gln Val Lys Ser  
 210 215 220  
 Val Leu Ala Ala Gly Ile Val Phe Phe Pro Leu Val Asn Pro Asp Gly  
 225 230 235 240  
 Val Ala Tyr Asp Gln Ser Ser Gly Ser Leu Trp Arg Lys Asn Arg Asn  
 245 250 255  
 Thr Arg Ser Gly Thr Ser Gly Ala Ser Val Gly Val Asp Ile Asn Arg  
 260 265 270  
 Asn Phe Asp Phe Leu Trp Asn Phe Lys Lys Phe Phe Asp Pro Ser Thr  
 275 280 285  
 Ser Pro Ala Ser Thr Ser Pro Ser Ser Glu Ala Phe Tyr Gly Thr Ala  
 290 295 300  
 Ala Ala Ser Glu Pro Glu Thr Lys Asn His Ile Ser Ile Tyr Asp Ser  
 305 310 315 320  
 Phe Pro Lys Ile Arg Trp Phe Met Asp Ile His Ser Ala Thr Gly Asp  
 325 330 335  
 Ile Leu Tyr Asn Trp Gly Asp Asp Glu Thr Gln Ser Thr Asn Ser Ala  
 340 345 350  
 Met Asn Phe Leu Asn Thr Ala Tyr Asp Gly Lys Arg Gly Arg Ile Gly  
 355 360 365  
 Asp Ser Thr Tyr Lys Glu Tyr Met Pro Ser Ala Asp Val Thr Gly Ile  
 370 375 380  
 Lys Ser Val Ala Ser Lys Thr Ala Ala Ala  
 385 390

&lt;210&gt; 197

&lt;211&gt; 43

&lt;212&gt; PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

&lt;400&gt; 197

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 Leu Tyr Ala Thr Ser Gly Ala Ser Asp Asp Tyr Ala Ala Ser Arg Val  
 20 25 30  
 Tyr Ala Lys Ser Gly Ala Asn Lys Val Phe Gly  
 35 40

&lt;210&gt; 198

&lt;211&gt; 42

&lt;212&gt; PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

10336256.txt

&lt;400&gt; 198

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 20 25 30  
 Ala Leu Ala Ala Ile Ala Val Gly Val Asn  
 35 40

&lt;210&gt; 199

&lt;211&gt; 1437

&lt;212&gt; DNA

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1437)

&lt;400&gt; 199

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ttc ctc gac att gtc aac aat ggc aca tac gat ctg ggc tgc cga cca Phe Leu Asp Ile Val Asn Asn Gly Thr Tyr Asp Leu Gly Cys Arg Pro 35 40 45	144
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acc gag gag caa att gcc cac ctc gaa agg gaa tat gag cac tct ggg Thr Glu Glu Gln Ile Ala His Leu Glu Arg Glu Tyr Glu His Ser Gly 65 70 75 80	240
gag atc tct ctc cac cga cgc gac ctc agc aag agg gct gcc gac gca Glu Ile Ser Leu His Arg Arg Asp Leu Ser Lys Arg Ala Ala Asp Ala 85 90 95	288
cca atc ggc act ggt gac agg tgg caa ggt ggt gcc gtc aca cct tca Pro Ile Gly Thr Gly Asp Arg Trp Gln Gly Gly Ala Val Thr Pro Ser 100 105 110	336
ggt ctt gga acc aaa gct gcg gga tca aca gtc agc tcc atc atg aac Gly Leu Gly Thr Lys Ala Ala Gly Ser Thr Val Ser Ser Ile Met Asn 115 120 125	384
cct acc gag atc aac tcg gca atc aag ggt ctc gtt aac ggt tat ggt Pro Thr Glu Ile Asn Ser Ala Ile Lys Gly Leu Val Asn Gly Tyr Gly 130 135 140	432
atc aac acc att act ctg cca tac aag act ttc cag ggt gct acg cag Ile Asn Thr Ile Thr Leu Pro Tyr Lys Thr Phe Gln Gly Ala Thr Gln 145 150 155 160	480
acc gct gga tac gtc ggt gct ggt acg gac aag tcg cag tac aag ctc Thr Ala Gly Tyr Val Gly Ala Gly Thr Asp Lys Ser Gln Tyr Lys Leu 165 170 175	528
tac ctc agt gct ggc atg cac gcc cgt gag cga ggt ggt ccc gat cag Tyr Leu Ser Ala Gly Met His Ala Arg Glu Arg Gly Gly Pro Asp Gln 180 185 190	576
ctc att tac tgg atc tcc gac ttg ctt gct gcc aac aag gct gga acc	624

10336256.txt

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	195						200					205					
ggt	ctc	aca	tac	ggc	agg	aag	acc	tac	acc	aac	gcc	cag	gtc	aag	agc		672
Gly	Leu	Thr	Tyr	Gly	Arg	Lys	Thr	Tyr	Thr	Asn	Ala	Gln	Val	Lys	Ser		
	210					215					220						
gtt	ctc	gct	gcc	ggt	att	gtc	ttc	ttc	ccc	ctt	gtc	aac	cct	gac	gga		720
Val	Leu	Ala	Ala	Gly	Ile	Val	Phe	Phe	Pro	Leu	Val	Asn	Pro	Asp	Gly		
	225				230					235					240		
gtt	gcc	tac	gat	caa	tcc	tct	ggc	tcc	ctc	tgg	cgc	aag	aac	cga	aac		768
Val	Ala	Tyr	Asp	Gln	Ser	Ser	Gly	Ser	Leu	Trp	Arg	Lys	Asn	Arg	Asn		
				245					250					255			
act	cgc	tcc	ggc	aca	agc	ggc	gca	tcc	gtc	ggt	gtc	gat	atc	aac	cgc		816
Thr	Arg	Ser	Gly	Thr	Ser	Gly	Ala	Ser	Val	Gly	Val	Asp	Ile	Asn	Arg		
			260				265						270				
aac	ttt	gat	ttc	ctc	tgg	aac	ttc	aag	aag	ttc	ttc	gac	cca	tcc	acc		864
Asn	Phe	Asp	Phe	Leu	Trp	Asn	Phe	Lys	Lys	Phe	Phe	Asp	Pro	Ser	Thr		
		275					280					285					
tcg	cct	gct	tcc	acc	tcg	ccc	agt	tcg	gag	gct	ttt	tac	ggc	act	gcc		912
Ser	Pro	Ala	Ser	Thr	Ser	Pro	Ser	Ser	Glu	Ala	Phe	Tyr	Gly	Thr	Ala		
	290					295					300						
gcc	gca	tct	gag	ccc	gag	acc	aag	aac	cac	atc	agc	atc	tac	gac	agc		960
Ala	Ala	Ser	Glu	Pro	Glu	Thr	Lys	Asn	His	Ile	Ser	Ile	Tyr	Asp	Ser		
	305				310					315					320		
ttc	ccc	aag	atc	agg	tgg	ttc	atg	gat	atc	cac	tct	gct	act	ggt	gac		1008
Phe	Pro	Lys	Ile	Arg	Trp	Phe	Met	Asp	Ile	His	Ser	Ala	Thr	Gly	Asp		
				325					330					335			
atc	cta	tac	aac	tgg	ggt	gac	gac	gag	aca	cag	tcc	aca	aac	agc	gct		1056
Ile	Leu	Tyr	Asn	Trp	Gly	Asp	Asp	Glu	Thr	Gln	Ser	Thr	Asn	Ser	Ala		
			340					345					350				
atg	aac	ttc	ctt	aac	act	gct	tat	gac	gga	aag	aga	ggt	cgt	atc	ggc		1104
Met	Asn	Phe	Leu	Asn	Thr	Ala	Tyr	Asp	Gly	Lys	Arg	Gly	Arg	Ile	Gly		
		355				360						365					
gac	agc	aca	tac	aag	gag	tac	atg	ccc	tct	gcc	gat	gtc	acc	ggc	atc		1152
Asp	Ser	Thr	Tyr	Lys	Glu	Tyr	Met	Pro	Ser	Ala	Asp	Val	Thr	Gly	Ile		
	370					375					380						
aag	agc	gtt	gcc	tcc	aag	acg	gct	gct	gct	gtg	gcc	gct	gta	ggt	gga		1200
Lys	Ser	Val	Ala	Ser	Lys	Thr	Ala	Ala	Ala	Val	Ala	Ala	Val	Gly	Gly		
	385				390					395				400			
cgt	tca	tac	aca	tcc	atg	caa	tcc	gtt	ggt	ctc	tac	gcc	act	tcc	ggt		1248
Arg	Ser	Tyr	Thr	Ser	Met	Gln	Ser	Val	Gly	Leu	Tyr	Ala	Thr	Ser	Gly		
				405					410					415			
gcc	tcg	gat	gac	tac	gcc	gcc	agc	cgc	gtg	tac	gcc	aaa	tcc	ggt	gct		1296
Ala	Ser	Asp	Asp	Tyr	Ala	Ala	Ser	Arg	Val	Tyr	Ala	Lys	Ser	Gly	Ala		
			420					425					430				
aac	aag	gtc	ttt	ggc	ttc	acc	atg	gag	ttt	gga	tac	gca	acc	aac	ttt		1344
Asn	Lys	Val	Phe	Gly	Phe	Thr	Met	Glu	Phe	Gly	Tyr	Ala	Thr	Asn	Phe		
		435					440					445					
tac	ccc	act	ctc	acc	gag	ttc	aac	cag	aac	atc	ctt	gac	acc	aat	gct		1392
Tyr	Pro	Thr	Leu	Thr	Glu	Phe	Asn	Gln	Asn	Ile	Leu	Asp	Thr	Asn	Ala		
	450				455						460						
ggt	ttc	atg	gat	tgg	gca	ctt	gct	gcc	att	gct	gtt	gga	gtt	aac			1437

10336256.txt

Gly Phe Met Asp Trp Ala Leu Ala Ala Ile Ala Val Gly Val Asn  
 465 470 475

&lt;210&gt; 200

&lt;211&gt; 479

&lt;212&gt; PRT

&lt;213&gt; Cochliobolus heterostrophus strain C4 (ATCC 48331)

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; (1)...(18)

&lt;221&gt; DOMAIN

&lt;222&gt; (124)...(344)

&lt;223&gt; Zinc carboxypeptidase

&lt;400&gt; 200

Met Lys Tyr Ser Leu Ala Ala Ala Leu Ile Leu Gln Gly Thr Thr Val  
 1 5 10 15  
 Leu Gly Ser Leu Leu Pro Val His Phe Lys Ala Pro Ser Pro Ser His  
 20 25 30  
 Phe Leu Asp Ile Val Asn Asn Gly Thr Tyr Asp Leu Gly Cys Arg Pro  
 35 40 45  
 Lys Ala Val Pro His Glu Asp Gly His Phe Glu Leu His Ala Leu Leu  
 50 55 60  
 Thr Glu Glu Gln Ile Ala His Leu Glu Arg Glu Tyr Glu His Ser Gly  
 65 70 75 80  
 Glu Ile Ser Leu His Arg Arg Asp Leu Ser Lys Arg Ala Ala Asp Ala  
 85 90 95  
 Pro Ile Gly Thr Gly Asp Arg Trp Gln Gly Gly Ala Val Thr Pro Ser  
 100 105 110  
 Gly Leu Gly Thr Lys Ala Ala Gly Ser Thr Val Ser Ser Ile Met Asn  
 115 120 125  
 Pro Thr Glu Ile Asn Ser Ala Ile Lys Gly Leu Val Asn Gly Tyr Gly  
 130 135 140  
 Ile Asn Thr Ile Thr Leu Pro Tyr Lys Thr Phe Gln Gly Ala Thr Gln  
 145 150 155 160  
 Thr Ala Gly Tyr Val Gly Ala Gly Thr Asp Lys Ser Gln Tyr Lys Leu  
 165 170 175  
 Tyr Leu Ser Ala Gly Met His Ala Arg Glu Arg Gly Gly Pro Asp Gln  
 180 185 190  
 Leu Ile Tyr Trp Ile Ser Asp Leu Leu Ala Ala Asn Lys Ala Gly Thr  
 195 200 205  
 Gly Leu Thr Tyr Gly Arg Lys Thr Tyr Thr Asn Ala Gln Val Lys Ser  
 210 215 220  
 Val Leu Ala Ala Gly Ile Val Phe Phe Pro Leu Val Asn Pro Asp Gly  
 225 230 235 240  
 Val Ala Tyr Asp Gln Ser Ser Gly Ser Leu Trp Arg Lys Asn Arg Asn  
 245 250 255  
 Thr Arg Ser Gly Thr Ser Gly Ala Ser Val Gly Val Asp Ile Asn Arg  
 260 265 270  
 Asn Phe Asp Phe Leu Trp Asn Phe Lys Lys Phe Phe Asp Pro Ser Thr  
 275 280 285  
 Ser Pro Ala Ser Thr Ser Pro Ser Ser Glu Ala Phe Tyr Gly Thr Ala  
 290 295 300  
 Ala Ala Ser Glu Pro Glu Thr Lys Asn His Ile Ser Ile Tyr Asp Ser  
 305 310 315 320  
 Phe Pro Lys Ile Arg Trp Phe Met Asp Ile His Ser Ala Thr Gly Asp  
 325 330 335  
 Ile Leu Tyr Asn Trp Gly Asp Asp Glu Thr Gln Ser Thr Asn Ser Ala  
 340 345 350  
 Met Asn Phe Leu Asn Thr Ala Tyr Asp Gly Lys Arg Gly Arg Ile Gly  
 355 360 365  
 Asp Ser Thr Tyr Lys Glu Tyr Met Pro Ser Ala Asp Val Thr Gly Ile  
 370 375 380  
 Lys Ser Val Ala Ser Lys Thr Ala Ala Ala Val Ala Val Gly Gly  
 385 390 395 400

10336256.txt

Arg Ser Tyr Thr Ser Met Gln Ser Val Gly Leu Tyr Ala Thr Ser Gly  
 405 410 415  
 Ala Ser Asp Asp Tyr Ala Ala Ser Arg Val Tyr Ala Lys Ser Gly Ala  
 420 425 430  
 Asn Lys Val Phe Gly Phe Thr Met Glu Phe Gly Tyr Ala Thr Asn Phe  
 435 440 445  
 Tyr Pro Thr Leu Thr Glu Phe Asn Gln Asn Ile Leu Asp Thr Asn Ala  
 450 455 460  
 Gly Phe Met Asp Trp Ala Leu Ala Ala Ile Ala Val Gly Val Asn  
 465 470 475

&lt;210&gt; 201

&lt;211&gt; 3380

&lt;212&gt; DNA

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1001)...(1592)

&lt;223&gt; Exon

&lt;221&gt; CDS

&lt;222&gt; (1641)...(2380)

&lt;223&gt; Exon

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(3380)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 201

tagctggaat	ctctttacat	tttatgttgt	taaatgcat	ttgggcttct	tgtttggtga	60
tttcgtttgt	cactttcggt	gcttttgaaa	tcgagtgcc	ttgccaaca	gtagggttga	120
tcatgaatgt	gtagttcccg	ccttgacttt	tcttgctacc	aggttcattg	tgtagaagta	180
aatgtatgta	ggaagccagt	cgtgaagttt	tgaatactag	gaacaattta	ctatggggca	240
atcgaaagcc	tgtttggtac	aggaatgtaa	gagaggggct	gggatacatg	ctcaaataag	300
cgagttggcc	aagcatgcag	aacaagcgtg	cttacggtag	ttgtgttcca	aaaccttata	360
catgactgtg	agtcctgttc	gccgggtatgc	cttttgtaata	agcttccaat	tctgcttgct	420
gtgttcatac	gcgtgaaact	tgcaaaacat	cgtagaccgt	agagacgtag	ctcaatgcga	480
cgatcatcaaa	gcaccgatat	cgtctcttga	ggagcatcat	ggtgaaacat	catttgcttc	540
tcaagaaaaa	gaacacgcag	gittccaatg	atcittggaa	tcaagcatga	ggctacagaa	600
tagctatgga	acaggaattt	tgtacggctt	ttcaacggct	ttcgacggga	tcagcaatat	660
acccggggggc	tgagggggag	ttgcataccc	gacctgcctt	gctccttggc	gatgcgtcta	720
gatcaggaag	ctgggggtac	ataagtatac	acaagcctgg	gcatcgctt	ggctagcggg	780
cgaacgcagc	tccacctact	gaatatgatt	ccagtgatgc	aaatgaacac	ggcaatgctg	840
tgcgagctag	catgacagtt	ccatggcgac	attcgattat	tgcaaccgagc	ttcccgcgc	900
gcagataagg	ttagaacagg	gggtccaaagt	catatttaag	aagtgtatat	gatgttgtaa	960
tgacttgtgt	gttgtgtttg	ttaactctcc	gaacttcaaa	atg aga ttg tca aag		1015
				Met Arg Leu Ser Lys		
				1 5		

ttg gtg gtg gcc gct caa ttg gca gca gcg tct cct ttg gca cac gac	1063
Leu Val Val Ala Ala Gln Leu Ala Ala Ala Ser Pro Leu Ala His Asp	
10 15 20	

gct agc tct gtg tct cgc agt gcc aac cca agc tac gat ggc tac caa	1111
Ala Ser Ser Val Ser Arg Ser Ala Asn Pro Ser Tyr Asp Gly Tyr Gln	
25 30 35	

atc tac tcc att acg cca tct tct gcc gaa gaa gct cat gat atc aac	1159
Ile Tyr Ser Ile Thr Pro Ser Ser Ala Glu Glu Ala His Asp Ile Asn	
40 45 50	

aag cgc ttc tcc aac tac cac act cac ccg att cgc aac acc ctg tca	1207
Lys Arg Phe Ser Asn Tyr His Thr His Pro Ile Arg Asn Thr Leu Ser	
55 60 65	

gtt gct att cca ccc gag gag att gac tct ttt cgt gca ctg ggt ttg	1255
Val Ala Ile Pro Pro Glu Glu Ile Asp Ser Phe Arg Ala Leu Gly Leu	

10336256.txt

70	75	80	85	
aac gct cgc ctg gtg aac tcg gat ctg ggc aag tac att cgc tct acc	Asn Ala Arg Leu Val 90	Asn Ser Asp Leu Gly 95	Lys Tyr Ile Arg Ser 100	1303
gac aag gaa gcc gta tac aag cgt gac ttg cat gca acg ggt cag ctc	Asp Lys Glu Ala Val 105	Asp Leu His Ala Thr 110	Gly Gln Leu 115	1351
ccg gac ctg tcg tgg ttc gac act tac cat gct tat tcc gac cac ctt	Pro Asp Leu Ser Trp Phe Asp Thr 125	Tyr His Ala Tyr Ser 130	Asp His Leu 135	1399
cag tac tgg gac gac ctt gtt gcg gcg ttc cct ggt aac tct gag aag	Gln Tyr Trp Asp Asp Leu Val 140	Ala Ala Phe Pro Gly 145	Asn Ser Glu Lys 150	1447
ttt tcg att ggc cag agt tat gag aac cgg aca att tgg gcg ttc cat	Phe Ser Ile Gly Gln Ser Tyr Glu Asn Arg Thr 155	Ile Trp Ala Phe His 160	165	1495
ttg ttt ggt gac aag agc act gaa gct gca acg caa gaa aag ccc att	Leu Phe Gly Asp Lys Ser Thr Glu Ala Thr Gln Glu Lys Pro Ile 170	175	180	1543
att ctt tgg cat gcc aca gtt cac gca aga gaa tgg atc tcc act atg	Ile Leu Trp His Ala Thr Val His Ala Arg Glu Trp Ile Ser Thr Met 185	190	195	1591
g gtaagcagaa cacgcatgag aaaaaggaat actagctaac gctcccag tc atc gag			Val Ile Glu 200	1648
tac cta gcc tac cag ctt att gac ggg tac caa aaa ggc gat gca aat	Tyr Leu Ala Tyr Gln Leu Ile Asp Gly Tyr 205	Gln Lys Gly Asp Ala Asn 210	215	1696
gtg act agt ttt ctg gac cac tac gac ttc tac ctc gtc ccc ttc cac	Val Thr Ser Phe Leu Asp His Tyr Asp Phe Tyr Leu Val Pro Phe His 220	225	230	1744
aac cca gac ggc ttc tcg tac aca caa acc aac gac cga cta tgg cgc	Asn Pro Asp Gly Phe Ser Tyr Thr Gln Thr Asn Asp Arg Leu Trp Arg 235	240	245	1792
aag aac cgg cag ccg cgc ccc caa cta aac acg gcc tgt gtc ggc acc	Lys Asn Arg Gln Pro Arg Pro Gln Leu Asn Thr Ala Cys Val Gly Thr 250	255	260	1840
gac ggc aac cgc aac tgg aag ttt gaa tgg gac gcc acg cct cca gac	Asp Gly Asn Arg Asn Trp Lys Phe Glu Trp Asp Ala Thr Pro Pro Asp 265	270	275	1888
ggt ggt tca acg ccc aat ccg tgc gga gag acg tac cgt ggc gaa gcc	Gly Gly Ser Thr Pro Asn Pro Cys Gly Glu Thr Tyr Arg Gly Glu Ala 285	290	295	1936
gcc ggc gac aca ccc gag aat caa gcc atg gac gga ctc tct gct aag	Ala Gly Asp Thr Pro Glu Asn Gln Ala Met Asp Gly Leu Ser Ala Lys 300	305	310	1984
ctt tcc agc acg ggc gct ggc atc cgg tcc ttc atc gac ttc cac tcg	Leu Ser Ser Thr Gly Ala Gly Ile Arg Ser Phe Ile Asp Phe His Ser 315	320	325	2032
tac agc cag ctt atc ctc act ccc tgg ggt ttc tcg tgc gac ccg ctc	Tyr Ser Gln Leu Ile Leu Thr Pro Trp Gly Phe Ser Cys Asp Pro Leu 330			2080

10336256.txt  
340

330 335  
 ccc gaa acg ctt ccc cgt atg ctc gag gta gca ggc ggc act gcc aga 2128  
 Pro Glu Thr Leu Pro Arg Met Leu Glu Val Ala Gly Gly Thr Ala Arg 360  
 345 350 355  
 gct atc cag gcg ggc agc gcg cga aac gtc acg tac gag ttt ggg cct 2176  
 Ala Ile Gln Ala Gly Ser Ala Arg Asn Val Thr Tyr Glu Phe Gly Pro 375  
 365 370 375  
 ggc tgt cag att ctg tac ttc tcc acg ggc aac tcg aga gac cac cac 2224  
 Gly Cys Gln Ile Leu Tyr Phe Ser Thr Gly Asn Ser Arg Asp His His 390  
 380 385 390  
 cat gct gtg cat ggc gcg gcg cac tcg tgg act atg gag ctg agc ccc 2272  
 His Ala Val His Gly Ala Ala His Ser Trp Thr Met Glu Leu Ser Pro 405  
 395 400 405  
 cag gac gcg gca gga ggc ggg ttt gtt ctg ccg cct gaa ctc att tgg 2320  
 Gln Asp Ala Ala Gly Gly Gly Phe Val Leu Pro Pro Glu Leu Ile Trp 420  
 410 415 420  
 ccg acg gtc aag gag cag tgg gcg ggc cag ttg tgg ttg ttg aat gat 2368  
 Pro Thr Val Lys Glu Gln Trp Ala Gly Gln Leu Trp Leu Leu Asn Asp 440  
 425 430 435 440  
 gtt tgg gat aac tgagcttttg gtgcaatggc acaggaatat catgcactgt 2420  
 Val Trp Asp Asn

tggatggcat atttgcttag attggctacg agatagatgc tatgaaacat tctgtgaact 2480  
 ggctcttgaa gcattgcaga tgttcaagtg atgtgtttat gattggagta agatctggag 2540  
 cttgacctat aagcagtgcc ttatacccac atcttctctt atccatatcg tcctcatgtc 2600  
 ctcatgtcct catgtcctca ttgtcccaac tcacagttac aaaatatcag gagcacaagt 2660  
 acaggtttca acattataatc tatttaaagt cgagacagtg gacagttagt aaatgaacag 2720  
 gtannnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn 2780  
 nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn 2840  
 nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn 2900  
 nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn 2960  
 nncatcatag gcgtcatgtg gcgtgaggag aaacactaaa gttggacaca agggcattgc 3020  
 tcactcagaca gagactatga gcttcattccg aacatgcggt tctcgtattg atagatgggc 3080  
 agactccatt aggggtagtc agtgcatact ggattggagc aagatcgaaa ctgagtcattc 3140  
 atcgcccaaa ggacgatttc gaaaagccca agacctaatac aacgagggtc gtatatggaa 3200  
 tcgaaaatct ctcagacgat gagtacttgt gagcatgaaa tgcgaagaat tgataatggc 3260  
 acgaggttct ggtgtagtga acgacaagaa gctgggtcgca ttgttgacgg cgggttgagg 3320  
 atttggatct gcaagtgcag tctcgaaaat ctttacgggc aggcctctcgt tgggtggtgac 3380

&lt;210&gt; 202

&lt;211&gt; 197

&lt;212&gt; PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

&lt;400&gt; 202

Met Arg Leu Ser Lys Leu Val Val Ala Ala Gln Leu Ala Ala Ala Ser  
 1 5 10 15  
 Pro Leu Ala His Asp Ala Ser Ser Val Ser Arg Ser Ala Asn Pro Ser  
 20 25 30  
 Tyr Asp Gly Tyr Gln Ile Tyr Ser Ile Thr Pro Ser Ser Ala Glu Glu  
 35 40 45  
 Ala His Asp Ile Asn Lys Arg Phe Ser Asn Tyr His Thr His Pro Ile  
 50 55 60  
 Arg Asn Thr Leu Ser Val Ala Ile Pro Pro Glu Glu Ile Asp Ser Phe  
 65 70 75 80  
 Arg Ala Leu Gly Leu Asn Ala Arg Leu Val Asn Ser Asp Leu Gly Lys  
 85 90 95  
 Tyr Ile Arg Ser Thr Asp Lys Glu Ala Val Tyr Lys Arg Asp Leu His  
 100 105 110  
 Ala Thr Gly Gln Leu Pro Asp Leu Ser Trp Phe Asp Thr Tyr His Ala

## 10336256.txt

Tyr Ser Asp His Leu Gln Tyr Trp Asp Asp Leu Val Ala Ala Phe Pro  
 115 120 125  
 130 135 140  
 Gly Asn Ser Glu Lys Phe Ser Ile Gly Gln Ser Tyr Glu Asn Arg Thr  
 145 150 155 160  
 Ile Trp Ala Phe His Leu Phe Gly Asp Lys Ser Thr Glu Ala Ala Thr  
 165 170 175  
 Gln Glu Lys Pro Ile Ile Leu Trp His Ala Thr Val His Ala Arg Glu  
 180 185 190  
 Trp Ile Ser Thr Met  
 195

&lt;210&gt; 203

&lt;211&gt; 247

&lt;212&gt; PRT

&lt;213&gt; Cochliobolus heterostrophus strain C4 (ATCC 48331)

&lt;400&gt; 203

Val Ile Glu Tyr Leu Ala Tyr Gln Leu Ile Asp Gly Tyr Gln Lys Gly  
 1 5 10 15  
 Asp Ala Asn Val Thr Ser Phe Leu Asp His Tyr Asp Phe Tyr Leu Val  
 20 25 30  
 Pro Phe His Asn Pro Asp Gly Phe Ser Tyr Thr Gln Thr Asn Asp Arg  
 35 40 45  
 Leu Trp Arg Lys Asn Arg Gln Pro Arg Pro Gln Leu Asn Thr Ala Cys  
 50 55 60  
 Val Gly Thr Asp Gly Asn Arg Asn Trp Lys Phe Glu Trp Asp Ala Thr  
 65 70 75 80  
 Pro Pro Asp Gly Gly Ser Thr Pro Asn Pro Cys Gly Glu Thr Tyr Arg  
 85 90 95  
 Gly Glu Ala Ala Gly Asp Thr Pro Glu Asn Gln Ala Met Asp Gly Leu  
 100 105 110  
 Ser Ala Lys Leu Ser Ser Thr Gly Ala Gly Ile Arg Ser Phe Ile Asp  
 115 120 125  
 Phe His Ser Tyr Ser Gln Leu Ile Leu Thr Pro Trp Gly Phe Ser Cys  
 130 135 140  
 Asp Pro Leu Pro Glu Thr Leu Pro Arg Met Leu Glu Val Ala Gly Gly  
 145 150 155 160  
 Thr Ala Arg Ala Ile Gln Ala Gly Ser Ala Arg Asn Val Thr Tyr Glu  
 165 170 175  
 Phe Gly Pro Gly Cys Gln Ile Leu Tyr Phe Ser Thr Gly Asn Ser Arg  
 180 185 190  
 Asp His His His Ala Val His Gly Ala Ala His Ser Trp Thr Met Glu  
 195 200 205  
 Leu Ser Pro Gln Asp Ala Ala Gly Gly Phe Val Leu Pro Pro Glu  
 210 215 220  
 Leu Ile Trp Pro Thr Val Lys Glu Gln Trp Ala Gly Gln Leu Trp Leu  
 225 230 235 240  
 Leu Asn Asp Val Trp Asp Asn  
 245

&lt;210&gt; 204

&lt;211&gt; 1332

&lt;212&gt; DNA

&lt;213&gt; Cochliobolus heterostrophus strain C4 (ATCC 48331)

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1332)

&lt;400&gt; 204

atg aga ttg tca aag ttg gtg gtg gcc gct caa ttg gca gca gcg tct  
 Met Arg Leu Ser Lys Leu Val Val Ala Ala Gln Leu Ala Ala Ala Ser  
 1 5 10 15  
 cct ttg gca cac gac gct agc tct gtg tct cgc agt gcc aac cca agc  
 Pro Leu Ala His Asp Ala Ser Ser Val Ser Arg Ser Ala Asn Pro Ser  
 20 25 30

48

96

## 10336256.txt

tac gat ggc tac caa atc tac tcc att acg cca tct tct gcc gaa gaa Tyr Asp Gly Tyr Gln Ile Tyr Ser Ile Thr Pro Ser Ser Ala Glu Glu 35 40 45	144
gct cat gat atc aac aag cgc ttc tcc aac tac cac act cac ccg att Ala His Asp Ile Asn Lys Arg Phe Ser Asn Tyr His Thr His Pro Ile 50 55 60	192
cgc aac acc ctg tca gtt gct att cca ccc gag gag att gac tct ttt Arg Asn Thr Leu Ser Val Ala Ile Pro Pro Glu Glu Ile Asp Ser Phe 65 70 75 80	240
cgt gca ctg ggt ttg aac gct cgc ctg gtg aac tcg gat ctg ggc aag Arg Ala Leu Gly Leu Asn Ala Arg Leu Val Asn Ser Asp Leu Gly Lys 85 90 95	288
tac att cgc tct acc gac aag gaa gcc gta tac aag cgt gac ttg cat Tyr Ile Arg Ser Thr Asp Lys Glu Ala Val Tyr Lys Arg Asp Leu His 100 105 110	336
gca acg ggt cag ctc ccg gac ctg tcg tgg ttc gac act tac cat gct Ala Thr Gly Gln Leu Pro Asp Leu Ser Trp Phe Asp Thr Tyr His Ala 115 120 125	384
tat tcc gac cac ctt cag tac tgg gac gac ctt gtt gcg gcg ttc cct Tyr Ser Asp His Leu Gln Tyr Trp Asp Asp Leu Val Ala Ala Phe Pro 130 135 140	432
ggt aac tct gag aag ttt tcg att ggc cag agt tat gag aac cgg aca Gly Asn Ser Glu Lys Phe Ser Ile Gly Gln Ser Tyr Glu Asn Arg Thr 145 150 155 160	480
att tgg gcg ttc cat ttg ttt ggt gac aag agc act gaa gct gca acg Ile Trp Ala Phe His Leu Phe Gly Asp Lys Ser Thr Glu Ala Ala Thr 165 170 175	528
caa gaa aag ccc att att ctt tgg cat gcc aca gtt cac gca aga gaa Gln Glu Lys Pro Ile Ile Leu Trp His Ala Thr Val His Ala Arg Glu 180 185 190	576
tgg atc tcc act atg gtc atc gag tac cta gcc tac cag ctt att gac Trp Ile Ser Thr Met Val Ile Glu Tyr Leu Ala Tyr Gln Leu Ile Asp 195 200 205	624
ggg tac caa aaa ggc gat gca aat gtg act agt ttt ctg gac cac tac Gly Tyr Gln Lys Gly Asp Ala Asn Val Thr Ser Phe Leu Asp His Tyr 210 215 220	672
gac ttc tac ctc gtc ccc ttc cac aac cca gac ggc ttc tcg tac aca Asp Phe Tyr Leu Val Pro Phe His Asn Pro Asp Gly Phe Ser Tyr Thr 225 230 235 240	720
caa acc aac gac cga cta tgg cgc aag aac cgg cag ccg cgc ccc caa Gln Thr Asn Asp Arg Leu Trp Arg Lys Asn Arg Gln Pro Arg Pro Gln 245 250 255	768
cta aac acg gcc tgt gtc ggc acc gac ggc aac cgc aac tgg aag ttt Leu Asn Thr Ala Cys Val Gly Thr Asp Gly Asn Arg Asn Trp Lys Phe 260 265 270	816
gaa tgg gac gcc acg cct cca gac ggt ggt tca acg ccc aat ccg tgc Glu Trp Asp Ala Thr Pro Pro Asp Gly Gly Ser Thr Pro Asn Pro Cys 275 280 285	864
gga gag acg tac cgt ggc gaa gcc gcc ggc gac aca ccc gag aat caa Gly Glu Thr Tyr Arg Gly Glu Ala Ala Gly Asp Thr Pro Glu Asn Gln 290 295 300	912

## 10336256.txt

```

gcc atg gac gga ctc tct gct aag ctt tcc agc acg ggc gct ggc atc      960
Ala Met Asp Gly Leu Ser Ala Lys Leu Ser Ser Thr Gly Ala Gly Ile
305                               310                               315                               320

cgg tcc ttc atc gac ttc cac tcg tac agc cag ctt atc ctc act ccc      1008
Arg Ser Phe Ile Asp Phe His Ser Tyr Ser Gln Leu Ile Leu Thr Pro
                               325                               330                               335

tgg ggt ttc tcg tgc gac ccg ctc ccc gaa acg ctt ccc cgt atg ctc      1056
Trp Gly Phe Ser Cys Asp Pro Leu Pro Glu Thr Leu Pro Arg Met Leu
                               340                               345                               350

gag gta gca ggc ggc act gcc aga gct atc cag gcg ggc agc gcg cga      1104
Glu Val Ala Gly Gly Thr Ala Arg Ala Ile Gln Ala Gly Ser Ala Arg
                               355                               360                               365

aac gtc acg tac gag ttt ggg cct ggc tgt cag att ctg tac ttc tcc      1152
Asn Val Thr Tyr Glu Phe Gly Pro Gly Cys Gln Ile Leu Tyr Phe Ser
                               370                               375                               380

acg ggc aac tcg aga gac cac cac cat gct gtg cat ggc gcg gcg cac      1200
Thr Gly Asn Ser Arg Asp His His His Ala Val His Gly Ala Ala His
385                               390                               395                               400

tcg tgg act atg gag ctg agc ccc cag gac gcg gca gga ggc ggg ttt      1248
Ser Trp Thr Met Glu Leu Ser Pro Gln Asp Ala Ala Gly Gly Gly Phe
                               405                               410                               415

gtt ctg ccg cct gaa ctc att tgg ccg acg gtc aag gag cag tgg gcg      1296
Val Leu Pro Pro Glu Leu Ile Trp Pro Thr Val Lys Glu Gln Trp Ala
                               420                               425                               430

ggc cag ttg tgg ttg ttg aat gat gtt tgg gat aac      1332
Gly Gln Leu Trp Leu Leu Asn Asp Val Trp Asp Asn
                               435                               440

```

&lt;210&gt; 205

&lt;211&gt; 444

&lt;212&gt; PRT

&lt;213&gt; Cochliobolus heterostrophus strain C4 (ATCC 48331)

&lt;220&gt;

&lt;221&gt; DOMAIN

&lt;222&gt; (124)...(340)

&lt;223&gt; Zinc carboxypeptidase

&lt;400&gt; 205

```

Met Arg Leu Ser Lys Leu Val Val Ala Ala Gln Leu Ala Ala Ala Ser
 1      5      10      15
Pro Leu Ala His Asp Ala Ser Ser Val Ser Arg Ser Ala Asn Pro Ser
 20      25      30
Tyr Asp Gly Tyr Gln Ile Tyr Ser Ile Thr Pro Ser Ser Ala Glu Glu
 35      40      45
Ala His Asp Ile Asn Lys Arg Phe Ser Asn Tyr His Thr His Pro Ile
 50      55      60
Arg Asn Thr Leu Ser Val Ala Ile Pro Pro Glu Ile Asp Ser Phe
 65      70      75      80
Arg Ala Leu Gly Leu Asn Ala Arg Leu Val Asn Ser Asp Leu Gly Lys
 85      90      95
Tyr Ile Arg Ser Thr Asp Lys Glu Ala Val Tyr Lys Arg Asp Leu His
100      105      110
Ala Thr Gly Gln Leu Pro Asp Leu Ser Trp Phe Asp Thr Tyr His Ala
115      120      125
Tyr Ser Asp His Leu Gln Tyr Trp Asp Asp Leu Val Ala Ala Phe Pro
130      135      140
Gly Asn Ser Glu Lys Phe Ser Ile Gly Gln Ser Tyr Glu Asn Arg Thr

```

## 10336256.txt

```

145      150      155      160
Ile Trp Ala Phe His Leu Phe Gly Asp Lys Ser Thr Glu Ala Ala Thr
165      170      175
Gln Glu Lys Pro Ile Ile Leu Trp His Ala Thr Val His Ala Arg Glu
180      185      190
Trp Ile Ser Thr Met Val Ile Glu Tyr Leu Ala Tyr Gln Leu Ile Asp
195      200      205
Gly Tyr Gln Lys Gly Asp Ala Asn Val Thr Ser Phe Leu Asp His Tyr
210      215      220
Asp Phe Tyr Leu Val Pro Phe His Asn Pro Asp Gly Phe Ser Tyr Thr
225      230      235      240
Gln Thr Asn Asp Arg Leu Trp Arg Lys Asn Arg Gln Pro Arg Pro Gln
245      250      255
Leu Asn Thr Ala Cys Val Gly Thr Asp Gly Asn Arg Asn Trp Lys Phe
260      265      270
Glu Trp Asp Ala Thr Pro Pro Asp Gly Gly Ser Thr Pro Asn Pro Cys
275      280      285
Gly Glu Thr Tyr Arg Gly Glu Ala Ala Gly Asp Thr Pro Glu Asn Gln
290      295      300
Ala Met Asp Gly Leu Ser Ala Lys Leu Ser Ser Thr Gly Ala Gly Ile
305      310      315      320
Arg Ser Phe Ile Asp Phe His Ser Tyr Ser Gln Leu Ile Leu Thr Pro
325      330      335
Trp Gly Phe Ser Cys Asp Pro Leu Pro Glu Thr Leu Pro Arg Met Leu
340      345      350
Glu Val Ala Gly Gly Thr Ala Arg Ala Ile Gln Ala Gly Ser Ala Arg
355      360      365
Asn Val Thr Tyr Glu Phe Gly Pro Gly Cys Gln Ile Leu Tyr Phe Ser
370      375      380
Thr Gly Asn Ser Arg Asp His His His Ala Val His Gly Ala Ala His
385      390      395      400
Ser Trp Thr Met Glu Leu Ser Pro Gln Asp Ala Ala Gly Gly Gly Phe
405      410      415
Val Leu Pro Pro Glu Leu Ile Trp Pro Thr Val Lys Glu Gln Trp Ala
420      425      430
Gly Gln Leu Trp Leu Leu Asn Asp Val Trp Asp Asn
435      440

```

<210> 206  
 <211> 3999  
 <212> DNA  
 <213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<220>  
 <221> CDS  
 <222> (1265)...(1549)  
 <223> Exon

<221> CDS  
 <222> (1609)...(1950)  
 <223> Exon

<221> CDS  
 <222> (2001)...(2999)  
 <223> Exon

<221> misc\_feature  
 <222> (1)...(3999)  
 <223> n = A,T,C or G

```

<400> 206
cgtgccgagc gtttacttct tttttcctga gccaaaggga cgcagtttgg aggagctgga      60
tgtcattttt gcgagtgcga atcagatggg ggtagtcct gtgaagagag cgagggagat      120
ggagaagctg gtggggaggg agttggatga ggagattgag agattttttg ggggtgatgt      180
ggaggagggt aggcggagga gcagagcttg agaggtggat tggaattttc gatgtgtagg      240
cacgcgtgca ggttgattgt cgtgattttg acgtggcctt gggcggtact ttttttcattg      300
cactctgccg gtgtagggtg tgcccggcca tcttgacacg agtttccggt caacagcaag      360
gttgtagcga gacggcctaa gttgggaaca tcaaattccat gcagcacgag ttgtactgca      420

```

## 10336256.txt

aatccaataa caccctatcg cgatgatcga tagatggcga cctgccgact gcagctagcg 480  
ttacacaccg gcaatatcga tgtcgcgggg ggctgggtgc ctcattctcc tcttttgcaa 540  
cgggtccaaaa cgccacaacg ctttcaacta cgccccaacc tccagattgg gggtacaact 600  
atgacgttga taagctttcc tcgggtcaac gaacgacttg gcaagaggcc ttattccacc 660  
attgcgcata gcgagcttct tgtttgggta aggtgtgtga tttgatgtgc gtagactact 720  
cggacctcat tggagaaaac acacacaaat cgtcactctc tttcatcgat ggaaaaacac 780  
gccttagaca gcagtttcga tggctgaaaa attgcggcat aggttgcatc tttgactcga 840  
tgccttttgt cctaagccat aattagtaac cgggtgataca aaatccaacc gcggcaaaca 900  
agttgtattt ctgaaagctc ttactagtat tgtcgcctta acgcggaact cgcaagatct 960  
tcatactcgt gttatcccgg ccaattgcaa tgaccagtac tactttgcag ttgcctgatt 1020  
cggattaaac ctacctgcac tggcctaccc acagatcgca tttggcctca catggagcca 1080  
gcccgccatg cagtgtcag ccatggcagg cggaaagaaa tgtacatagc cgcatcattg 1140  
catgttgtaa aacggcttag cctcgtacgc attcagtgtg ttaagaagg ccgagagaag 1200  
cggccttctc ggcaagcccg ctgcttaagc cttggtcatt cttcttcacg acaagctatt 1260  
cacc atg gcg cgc ttc acc cag att gtt gct gtc ttg gca gca gcg acg 1309  
Met Ala Arg Phe Thr Gln Ile Val Ala Val Leu Ala Ala Ala Thr  
1 5 10 15  
ctc agt cat gct cgc aag cca ttc atc act gag cgt cag gtc ccg gct 1357  
Leu Ser His Ala Arg Lys Pro Phe Ile Thr Glu Arg Gln Val Pro Ala  
20 25 30  
gac ccc act ggc gtc aca acc atc aag tct gct cag ggt gcc gag att 1405  
Asp Pro Thr Gly Val Thr Thr Ile Lys Ser Ala Gln Gly Ala Glu Ile  
35 40 45  
cgc tac aag cag cct gga aag gcg gga gtt tgc gag act act gaa ggt 1453  
Arg Tyr Lys Gln Pro Gly Lys Ala Gly Val Cys Glu Thr Thr Glu Gly  
50 55 60  
gtt gac gat tat gcc ggt tac atc agt ctc aat cct act acc aac atg 1501  
Val Asp Asp Tyr Ala Gly Tyr Ile Ser Leu Asn Pro Thr Thr Asn Met  
65 70 75  
ttc ttt tgg ttc ttc gag gcg cgt gaa aac ccc tcc gaa aag ccg ttg 1549  
Phe Phe Trp Phe Phe Glu Ala Arg Glu Asn Pro Ser Glu Lys Pro Leu  
80 85 90 95  
gcaagtacaa cctatatattc agctcagaat tcggtagcag attctaactt tgtttccag 1608  
aca ctt tgg ttg aat ggt gga cca gga agt gac tcg ctc atc ggt ctc 1656  
Thr Leu Trp Leu Asn Gly Gly Pro Gly Ser Asp Ser Leu Ile Gly Leu  
100 105 110  
ttc caa gaa cac ggc cca tgt aat gtc act gag gat ttg aag aca caa 1704  
Phe Gln Glu His Gly Pro Cys Asn Val Thr Glu Asp Leu Lys Thr Gln  
115 120 125  
ttg aat cct tat tca tgg aac gag cac agc aac atg ctc tac ctc tcg 1752  
Leu Asn Pro Tyr Ser Trp Asn Glu His Ser Asn Met Leu Tyr Leu Ser  
130 135 140  
cag cct gtt ggt gta ggc ttc tcc tac gag acc aca gaa acc gac gcg 1800  
Gln Pro Val Gly Val Gly Phe Ser Tyr Glu Thr Thr Glu Thr Asp Ala  
145 150 155  
gac ggt cga tac tcg ctt gtt gat ccc gat acc aca aac act acc gat 1848  
Asp Gly Arg Tyr Ser Leu Val Asp Pro Asp Thr Thr Asn Thr Thr Asp  
160 165 170  
gct gca gcc atc ggt gcg tgg cac att ctc cag gct ttc ttg gac ctg 1896  
Ala Ala Ala Ile Gly Ala Trp His Ile Leu Gln Ala Phe Leu Asp Leu  
180 185 190  
agc ccc cag ctc gac ccg gat atc act aac ttt aca ttc aat ctt tgg 1944  
Ser Pro Gln Leu Asp Pro Asp Ile Thr Asn Phe Thr Phe Asn Leu Trp  
195 200 205  
act gag aggttagtga ttcagcaaca agactgaaaa cgtattgctc accagtttct 2000

10336256.txt

Thr Glu

agc Ser 210	tac Tyr	gga Gly	gga Gly	cat His	tac Tyr 215	ggc Gly	ccc Pro	ggt Gly	ttc Phe	tac Tyr 220	aac Asn	tac Tyr	ttc Phe	tac Tyr	caa Gln 225	2048
caa Gln	aat Asn	gag Glu	aag Lys	atc Ile 230	aag Lys	aac Asn	ggc Gly	tct Ser	tcc Ser 235	cct Pro	ggt Gly	gtc Val	gag Glu	att Ile 240	cgc Arg	2096
atg Met	gac Asp	act Thr	ctc Leu 245	ggt Gly	ata Ile	atc Ile	aac Asn	gga Gly 250	att Ile	gtc Val	gat Asp	gag Glu	cag Gln 255	atc Ile	cag Gln	2144
gcc Ala	cct Pro	tac Tyr 260	tac Tyr	ccc Pro	gag Glu	ttt Phe	gct Ala 265	gtc Val	aac Asn	aac Asn	acc Thr	tat Tyr 270	ggc Gly	atc Ile	aaa Lys	2192
gca Ala	gtt Val 275	aac Asn	gac Asp	acg Thr	gtt Val	tac Tyr 280	act Thr	ttc Phe	atg Met	aag Lys	aac Asn 285	gcc Ala	tac Tyr	tac Tyr	atg Met	2240
cca Pro 290	gaa Glu	ggc Gly	tgc Cys	cac His	gat Asp 295	caa Gln	atc Ile	gaa Glu	tac Tyr	tgc Cys 300	aag Lys	caa Gln	tcc Ser	gac Asp	cgc Arg 305	2288
acc Thr	acc Thr	caa Gln	gac Asp	ggc Gly 310	tat Tyr	cta Leu	act Thr	tgt Cys	tca Ser 315	tcc Ser	gca Ala	acc Thr	aac Asn	ctc Leu 320	tgc Cys	2336
cga Arg	tcg Ser	ctc Leu	gtc Val 325	gaa Glu	gag Glu	cca Pro	tat Tyr	tac Tyr 330	gca Ala	ttt Phe	ggc Gly	ggg Gly	cgt Arg 335	ggc Gly	gtc Val	2384
tac Tyr	gac Asp	atc Ile 340	cgc Arg	cat His	ccc Pro	tac Tyr	gac Asp 345	gac Asp	cct Pro	acg Thr	ccc Pro	ccc Pro 350	gac Asp	tat Tyr	ttc Phe	2432
gag Glu 355	tcc Ser	ttc Phe	ctg Leu	aac Asn	ctg Leu	gcc Ala 360	tca Ser	acc Thr	caa Gln	gaa Glu	gcc Ala 365	atc Ile	ggc Gly	gta Val	aac Asn	2480
atc Ile 370	aac Asn	tac Tyr	acg Thr	agc Ser	acc Thr 375	aac Asn	gcc Ala	cgc Arg	aac Asn	gtg Val 380	tcc Ser	ctc Leu	ggc Gly	ttc Phe	agt Ser 385	2528
cgc Arg	acc Thr	ggc Gly	gac Asp	ttc Phe 390	gtc Val	ttc Phe	ccc Pro	aac Asn	ttc Phe 395	ctc Leu	gag Glu	gac Asp	ctc Leu	gaa Glu 400	gaa Glu	2576
atc Ile	ctc Leu	gcc Ala	tac Tyr 405	ggc Gly	gtc Val	cgc Arg	gtc Val	gcc Ala 410	ctc Leu	ctc Leu	tac Tyr	ggc Gly 415	gac Asp	gca Ala	gac Asp	2624
tac Tyr	atc Ile	tgc Cys 420	aac Asn	tgg Trp	ttc Phe	ggc Gly	ggc Gly 425	gaa Glu	gcc Ala	gtc Val	tct Ser	ctg Leu 430	gcc Ala	gtc Val	aac Asn	2672
ttc Phe 435	acg Thr	cac His	gcc Ala	gcc Ala	gac Asp	ttc Phe 440	cgc Arg	tcc Ser	gcg Ala	ggc Gly	tac Tyr 445	acg Thr	ccc Pro	ttt Phe	ctc Leu	2720
gtt Val 450	gac Asp	ggc Gly	gtc Val	gag Glu	tac Tyr 455	ggc Gly	gag Glu	gtg Val	cgc Arg	gag Glu 460	tac Tyr	ggc Gly	aac Asn	ttc Phe	tcc Ser 465	2768
ttc acc	acc cgc	atc tac	gag gag	gcc gag	ggc cac	gag gag	gtc gtc	ccg tat	tac tac	cag cct						2816

10336256.txt

```

Phe Thr Arg Ile Tyr Glu Ala Gly His Glu Val Pro Tyr Tyr Gln Pro
      470      475      480
gaa gct agt ctg gag cat ttt agg cgc gtc ctg cat cat gtc gtt gtt 2864
Glu Ala Ser Leu Glu His Phe Arg Arg Val Leu His His Val Val Val
      485      490      495
gcg gat ggg agc cag gtg gtc acg agt gat tac aag acg aat ggc acc 2912
Ala Asp Gly Ser Gln Val Val Thr Ser Asp Tyr Lys Thr Asn Gly Thr
      500      505      510
gcc aag gcg acg cat aca gag gag ttt gtc ccg ttg ccg ccg acg agt 2960
Ala Lys Ala Thr His Thr Glu Glu Phe Val Pro Leu Pro Pro Thr Ser
      515      520      525
acg ccg agt gct gct agt agg gtg agg agg gga tcg gtg tagattggcc 3009
Thr Pro Ser Ala Ala Ser Arg Val Arg Arg Gly Ser Val
      530      535      540
gtggggggcgg tgagacgggt gatgaagttt agagccttgt gtgaggcatt gatgtatgac 3069
gttaatgact tgaaatgaaa gtaattgaat catgagttca gaggaataac tgcttgtcta 3129
ctgttataag acgtctgaaa tgagtaggtt tgaccctttt accatttgca caatcttttc 3189
tttcgtgtgc acattgcttt ttgtaaactt gttttggctt tcttttaaga gtatcacgcc 3249
ttgttgccga ctgtaccgac gcgtttactt ggcaaatgaa agtcgtttcg aggaaagcta 3309
gggtccgattg attactgttt acttcccttt ccgatcgttc tggatnnnnn nnnnnnnnnn 3369
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 3429
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 3489
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 3549
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnncccccac 3609
caaactcaca cacctctccc atcttatcat acaatggctc aacgcagcgc tactctatta 3669
gcttcaaatg aattagatat tcagcttgcg atctctttaa ttaattctaa gcagattcta 3729
agtaatcgga gtgctgtgct tatctacaac gtgtttaaat gaacgatccg ccgccaacgc 3789
gctggtgtcc ctgcgcgacg tgattgccag cctaacttaa agaagctaac ctagctagaa 3849
gaggaggtaa ttgttagcta tatactcaat ctagattagc gtggattcgc gcctacgtac 3909
gcagccgtgc gcgatatagc taataagctg ctagctacgc gtagtagagg acgcgttaga 3969
gttaactagc cgtctacctt tattaagcgt

```

&lt;210&gt; 207

&lt;211&gt; 95

&lt;212&gt; PRT

&lt;213&gt; Cochliobolus heterostrophus strain C4 (ATCC 48331)

&lt;400&gt; 207

```

Met Ala Arg Phe Thr Gln Ile Val Ala Val Leu Ala Ala Ala Thr Leu
 1      5      10      15
Ser His Ala Arg Lys Pro Phe Ile Thr Glu Arg Gln Val Pro Ala Asp
      20      25      30
Pro Thr Gly Val Thr Thr Ile Lys Ser Ala Gln Gly Ala Glu Ile Arg
      35      40      45
Tyr Lys Gln Pro Gly Lys Ala Gly Val Cys Glu Thr Thr Glu Gly Val
      50      55      60
Asp Asp Tyr Ala Gly Tyr Ile Ser Leu Asn Pro Thr Thr Asn Met Phe
      65      70      75      80
Phe Trp Phe Phe Glu Ala Arg Glu Asn Pro Ser Glu Lys Pro Leu
      85      90      95

```

&lt;210&gt; 208

&lt;211&gt; 114

&lt;212&gt; PRT

&lt;213&gt; Cochliobolus heterostrophus strain C4 (ATCC 48331)

&lt;400&gt; 208

```

Thr Leu Trp Leu Asn Gly Gly Pro Gly Ser Asp Ser Leu Ile Gly Leu
 1      5      10      15
Phe Gln Glu His Gly Pro Cys Asn Val Thr Glu Asp Leu Lys Thr Gln
      20      25      30
Leu Asn Pro Tyr Ser Trp Asn Glu His Ser Asn Met Leu Tyr Leu Ser
      35      40      45

```

10336256.txt

Gln Pro Val Gly Val Gly Phe Ser Tyr Glu Thr Thr Glu Thr Asp Ala  
 50 55 60  
 Asp Gly Arg Tyr Ser Leu Val Asp Pro Asp Thr Thr Asn Thr Thr Asp  
 65 70 75 80  
 Ala Ala Ala Ile Gly Ala Trp His Ile Leu Gln Ala Phe Leu Asp Leu  
 85 90 95  
 Ser Pro Gln Leu Asp Pro Asp Ile Thr Asn Phe Thr Phe Asn Leu Trp  
 100 105 110  
 Thr Glu

&lt;210&gt; 209

&lt;211&gt; 333

&lt;212&gt; PRT

&lt;213&gt; Cochliobolus heterostrophus strain C4 (ATCC 48331)

&lt;400&gt; 209

Ser Tyr Gly Gly His Tyr Gly Pro Gly Phe Tyr Asn Tyr Phe Tyr Gln  
 1 5 10 15  
 Gln Asn Glu Lys Ile Lys Asn Gly Ser Ser Pro Gly Val Glu Ile Arg  
 20 25 30  
 Met Asp Thr Leu Gly Ile Ile Asn Gly Ile Val Asp Glu Gln Ile Gln  
 35 40 45  
 Ala Pro Tyr Tyr Pro Glu Phe Ala Val Asn Asn Thr Tyr Gly Ile Lys  
 50 55 60  
 Ala Val Asn Asp Thr Val Tyr Thr Phe Met Lys Asn Ala Tyr Tyr Met  
 65 70 75 80  
 Pro Glu Gly Cys His Asp Gln Ile Glu Tyr Cys Lys Gln Ser Asp Arg  
 85 90 95  
 Thr Thr Gln Asp Gly Tyr Leu Thr Cys Ser Ser Ala Thr Asn Leu Cys  
 100 105 110  
 Arg Ser Leu Val Glu Glu Pro Tyr Tyr Ala Phe Gly Gly Arg Gly Val  
 115 120 125  
 Tyr Asp Ile Arg His Pro Tyr Asp Asp Pro Thr Pro Pro Asp Tyr Phe  
 130 135 140  
 Glu Ser Phe Leu Asn Leu Ala Ser Thr Gln Glu Ala Ile Gly Val Asn  
 145 150 155 160  
 Ile Asn Tyr Thr Ser Thr Asn Ala Arg Asn Val Ser Leu Gly Phe Ser  
 165 170 175  
 Arg Thr Gly Asp Phe Val Phe Pro Asn Phe Leu Glu Asp Leu Glu Glu  
 180 185 190  
 Ile Leu Ala Tyr Gly Val Arg Val Ala Leu Leu Tyr Gly Asp Ala Asp  
 195 200 205  
 Tyr Ile Cys Asn Trp Phe Gly Gly Glu Ala Val Ser Leu Ala Val Asn  
 210 215 220  
 Phe Thr His Ala Ala Asp Phe Arg Ser Ala Gly Tyr Thr Pro Phe Leu  
 225 230 235 240  
 Val Asp Gly Val Glu Tyr Gly Glu Val Arg Glu Tyr Gly Asn Phe Ser  
 245 250 255  
 Phe Thr Arg Ile Tyr Glu Ala Gly His Glu Val Pro Tyr Tyr Gln Pro  
 260 265 270  
 Glu Ala Ser Leu Glu His Phe Arg Arg Val Leu His His Val Val Val  
 275 280 285  
 Ala Asp Gly Ser Gln Val Val Thr Ser Asp Tyr Lys Thr Asn Gly Thr  
 290 295 300  
 Ala Lys Ala Thr His Thr Glu Glu Phe Val Pro Leu Pro Pro Thr Ser  
 305 310 315 320  
 Thr Pro Ser Ala Ala Ser Arg Val Arg Arg Gly Ser Val  
 325 330

&lt;210&gt; 210

&lt;211&gt; 1626

&lt;212&gt; DNA

&lt;213&gt; Cochliobolus heterostrophus strain C4 (ATCC 48331)

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1626)

## 10336256.txt

<400> 210  
 atg gcg cgc ttc acc cag att gtt gct gtc ttg gca gca gcg acg ctc 48  
 Met Ala Arg Phe Thr 5 Gln Ile Val Ala Val 10 Leu Ala Ala Ala Thr 15 Leu

agt cat gct cgc aag cca ttc atc act gag cgt cag gtc ccg gct gac 96  
 Ser His Ala Arg 20 Lys Pro Phe Ile Thr 25 Glu Arg Gln Val 30 Pro Ala Asp

ccc act ggc gtc aca acc atc aag tct gct cag ggt gcc gag att cgc 144  
 Pro Thr Gly Val Thr Thr Ile Lys 40 Ser Ala Gln Gly Ala 45 Glu Ile Arg

tac aag cag cct gga aag gcg gga gtt tgc gag act act gaa ggt gtt 192  
 Tyr Lys 50 Gln Pro Gly Lys Ala 55 Gly Val Cys Glu Thr 60 Thr Glu Gly Val

gac gat tat gcc ggt tac atc agt ctc aat cct act acc aac atg ttc 240  
 Asp Asp Tyr Ala Gly Tyr 70 Ile Ser Leu Asn Pro 75 Thr Thr Asn Met Phe 80

ttt tgg ttc ttc gag gcg cgt gaa aac ccc tcc gaa aag ccg ttg aca 288  
 Phe Trp Phe Phe Glu 85 Ala Arg Glu Asn Pro 90 Ser Glu Lys Pro Leu Thr 95

ctt tgg ttg aat ggt gga cca gga agt gac tcg ctc atc ggt ctc ttc 336  
 Leu Trp Leu Asn 100 Gly Gly Pro Gly Ser 105 Asp Ser Leu Ile Gly 110 Leu Phe

caa gaa cac ggc cca tgt aat gtc act gag gat ttg aag aca caa ttg 384  
 Gln Glu His 115 Gly Pro Cys Asn Val 120 Thr Glu Asp Leu Lys 125 Thr Gln Leu

aat cct tat tca tgg aac gag cac agc aac atg ctc tac ctc tcg cag 432  
 Asn Pro 130 Tyr Ser Trp Asn Glu 135 His Ser Asn Met 140 Tyr Leu Ser Gln

cct gtt ggt gta ggc ttc tcc tac gag acc aca gaa acc gac gcg gac 480  
 Pro Val Gly Val Gly Phe 150 Ser Tyr Glu Thr 155 Glu Thr Asp Ala Asp 160

ggt cga tac tcg ctt gtt gat ccc gat acc aca aac act acc gat gct 528  
 Gly Arg Tyr Ser Leu 165 Val Asp Pro Asp Thr 170 Thr Asn Thr Thr Asp 175 Ala

gca gcc atc ggt gcg tgg cac att ctc cag gct ttc ttg gac ctg agc 576  
 Ala Ala Ile Gly Ala Trp His Ile Leu 185 Gln Ala Phe Leu 190 Asp Leu Ser

ccc cag ctc gac ccg gat atc act aac ttt aca ttc aat ctt tgg act 624  
 Pro Gln Leu 195 Asp Pro Asp Ile Thr 200 Asn Phe Thr Phe 205 Asn Leu Trp Thr

gag agc tac gga gga cat tac ggc ccc ggt ttc tac aac tac ttc tac 672  
 Glu Ser 210 Tyr Gly Gly His Tyr 215 Gly Pro Gly Phe Tyr 220 Asn Tyr Phe Tyr

caa caa aat gag aag atc aag aac ggc tct tcc cct ggt gtc gag att 720  
 Gln Gln Asn Glu Lys 230 Ile Lys Asn Gly Ser 235 Pro Gly Val Glu Ile 240

cgc atg gac act ctc ggt ata atc aac gga att gtc gat gag cag atc 768  
 Arg Met Asp Thr 245 Gly Ile Ile Asn Gly 250 Ile Val Asp Glu Gln 255 Ile

cag gcc cct tac tac ccc gag ttt gct gtc aac aac acc tat ggc atc 816  
 Gln Ala Pro Tyr Tyr Pro Glu Phe Ala Val Asn Asn Thr Tyr Gly Ile

10336256.txt																
260						265						270				
aaa Lys	gca Ala	gtt Val 275	aac Asn	gac Asp	acg Thr	gtt Val	tac Tyr 280	act Thr	ttc Phe	atg Met	aag Lys	aac Asn 285	gcc Ala	tac Tyr	tac Tyr	864
atg Met	cca Pro 290	gaa Glu	ggc Gly	tgc Cys	cac His	gat Asp 295	caa Gln	atc Ile	gaa Glu	tac Tyr	tgc Cys 300	aag Lys	caa Gln	tcc Ser	gac Asp	912
cgc Arg 305	acc Thr	acc Thr	caa Gln	gac Asp	ggc Gly 310	tat Tyr	cta Leu	act Thr	tgt Cys	tca Ser 315	tcc Ser	gca Ala	acc Thr	aac Asn	ctc Leu 320	960
tgc Cys	cga Arg	tcg Ser	ctc Leu	gtc Val 325	gaa Glu	gag Glu	cca Pro	tat Tyr	tac Tyr 330	gca Ala	ttt Phe	ggc Gly	ggg Gly	cgt Arg 335	ggc Gly	1008
gtc Val	tac Tyr	gac Asp	atc Ile 340	cgc Arg	cat His	ccc Pro	tac Tyr	gac Asp 345	gac Asp	cct Pro	acg Thr	ccc Pro	ccc Pro 350	gac Asp	tat Tyr	1056
ttc Phe	gag Glu	tcc Ser 355	ttc Phe	ctg Leu	aac Asn	ctg Leu	gcc Ala 360	tca Ser	acc Thr	caa Gln	gaa Glu	gcc Ala 365	atc Ile	ggc Gly	gta Val	1104
aac Asn	atc Ile 370	aac Asn	tac Tyr	acg Thr	agc Ser	acc Thr 375	aac Asn	gcc Ala	cgc Arg	aac Asn	gtg Val 380	tcc Ser	ctc Leu	ggc Gly	ttc Phe	1152
agt Ser 385	cgc Arg	acc Thr	ggc Gly	gac Asp	ttc Phe 390	gtc Val	ttc Phe	ccc Pro	aac Asn	ttc Phe 395	ctc Leu	gag Glu	gac Asp	ctc Leu	gaa Glu 400	1200
gaa Glu	atc Ile	ctc Leu	gcc Ala	tac Tyr 405	ggc Gly	gtc Val	cgc Arg	gtc Val	gcc Ala 410	ctc Leu	ctc Leu	tac Tyr	ggc Gly	gac Asp 415	gca Ala	1248
gac Asp	tac Tyr	atc Ile	tgc Cys 420	aac Asn	tgg Trp	ttc Phe	ggc Gly	ggc Gly 425	gaa Glu	gcc Ala	gtc Val	tct Ser	ctg Leu 430	gcc Ala	gtc Val	1296
aac Asn	ttc Phe	acg Thr 435	cac His	gcc Ala	gcc Ala	gac Asp	ttc Phe 440	cgc Arg	tcc Ser	gcg Ala	ggc Gly	tac Tyr 445	acg Thr	ccc Pro	ttt Phe	1344
ctc Leu	gtt Val 450	gac Asp	ggc Gly	gtc Val	gag Glu	tac Tyr 455	ggc Gly	gag Glu	gtg Val	cgc Arg	gag Glu 460	tac Tyr	ggc Gly	aat Asn	ttc Phe	1392
tcc Ser 465	ttc Phe	acc Thr	cgc Arg	atc Ile	tac Tyr 470	gag Glu	gcc Ala	ggc Gly	cac His	gag Glu 475	gtc Val	ccg Pro	tat Tyr	tac Tyr	cag Gln 480	1440
cct Pro	gaa Glu	gct Ala	agt Ser	ctg Leu 485	gag Glu	cat His	ttt Phe	agg Arg	cgc Arg 490	gtc Val	ctg Leu	cat His	cat His	gtc Val 495	gtt Val	1488
gtt Val	gcg Ala	gat Asp	ggg Gly 500	agc Ser	cag Gln	gtg Val	gtc Val	acg Thr 505	agt Ser	gat Asp	tac Tyr	aag Lys	acg Thr 510	aat Asn	ggc Gly	1536
acc Thr	gcc Ala	aag Lys 515	gcg Ala	acg Thr	cat His	aca Thr	gag Glu 520	gag Glu	ttt Phe	gtc Val	ccg Pro	ttg Leu 525	ccg Pro	ccg Pro	acg Thr	1584
agt Ser	acg Thr	ccg Pro	agt Ser	gct Ala	gct Ala	agt Ser	agg Arg	gtg Val	agg Arg	agg Arg	gga Gly	tcg Ser	gtg Val			1626

530

535

10336256.txt  
540

<210> 211  
 <211> 542  
 <212> PRT  
 <213> Cochliobolus heterostrophus strain C4 (ATCC 48331)

<220>  
 <221> SIGNAL  
 <222> (1)...(19)

<221> DOMAIN  
 <222> (52)...(494)  
 <223> Serine carboxypeptidase

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 Pro Thr Gly Val Thr Thr Ile Lys Ser Ala Gln Gly Ala Glu Ile Arg  
 35 40 45  
 Tyr Lys Gln Pro Gly Lys Ala Gly Val Cys Glu Thr Thr Glu Gly Val  
 50 55 60  
 Asp Asp Tyr Ala Gly Tyr Ile Ser Leu Asn Pro Thr Thr Asn Met Phe  
 65 70 75 80  
 Phe Trp Phe Phe Glu Ala Arg Glu Asn Pro Ser Glu Lys Pro Leu Thr  
 85 90 95  
 Leu Trp Leu Asn Gly Gly Pro Gly Ser Asp Ser Leu Ile Gly Leu Phe  
 100 105 110  
 Gln Glu His Gly Pro Cys Asn Val Thr Glu Asp Leu Lys Thr Gln Leu  
 115 120 125  
 Asn Pro Tyr Ser Trp Asn Glu His Ser Asn Met Leu Tyr Leu Ser Gln  
 130 135 140  
 Pro Val Gly Val Gly Phe Ser Tyr Glu Thr Thr Glu Thr Asp Ala Asp  
 145 150 155 160  
 Gly Arg Tyr Ser Leu Val Asp Pro Asp Thr Thr Asn Thr Thr Asp Ala  
 165 170 175  
 Ala Ala Ile Gly Ala Trp His Ile Leu Gln Ala Phe Leu Asp Leu Ser  
 180 185 190  
 Pro Gln Leu Asp Pro Asp Ile Thr Asn Phe Thr Phe Asn Leu Trp Thr  
 195 200 205  
 Glu Ser Tyr Gly Gly His Tyr Gly Pro Gly Phe Tyr Asn Tyr Phe Tyr  
 210 215 220  
 Gln Gln Asn Glu Lys Ile Lys Asn Gly Ser Ser Pro Gly Val Glu Ile  
 225 230 235 240  
 Arg Met Asp Thr Leu Gly Ile Ile Asn Gly Ile Val Asp Glu Gln Ile  
 245 250 255  
 Gln Ala Pro Tyr Tyr Pro Glu Phe Ala Val Asn Asn Thr Tyr Gly Ile  
 260 265 270  
 Lys Ala Val Asn Asp Thr Val Tyr Thr Phe Met Lys Asn Ala Tyr Tyr  
 275 280 285  
 Met Pro Glu Gly Cys His Asp Gln Ile Glu Tyr Cys Lys Gln Ser Asp  
 290 295 300  
 Arg Thr Thr Gln Asp Gly Tyr Leu Thr Cys Ser Ser Ala Thr Asn Leu  
 305 310 315 320  
 Cys Arg Ser Leu Val Glu Glu Pro Tyr Tyr Ala Phe Gly Gly Arg Gly  
 325 330 335  
 Val Tyr Asp Ile Arg His Pro Tyr Asp Asp Pro Thr Pro Pro Asp Tyr  
 340 345 350  
 Phe Glu Ser Phe Leu Asn Leu Ala Ser Thr Gln Glu Ala Ile Gly Val  
 355 360 365  
 Asn Ile Asn Tyr Thr Ser Thr Asn Ala Arg Asn Val Ser Leu Gly Phe  
 370 375 380  
 Ser Arg Thr Gly Asp Phe Val Phe Pro Asn Phe Leu Glu Asp Leu Glu  
 385 390 395 400  
 Glu Ile Leu Ala Tyr Gly Val Arg Val Ala Leu Leu Tyr Gly Asp Ala

## 10336256.txt

Asp Tyr Ile Cys Asn Trp Phe Gly Gly Glu Ala Val Ser Leu Ala Val  
 405 410 415  
 Asn Phe Thr His Ala Ala Asp Phe Arg Ser Ala Gly Tyr Thr Pro Phe  
 420 425 430  
 Leu Val Asp Gly Val Glu Tyr Gly Glu Val Arg Glu Tyr Gly Asn Phe  
 435 440 445  
 Ser Phe Thr Arg Ile Tyr Glu Ala Gly His Glu Val Pro Tyr Tyr Gln  
 450 455 460  
 Pro Glu Ala Ser Leu Glu His Phe Arg Arg Val Leu His His Val Val  
 465 470 475  
 Val Ala Asp Gly Ser Gln Val Val Thr Ser Asp Tyr Lys Thr Asn Gly  
 480 485 490 495  
 Thr Ala Lys Ala Thr His Thr Glu Glu Phe Val Pro Leu Pro Pro Thr  
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 Ser Thr Pro Ser Ala Ala Ser Arg Val Arg Arg Gly Ser Val  
 515 520 525 530 535 540

&lt;210&gt; 212

&lt;211&gt; 4330

&lt;212&gt; DNA

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (861)...(1172)

&lt;223&gt; Exon

&lt;221&gt; CDS

&lt;222&gt; (1222)...(1461)

&lt;223&gt; Exon

&lt;221&gt; CDS

&lt;222&gt; (1520)...(1714)

&lt;223&gt; Exon

&lt;221&gt; CDS

&lt;222&gt; (1768)...(1931)

&lt;223&gt; Exon

&lt;221&gt; CDS

&lt;222&gt; (2000)...(2330)

&lt;223&gt; Exon

&lt;400&gt; 212

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tgcatgcctg	tctaccactt	ggcggccgcc	ttccaatgat	ctccttccc	tttcagctca	300
tcgcttcgaa	ccagctatgc	ccttgctaca	ctgcatcggg	tcgactagtt	gcccatacag	360
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gccaatcatgc	tctccgagaa	ttccggggccc	tacacctgcc	taaccgggta	agcacatacg	480
actccggacc	aatcatcttg	ttcgcgcccc	cgtctctcct	ccagcgcgcc	aagtgattcc	540
ataaattaat	cctccatcca	tggcccaggc	gtttactccg	acctccttcg	aatgaccatc	600
tcccgcgctt	gtaaggccta	tcttggtctt	cttattcgag	tgcacatctc	ccgttcgtgc	660
agacgactac	cacgaaactg	gggtacctgc	ctattccata	caatttcgat	taagagacag	720
ggacatgtcg	gccatgctac	ttgacaggaa	ggtagatcgt	aactagggtat	gactatggag	780
aagcataaaa	agcagcgctc	cccacggcct	gtattacgtt	gcaccttgct	tctacagagt	840
cagtgtctcc	atctctcatc	atg aag act act atc ttt acc tcc gcc ctt ctc				893

Met Lys Thr Thr Ile Phe Thr Ser Ala Leu Leu  
 1 5 10

ctt ggc tcc act gcc ttg ggc agc gct gtc cca acc gct ggc aag aag	941
Leu Gly Ser Thr Ala Leu Gly Ser Ala Val Pro Thr Ala Gly Lys Lys	
15 20 25	

gtc gat tac aat ggc ttc aag gtc ctg cgc gtt tct agc acc gac gct	989
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10336256.txt

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Val	Lys	Ser	Gln	Ile	Glu	Asn	Leu	Ala	Ala	His	Ile	Leu	Asn	Pro	Gly		
	45					50					55						
aag	tct	gcc	gag	atg	gat	gta	gtt	gtt	gca	ccc	gaa	aac	gtt	gcg	gca	1085	
Lys	Ser	Ala	Glu	Met	Asp	Val	Val	Val	Ala	Pro	Glu	Asn	Val	Ala	Ala		
	60				65					70					75		
ttg	act	gcg	ttg	gct	tcc	gag	agc	aag	gtc	atc	aat	gag	gat	gtt	ggc	1133	
Leu	Thr	Ala	Leu	Ala	Ser	Glu	Ser	Lys	Val	Ile	Asn	Glu	Asp	Val	Gly		
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gct	gcc	ctc	aag	gaa	gaa	ggc	gag	atg	gga	atc	tac	gct	ggtttgtaat			1182	
Ala	Ala	Leu	Lys	Glu	Glu	Gly	Glu	Met	Gly	Ile	Tyr	Ala					
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tggtctcaata	tcttcgaggt	tacacactca	ccgaatata	ggt	ccc	agc	gag	tcg								1236	
				Val	Pro	Ser	Glu	Ser									
								105									
tggttc	aca	gca	tac	cac	cca	tat	gcc	gat	cat	ctt	caa	ttc	ctc	cgc		1284	
Trp	Phe	Thr	Ala	Tyr	His	Pro	Tyr	Ala	Asp	His	Leu	Gln	Phe	Leu	Arg		
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gat	ctg	caa	gcc	ggc	tac	act	agc	aat	tcc	gag	att	gtc	acc	ctt	ggc	1332	
Asp	Leu	Gln	Ala	Gly	Tyr	Thr	Ser	Asn	Ser	Glu	Ile	Val	Thr	Leu	Gly		
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aac	tca	gtc	caa	gga	cgt	acc	ttg	act	ggc	atc	cat	atc	tgg	ggc	agc	1380	
Asn	Ser	Val	Gln	Gly	Arg	Thr	Leu	Thr	Gly	Ile	His	Ile	Trp	Gly	Ser		
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ggc	ggc	aag	gga	tcc	aag	cct	gcc	gtt	att	atc	cac	gga	aac	gtt	cac	1428	
Gly	Gly	Lys	Gly	Ser	Lys	Pro	Ala	Val	Ile	Ile	His	Gly	Asn	Val	His		
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gcc	cga	gag	tgg	atc	act	tcc	atg	acc	act	gag	taagccaccc	tgctatgaga				1481	
Ala	Arg	Glu	Trp	Ile	Thr	Ser	Met	Thr	Thr	Glu							
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ttattattga	aaaaaaacaa	gctaattctcc	acctcagg	tac	ttc	gcg	tgg	caa	ctt							1537	
				Tyr	Phe	Ala	Trp	Gln	Leu								
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cta	acc	aag	tac	gcc	tcc	gac	tca	agc	gtc	aag	gct	ctc	gtc	gac	aag	1585	
Leu	Thr	Lys	Tyr	Ala	Ser	Asp	Ser	Ser	Val	Lys	Ala	Leu	Val	Asp	Lys		
				195					200					205			
ttc	gac	ttt	tac	atc	acc	ccc	atc	gtc	aac	ccc	gac	gga	ttc	gtc	tac	1633	
Phe	Asp	Phe	Tyr	Ile	Thr	Pro	Ile	Val	Asn	Pro	Asp	Gly	Phe	Val	Tyr		
				210				215					220				
tcg	cag	acc	acg	gac	cgt	ctc	tgg	cgc	aag	aac	cgt	cag	act	gtc	agc	1681	
Ser	Gln	Thr	Thr	Asp	Arg	Leu	Trp	Arg	Lys	Asn	Arg	Gln	Thr	Val	Ser		
		225					230					235					
acc	agc	tcg	tgt	gtt	ggc	cgc	gat	atc	aac	cgt	aagggacccat	agaaattatt				1734	
Thr	Ser	Ser	Cys	Val	Gly	Arg	Asp	Ile	Asn	Arg							
		240				245											
gtatgattaa	catgctaaca	ttttatcaaa	ggc	aac	tgg	cca	tac	aag	tgg	gag						1788	
				Asn	Trp	Pro	Tyr	Lys	Trp	Glu							
					250					255							
gta	act	ggc	gga	gcc	tcc	acc	aac	cct	tgc	tcg	gag	acc	tac	aag	ggc	1836	

10336256.txt

Val	Thr	Gly	Gly	Ala	Ser	Thr	Asn	Pro	Cys	Ser	Glu	Thr	Tyr	Lys	Gly		
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cag	gcc	gct	gga	gac	gcc	ccc	gag	ctc	agg	gcc	atc	aaa	gcc	caa	gtc	1884	
Gln	Ala	Ala	Gly	Asp	Ala	Pro	Glu	Leu	Arg	Ala	Ile	Lys	Ala	Gln	Val		
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gat	gct	ctg	aag	gga	acg	cgc	gga	atc	agc	ctc	tac	ctc	gac	gtg	ca	1931	
Asp	Ala	Leu	Lys	Gly	Thr	Arg	Gly	Ile	Ser	Leu	Tyr	Leu	Asp	Val	His		
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	Ser	Tyr	Gly	Gln	Tyr	Ile	Leu	Trp	Pro	Tyr	Gly	Tyr	Asp				
		305				310					315						
tgc	agt	ctc	cgc	ccc	gaa	aac	gac	gcc	cag	ctc	cgc	agt	ctc	gca	tcc	2087	
Cys	Ser	Leu	Arg	Pro	Glu	Asn	Asp	Ala	Gln	Leu	Arg	Ser	Leu	Ala	Ser		
		320					325					330					
cgc	gct	caa	tca	gcc	atc	cgt	gct	gtc	tca	gga	act	gca	tac	acc	att	2135	
Arg	Ala	Gln	Ser	Ala	Ile	Arg	Ala	Val	Ser	Gly	Thr	Ala	Tyr	Thr	Ile		
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ggc	ccc	agc	tgc	tct	act	ctc	tac	gcc	acc	act	ggc	tct	tcc	act	gat	2183	
Gly	Pro	Ser	Cys	Ser	Thr	Leu	Tyr	Ala	Thr	Thr	Gly	Ser	Ser	Thr	Asp		
		350				355				360					365		
tac	acc	gat	gtc	gag	ggt	aat	gct	acc	tac	tgc	tac	act	tat	gag	ctg	2231	
Tyr	Thr	Asp	Val	Glu	Gly	Asn	Ala	Thr	Tyr	Ser	Tyr	Thr	Tyr	Glu	Leu		
				370					375					380			
agg	gat	acc	ggt	aca	tac	ggc	ttc	tgc	ctc	cct	gcc	aac	cag	att	cgt	2279	
Arg	Asp	Thr	Gly	Thr	Tyr	Gly	Phe	Ser	Leu	Pro	Ala	Asn	Gln	Ile	Arg		
			385					390					395				
ccc	act	gtt	ttg	gag	act	tgg	gct	ggt	gtt	act	agc	atg	ctc	cgc	gat	2327	
Pro	Thr	Val	Leu	Glu	Thr	Trp	Ala	Gly	Val	Thr	Ser	Met	Leu	Arg	Asp		
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## 10336256.txt

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&lt;210&gt; 213

&lt;211&gt; 104

&lt;212&gt; PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

&lt;400&gt; 213

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Met Lys Thr Thr Ile Phe Thr Ser Ala Leu Leu Leu Gly Ser Thr Ala
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Leu Gly Ser Ala Val Pro Thr Ala Gly Lys Lys Val Asp Tyr Asn Gly
20      25      30
Phe Lys Val Leu Arg Val Ser Ser Thr Asp Ala Val Lys Ser Gln Ile
35      40      45
Glu Asn Leu Ala Ala His Ile Leu Asn Pro Gly Lys Ser Ala Glu Met
50      55      60
Asp Val Val Val Ala Pro Glu Asn Val Ala Ala Leu Thr Ala Leu Ala
65      70      75      80
Ser Glu Ser Lys Val Ile Asn Glu Asp Val Gly Ala Ala Leu Lys Glu
85      90      95
Glu Gly Glu Met Gly Ile Tyr Ala
100

```

&lt;210&gt; 214

&lt;211&gt; 80

&lt;212&gt; PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

&lt;400&gt; 214

```

Val Pro Ser Glu Ser Trp Phe Thr Ala Tyr His Pro Tyr Ala Asp His
1      5      10      15
Leu Gln Phe Leu Arg Asp Leu Gln Ala Gly Tyr Thr Ser Asn Ser Glu
20      25      30
Ile Val Thr Leu Gly Asn Ser Val Gln Gly Arg Thr Leu Thr Gly Ile
35      40      45
His Ile Trp Gly Ser Gly Gly Lys Gly Ser Lys Pro Ala Val Ile Ile
50      55      60
His Gly Asn Val His Ala Arg Glu Trp Ile Thr Ser Met Thr Thr Glu
65      70      75      80

```

&lt;210&gt; 215

&lt;211&gt; 65

&lt;212&gt; PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

&lt;400&gt; 215

```

Tyr Phe Ala Trp Gln Leu Leu Thr Lys Tyr Ala Ser Asp Ser Ser Val
1      5      10      15
Lys Ala Leu Val Asp Lys Phe Asp Phe Tyr Ile Thr Pro Ile Val Asn
20      25      30
Pro Asp Gly Phe Val Tyr Ser Gln Thr Thr Asp Arg Leu Trp Arg Lys
35      40      45
Asn Arg Gln Thr Val Ser Thr Ser Ser Cys Val Gly Arg Asp Ile Asn
50      55      60
Arg
65

```

&lt;210&gt; 216

&lt;211&gt; 55

&lt;212&gt; PRT

10336256.txt

&lt;213&gt; Cochliobolus heterostrophus strain C4 (ATCC 48331)

&lt;400&gt; 216

Asn Trp Pro Tyr Lys Trp Glu Val Thr Gly Gly Ala Ser Thr Asn Pro  
 1 5 10 15  
 Cys Ser Glu Thr Tyr Lys Gly Gln Ala Ala Gly Asp Ala Pro Glu Leu  
 20 25 30  
 Arg Ala Ile Lys Ala Gln Val Asp Ala Leu Lys Gly Thr Arg Gly Ile  
 35 40 45  
 Ser Leu Tyr Leu Asp Val His  
 50 55

&lt;210&gt; 217

&lt;211&gt; 110

&lt;212&gt; PRT

&lt;213&gt; Cochliobolus heterostrophus strain C4 (ATCC 48331)

&lt;400&gt; 217

Ser Tyr Gly Gln Tyr Ile Leu Trp Pro Tyr Gly Tyr Asp Cys Ser Leu  
 1 5 10 15  
 Arg Pro Glu Asn Asp Ala Gln Leu Arg Ser Leu Ala Ser Arg Ala Gln  
 20 25 30  
 Ser Ala Ile Arg Ala Val Ser Gly Thr Ala Tyr Thr Ile Gly Pro Ser  
 35 40 45  
 Cys Ser Thr Leu Tyr Ala Thr Thr Gly Ser Ser Thr Asp Tyr Thr Asp  
 50 55 60  
 Val Glu Gly Asn Ala Thr Tyr Ser Tyr Thr Tyr Glu Leu Arg Asp Thr  
 65 70 75 80  
 Gly Thr Tyr Gly Phe Ser Leu Pro Ala Asn Gln Ile Arg Pro Thr Val  
 85 90 95  
 Leu Glu Thr Trp Ala Gly Val Thr Ser Met Leu Arg Asp Ala  
 100 105 110

&lt;210&gt; 218

&lt;211&gt; 1242

&lt;212&gt; DNA

&lt;213&gt; Cochliobolus heterostrophus strain C4 (ATCC 48331)

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1242)

&lt;400&gt; 218

atg aag act act atc ttt acc tcc gcc ctt ctc ctt ggc tcc act gcc Met Lys Thr Thr Ile Phe Thr Ser Ala Leu Leu Gly Ser Thr Ala 1 5 10 15	48
ttg ggc agc gct gtc cca acc gct ggc aag aag gtc gat tac aat ggc Leu Gly Ser Ala Val Pro Thr Ala Gly Lys Lys Val Asp Tyr Asn Gly 20 25 30	96
ttc aag gtc ctg cgc gtt tct agc acc gac gct gtc aag agt caa atc Phe Lys Val Leu Arg Val Ser Ser Thr Asp Ala Val Lys Ser Gln Ile 35 40 45	144
gag aac ttg gct gcc cac atc ctc aac cct ggc aag tct gcc gag atg Glu Asn Leu Ala Ala His Ile Leu Asn Pro Gly Lys Ser Ala Glu Met 50 55 60	192
gat gta gtt gtt gca ccc gaa aac gtt gcg gca ttg act gcg ttg gct Asp Val Val Val Ala Pro Glu Asn Val Ala Ala Leu Thr Ala Leu Ala 65 70 75 80	240
tcc gag agc aag gtc atc aat gag gat gtt ggt gct gcc ctc aag gaa Ser Glu Ser Lys Val Ile Asn Glu Asp Val Gly Ala Ala Leu Lys Glu 85 90 95	288
gaa ggc gag atg gga atc tac gct gtt ccc agc gag tcg tgg ttc aca	336

10336256.txt															
Glu	Gly	Glu	Met	Gly	Ile	Tyr	Ala	Val	Pro	Ser	Glu	Ser	Trp	Phe	Thr
			100					105					110		
gca	tac	cac	cca	tat	gcc	gat	cat	ctt	caa	ttc	ctc	cgc	gat	ctg	caa
Ala	Tyr	His	Pro	Tyr	Ala	Asp	His	Leu	Gln	Phe	Leu	Arg	Asp	Leu	Gln
		115					120					125			
gcc	ggc	tac	act	agc	aat	tcc	gag	att	gtc	acc	ctt	ggc	aac	tca	gtc
Ala	Gly	Tyr	Thr	Ser	Asn	Ser	Glu	Ile	Val	Thr	Leu	Gly	Asn	Ser	Val
	130					135					140				
caa	gga	cgt	acc	ttg	act	ggc	atc	cat	atc	tgg	ggc	agc	ggc	ggc	aag
Gln	Gly	Arg	Thr	Leu	Thr	Gly	Ile	His	Ile	Trp	Gly	Ser	Gly	Gly	Lys
145					150					155					160
gga	tcc	aag	cct	gcc	gtt	att	atc	cac	gga	aac	gtt	cac	gcc	cga	gag
Gly	Ser	Lys	Pro	Ala	Val	Ile	Ile	His	Gly	Asn	Val	His	Ala	Arg	Glu
				165					170					175	
tgg	atc	act	tcc	atg	acc	act	gag	tac	ttc	gcg	tgg	caa	ctt	cta	acc
Trp	Ile	Thr	Ser	Met	Thr	Thr	Glu	Tyr	Phe	Ala	Trp	Gln	Leu	Leu	Thr
			180					185					190		
aag	tac	gcc	tcc	gac	tca	agc	gtc	aag	gct	ctc	gtc	gac	aag	ttc	gac
Lys	Tyr	Ala	Ser	Asp	Ser	Ser	Val	Lys	Ala	Leu	Val	Asp	Lys	Phe	Asp
		195					200					205			
ttt	tac	atc	acc	ccc	atc	gtc	aac	ccc	gac	gga	ttc	gtc	tac	tcg	cag
Phe	Tyr	Ile	Thr	Pro	Ile	Val	Asn	Pro	Asp	Gly	Phe	Val	Tyr	Ser	Gln
	210					215					220				
acc	acg	gac	cgt	ctc	tgg	cgc	aag	aac	cgt	cag	act	gtc	agc	acc	agc
Thr	Thr	Asp	Arg	Leu	Trp	Arg	Lys	Asn	Arg	Gln	Thr	Val	Ser	Thr	Ser
225					230					235					240
tcg	tgt	gtt	ggc	cgc	gat	atc	aac	cgt	aac	tgg	cca	tac	aag	tgg	gag
Ser	Cys	Val	Gly	Arg	Asp	Ile	Asn	Arg	Asn	Trp	Pro	Tyr	Lys	Trp	Glu
				245					250					255	
gta	act	ggc	gga	gcc	tcc	acc	aac	cct	tgc	tcg	gag	acc	tac	aag	ggc
Val	Thr	Gly	Gly	Ala	Ser	Thr	Asn	Pro	Cys	Ser	Glu	Thr	Tyr	Lys	Gly
			260					265					270		
cag	gcc	gct	gga	gac	gcc	ccc	gag	ctc	agg	gcc	atc	aaa	gcc	caa	gtc
Gln	Ala	Ala	Gly	Asp	Ala	Pro	Glu	Leu	Arg	Ala	Ile	Lys	Ala	Gln	Val
		275					280					285			
gat	gct	ctg	aag	gga	acg	cgc	gga	atc	agc	ctc	tac	ctc	gac	gtg	cac
Asp	Ala	Leu	Lys	Gly	Thr	Arg	Gly	Ile	Ser	Leu	Tyr	Leu	Asp	Val	His
	290					295					300				
tcc	tac	ggc	caa	tac	atc	ctc	tgg	ccc	tac	ggc	tac	gac	tgc	agt	ctc
Ser	Tyr	Gly	Gln	Tyr	Ile	Leu	Trp	Pro	Tyr	Gly	Tyr	Asp	Cys	Ser	Leu
305					310					315					320
cgc	ccc	gaa	aac	gac	gcc	cag	ctc	cgc	agt	ctc	gca	tcc	cgc	gct	caa
Arg	Pro	Glu	Asn	Asp	Ala	Gln	Leu	Arg	Ser	Leu	Ala	Ser	Arg	Ala	Gln
				325					330					335	
tca	gcc	atc	cgt	gct	gtc	tca	gga	act	gca	tac	acc	att	ggc	ccc	agc
Ser	Ala	Ile	Arg	Ala	Val	Ser	Gly	Thr	Ala	Tyr	Thr	Ile	Gly	Pro	Ser
			340				345						350		
tgc	tct	act	ctc	tac	gcc	acc	act	ggc	tct	tcc	act	gat	tac	acc	gat
Cys	Ser	Thr	Leu	Tyr	Ala	Thr	Thr	Gly	Ser	Ser	Thr	Asp	Tyr	Thr	Asp
		355					360					365			
gtc	gag	ggc	aat	gct	acc	tac	tcg	tac	act	tat	gag	ctg	agg	gat	acc

10336256.txt

Val Glu Gly Asn Ala Thr Tyr Ser Tyr Thr Tyr Glu Leu Arg Asp Thr  
 370 375 380

ggt aca tac ggc ttc tcg ctc cct gcc aac cag att cgt ccc act gtt 1200  
 Gly Thr Tyr Gly Phe Ser Leu Pro Ala Asn Gln Ile Arg Pro Thr Val 400  
 385 390 395 400

ttg gag act tgg gct ggt gtt act agc atg ctc cgc gat gct 1242  
 Leu Glu Thr Trp Ala Gly Val Thr Ser Met Leu Arg Asp Ala  
 405 410

&lt;210&gt; 219

&lt;211&gt; 414

&lt;212&gt; PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

&lt;220&gt;

&lt;221&gt; DOMAIN

&lt;222&gt; (112)...(317)

&lt;223&gt; Zinc carboxypeptidase

&lt;400&gt; 219

Met Lys Thr Thr Ile Phe Thr Ser Ala Leu Leu Leu Gly Ser Thr Ala  
 1 5 10 15

Leu Gly Ser Ala Val Pro Thr Ala Gly Lys Lys Val Asp Tyr Asn Gly  
 20 25 30

Phe Lys Val Leu Arg Val Ser Ser Thr Asp Ala Val Lys Ser Gln Ile  
 35 40 45

Glu Asn Leu Ala Ala His Ile Leu Asn Pro Gly Lys Ser Ala Glu Met  
 50 55 60

Asp Val Val Val Ala Pro Glu Asn Val Ala Ala Leu Thr Ala Leu Ala  
 65 70 75 80

Ser Glu Ser Lys Val Ile Asn Glu Asp Val Gly Ala Ala Leu Lys Glu  
 85 90 95

Glu Gly Glu Met Gly Ile Tyr Ala Val Pro Ser Glu Ser Trp Phe Thr  
 100 105 110

Ala Tyr His Pro Tyr Ala Asp His Leu Gln Phe Leu Arg Asp Leu Gln  
 115 120 125

Ala Gly Tyr Thr Ser Asn Ser Glu Ile Val Thr Leu Gly Asn Ser Val  
 130 135 140

Gln Gly Arg Thr Leu Thr Gly Ile His Ile Trp Gly Ser Gly Gly Lys  
 145 150 155 160

Gly Ser Lys Pro Ala Val Ile Ile His Gly Asn Val His Ala Arg Glu  
 165 170 175

Trp Ile Thr Ser Met Thr Thr Glu Tyr Phe Ala Trp Gln Leu Leu Thr  
 180 185 190

Lys Tyr Ala Ser Asp Ser Ser Val Lys Ala Leu Val Asp Lys Phe Asp  
 195 200 205

Phe Tyr Ile Thr Pro Ile Val Asn Pro Asp Gly Phe Val Tyr Ser Gln  
 210 215 220

Thr Thr Asp Arg Leu Trp Arg Lys Asn Arg Gln Thr Val Ser Thr Ser  
 225 230 235 240

Ser Cys Val Gly Arg Asp Ile Asn Arg Asn Trp Pro Tyr Lys Trp Glu  
 245 250 255

Val Thr Gly Gly Ala Ser Thr Asn Pro Cys Ser Glu Thr Tyr Lys Gly  
 260 265 270

Gln Ala Ala Gly Asp Ala Pro Glu Leu Arg Ala Ile Lys Ala Gln Val  
 275 280 285

Asp Ala Leu Lys Gly Thr Arg Gly Ile Ser Leu Tyr Leu Asp Val His  
 290 295 300

Ser Tyr Gly Gln Tyr Ile Leu Trp Pro Tyr Gly Tyr Asp Cys Ser Leu  
 305 310 315 320

Arg Pro Glu Asn Asp Ala Gln Leu Arg Ser Leu Ala Ser Arg Ala Gln  
 325 330 335

Ser Ala Ile Arg Ala Val Ser Gly Thr Ala Tyr Thr Ile Gly Pro Ser  
 340 345 350

Cys Ser Thr Leu Tyr Ala Thr Thr Gly Ser Ser Thr Asp Tyr Thr Asp

10336256.txt

355 360 365  
 Val Glu Gly Asn Ala Thr Tyr Ser Tyr Thr Tyr Glu Leu Arg Asp Thr  
 370 375 380  
 Gly Thr Tyr Gly Phe Ser Leu Pro Ala Asn Gln Ile Arg Pro Thr Val  
 385 390 395 400  
 Leu Glu Thr Trp Ala Gly Val Thr Ser Met Leu Arg Asp Ala  
 405 410

<210> 220  
 <211> 3554  
 <212> DNA  
 <213> Cochliobolus heterostrophus strain C4 (ATCC 48331)

<220>  
 <221> CDS  
 <222> (1001)...(2554)  
 <223> Exon

<221> misc\_feature  
 <222> (1)...(3554)  
 <223> n = A,T,C or G

<400> 220  
 cggcggcggc agcgttgact ttgttggaac ttggctcgagc tacgcgctct tcaagagcgg 60  
 acacatccta gtcaacacta tggagcgtgg cgcattcggt gtcaagttgc aggcggggtt 120  
 cgacaaataa gcaaagaagg aataatgata atgatggcct aggccttctt gtatctagtc 180  
 gagacgttgt agttctgtaa atatctatcg gtcctagtcg tattcggccg gtgcgagtgt 240  
 ggcttgactt atcaattcgt aatttggcca aacatactcg gctttattcc ttgcccgctc 300  
 tttttttgat catatacccg ttgccaagtc cagcgcataa tagccgtagc agtagcgtag 360  
 tgaaggctac cgaggctcgg tttggctctgg cacaacaagc cactttagtc acacattgct 420  
 tattcttttg atcaaaatgg gaacaacctg ctgctaagcc gagagcttct cgaagtgttc 480  
 cagtggcggg atcgctcgttt tgcctcctcc attatcatcc gccctgattc tggcgctatc 540  
 atgccaaggc gattcgatgg gggatggatg tctcttgccg gggagtagat tcttggccgc 600  
 catctagctt cccaatcaag tgtcgtctgg ccgtgagcta ggtatgtccg agagatgatg 660  
 cggctattct ccttctcat acaacacagc atcacgcagc caagtcgact ttcattcaatt 720  
 tcgtcgctt cgccccagc ccttcaccgg gctaccgct accaataacc cacagcatgc 780  
 cttgaatacc catttcccg ttcccgaaaa ttgggtcaact agcgatcgcg atagcagctg 840  
 cctgaactgg ctaggccagg gagcacgcga ctatgctaac ccaactctcg tagtcgttta 900  
 tgaggatgtc agccagagta tatagagcca tgcaattccg gctgcatctg gcacggcagc 960  
 cctctcagtc tttgctcatc cctcgttctc aatattcaag atg agg ttc gtt cca 1015  
 Met Arg Phe Val Pro  
 1 5

ttc gtt gcg ctc gct gcg cct gtc ctt gcc cag gtc ggt ccc aag cca 1063  
 Phe Val Ala Leu Ala Pro Val Leu Ala Gln Val Gly Pro Lys Pro  
 10 15 20

aac cca aac aca aag ccc ggc aag cct cca aag cct gac gac aag cct 1111  
 Asn Pro Asn Thr Lys Pro Gly Lys Pro Pro Lys Pro Asp Asp Lys Pro  
 25 30 35

aag aag ctc gtc act ccc aag gat ctg atc aag gac atc aaa ctt gag 1159  
 Lys Lys Leu Val Thr Pro Lys Asp Leu Ile Lys Asp Ile Lys Leu Glu  
 40 45 50

gat ctg ctc aag ggc tcc caa aag ctc caa gac att gcc gac gaa gct 1207  
 Asp Leu Leu Lys Gly Ser Gln Lys Leu Gln Asp Ile Ala Asp Glu Ala  
 55 60 65

ggc ggt aac cgt gct ttt ggt ggc aca ggg cac aac gcg acc acc gaa 1255  
 Gly Gly Asn Arg Ala Phe Gly Gly Thr Gly His Asn Ala Thr Thr Glu  
 70 75 80 85

tgg ttg tac cag act ttg ttg gcc act ggt tac tat gac gtg tac aag 1303  
 Trp Leu Tyr Gln Thr Leu Leu Ala Thr Gly Tyr Tyr Asp Val Tyr Lys  
 90 95 100

cag cca ttc gtt gag ctt ttc acc gct gct acg acc aag ttc act gct 1351  
 Page 212

10336256.txt															
Gln	Pro	Phe	Val	Glu	Leu	Phe	Thr	Ala	Ala	Thr	Thr	Lys	Phe	Thr	Ala
			105					110					115		
ggt	ggt	gaa	gag	att	ccc	gtc	tct	tac	atg	acc	ttt	ggc	ccc	tct	ggc
Gly	Gly	Glu	Glu	Ile	Pro	Val	Ser	Tyr	Met	Thr	Phe	Gly	Pro	Ser	Gly
		120					125					130			1399
gat	gcc	act	gcc	aac	att	gtc	aag	gtt	aac	aac	ctg	gga	tgc	gcc	gcc
Asp	Ala	Thr	Ala	Asn	Ile	Val	Lys	Val	Asn	Asn	Leu	Gly	Cys	Ala	Ala
	135					140					145				1447
gaa	gac	tac	ccc	gct	agt	gtt	tct	ggc	caa	cac	gca	ctc	gtc	tcc	cga
Glu	Asp	Tyr	Pro	Ala	Ser	Val	Ser	Gly	Gln	His	Ala	Leu	Val	Ser	Arg
150					155				160						1495
ggc	aca	tgt	act	ttt	gcc	caa	aag	tct	acc	ctg	gcc	aag	gct	gct	ggt
Gly	Thr	Cys	Thr	Phe	Ala	Gln	Lys	Ser	Thr	Leu	Ala	Lys	Ala	Ala	Gly
				170					175					180	1543
gct	gta	ggc	gcg	ctc	atc	tac	aac	aat	gag	cca	gag	cag	ccc	ctc	tca
Ala	Val	Gly	Ala	Leu	Ile	Tyr	Asn	Asn	Glu	Pro	Glu	Gln	Pro	Leu	Ser
			185					190					195		
ggt	act	ctt	gga	ggt	gca	ggt	gac	tac	gct	cct	act	gtc	ggt	atg	acc
Gly	Thr	Leu	Gly	Gly	Ala	Gly	Asp	Tyr	Ala	Pro	Thr	Val	Gly	Met	Thr
		200					205					210			1639
aag	gag	gct	gga	gag	tct	ctc	att	gct	aag	ctt	gga	aac	ggc	act	aca
Lys	Glu	Ala	Gly	Glu	Ser	Leu	Ile	Ala	Lys	Leu	Gly	Asn	Gly	Thr	Thr
	215					220					225				1687
ctt	gag	gga	acc	ctc	ttc	atc	gat	gcc	atc	cag	gaa	aac	cgc	acc	aac
Leu	Glu	Gly	Thr	Leu	Phe	Ile	Asp	Ala	Ile	Gln	Glu	Asn	Arg	Thr	Asn
230					235					240					245
tac	aac	gtc	att	gct	gag	aca	aag	gag	ggc	gac	cac	aac	aac	gtt	ctc
Tyr	Asn	Val	Ile	Ala	Glu	Thr	Lys	Glu	Gly	Asp	His	Asn	Asn	Val	Leu
				250					255					260	1783
atg	att	ggt	ggc	cac	acc	gac	tcc	gtc	ttc	cag	ggt	cct	ggt	atc	aac
Met	Ile	Gly	Gly	His	Thr	Asp	Ser	Val	Phe	Gln	Gly	Pro	Gly	Ile	Asn
			265					270					275		1831
gat	gac	gga	tct	ggt	act	att	ggt	act	ctg	gtt	act	ggt	ctt	gct	ctc
Asp	Asp	Gly	Ser	Gly	Thr	Ile	Gly	Thr	Leu	Val	Thr	Gly	Leu	Ala	Leu
		280					285					290			1879
acc	aag	tac	aag	atc	aag	aac	gcc	gtt	cgt	ctt	ggt	ttc	tgg	ggc	gcc
Thr	Lys	Tyr	Lys	Ile	Lys	Asn	Ala	Val	Arg	Leu	Gly	Phe	Trp	Gly	Ala
	295					300					305				1927
gag	gag	ttt	ggc	aag	ctt	gga	tcc	ttc	tac	tac	atg	aag	acc	atc	aac
Glu	Glu	Phe	Gly	Lys	Leu	Gly	Ser	Phe	Tyr	Tyr	Met	Lys	Thr	Ile	Asn
310					315					320					325
ggt	act	ttc	ggc	ggc	agc	acc	gca	gag	gct	aac	aag	atc	cgt	gcc	tac
Gly	Thr	Phe	Gly	Gly	Ser	Thr	Ala	Glu	Ala	Asn	Lys	Ile	Arg	Ala	Tyr
				330					335					340	2023
ctc	aac	ttc	gac	atg	att	gcc	tcg	ccc	aac	tat	gtc	ctc	ggt	atc	tac
Leu	Asn	Phe	Asp	Met	Ile	Ala	Ser	Pro	Asn	Tyr	Val	Leu	Gly	Ile	Tyr
			345					350					355		2071
gat	ggt	gat	ggc	agt	gca	ttc	aac	ttt	tct	ggc	gca	gcc	ggt	tcc	gac
Asp	Gly	Asp	Gly	Ser	Ala	Phe	Asn	Phe	Ser	Gly	Ala	Ala	Gly	Ser	Asp
		360					365					370			2119
aag	atc	gag	aag	gac	ttt	gaa	gag	ttt	tac	gag	gag	cgt	ggc	ctt	cct
															2167

10336256.txt

Lys Ile Glu Lys Asp Phe Glu Glu Phe Tyr Glu Glu Arg Gly Leu Pro  
 375 380 385

cac gtc ccc tcc ctc ttt acc ctc cgc tcc gac tac gct gcc ttc ctc 2215  
 His Val Pro Ser Leu Phe Thr Leu Arg Ser Asp Tyr Ala Ala Phe Leu  
 390 395 400 405

gag aac ggt atc ccc tct ggc ggt ctc ttc acc ggt gcc gaa gtc ctc 2263  
 Glu Asn Gly Ile Pro Ser Gly Gly Leu Phe Thr Gly Ala Glu Val Leu  
 410 415 420

aag acc gag gag gag gcc cag ctc ttc ggc ggt gaa gcc ggc aag ccc 2311  
 Lys Thr Glu Glu Glu Ala Gln Leu Phe Gly Gly Glu Ala Gly Lys Pro  
 425 430 435

ctc gac gga tgc tac cac cag gcc tgc gac gac atc aac aac ctt gcc 2359  
 Leu Asp Gly Cys Tyr His Gln Ala Cys Asp Asp Ile Asn Asn Leu Ala  
 440 445 450

cac gac gcc tac ctc ctc aac acc cag agc att gcc aac tcc gtt gcc 2407  
 His Asp Ala Tyr Leu Leu Asn Thr Gln Ser Ile Ala Asn Ser Val Ala  
 455 460 465

aag tac gcc gtc tct ttc gag ggt atc ccc aag gcc aac gct act ctc 2455  
 Lys Tyr Ala Val Ser Phe Glu Gly Ile Pro Lys Ala Asn Ala Thr Leu  
 470 475 480 485

cgc aaa cgc ggt gct gag tgc gca agg ttc atg agc agg ttc gac cac 2503  
 Arg Lys Arg Gly Ala Glu Ser Ala Arg Phe Met Ser Arg Phe Asp His  
 490 495 500

ggt ggc cat gag cac ctt ggt cag cct tgc ggt gct gga aag cac gct 2551  
 Gly Gly His Glu His Leu Gly Gln Pro Cys Gly Ala Gly Lys His Ala  
 505 510 515

att taaatttcaa tgtctataat gatttgctgg ggtgaaagga aatgatgaga 2604  
 Ile

tgataccatg agagaaatct tttgtaaaag tagatgaaga ataataccca tttttttgtg 2664  
 ttcatttttga ctagtcttat gctgtgcctg gcgattgaat gctgtgaaat ttcttttggg 2724  
 tccttttttgt cagtttttcg tagttgtact attgctgttt gaaagagtca agccatctag 2784  
 atatgtggca ccctaaccac ctagacaaag gcatttaagt ctgcttcctc actactaaat 2844  
 atccattacc ctggaacatt catgtcagaa aagcacaagt tttaaaacaa atagtttctt 2904  
 ccagttcaac tatcaaatat atattaaacc gcacaccctc ccccttatat taccactcaa 2964  
 gtccaacaac gaaaagatta tatactgaaa aatctcctac ccactcttat ccactcctgc 3024  
 aaacaaaaaa accccaggcc gagattgaac tttcctcctt tctcctcaca aaccacgtga 3084  
 ttggtgatat acagtagcta aatgccaccg aaaccctgta ccacgctccc tactcaaatc 3144  
 cacgttagtt ttatatactt tttgtaattc gagatttcta cacaatccat tccaacgaa 3204  
 gatccgnnnn nnnnnnnnnn nnnnnncccc ccaaaaaaga atgatagtga gagatgtaga 3264  
 gaaacggggg aagtttagca agggaaagaa aagagacata cgctcagatg ttatcggtgg 3324  
 ccgagaagtc cgtaagagca actgtgattt caccgactac cgggttgga tctcctcggc 3384  
 gctgtgagaa agttagctat gtatgtgcgt gtgtgttggg aggggggaaa gggcgtactt 3444  
 ctgatgggac agctccggag agagcttcgg aggcagagtc agataccatt gtgaggtcca 3504  
 gctctggagc ctcaatgggt ctggcctggg cgactgaggc gaggacgagg 3554

&lt;210&gt; 221

&lt;211&gt; 518

&lt;212&gt; PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

&lt;400&gt; 221

Met Arg Phe Val Pro Phe Val Ala Leu Ala Ala Pro Val Leu Ala Gln  
 1 5 10 15  
 Val Gly Pro Lys Pro Asn Pro Asn Thr Lys Pro Gly Lys Pro Pro Lys  
 20 25 30  
 Pro Asp Asp Lys Pro Lys Lys Leu Val Thr Pro Lys Asp Leu Ile Lys  
 35 40 45

10336256.txt

Asp Ile Lys Leu Glu Asp Leu Leu Lys Gly Ser Gln Lys Leu Gln Asp  
 50 55 60  
 Ile Ala Asp Glu Ala Gly Gly Asn Arg Ala Phe Gly Gly Thr Gly His  
 65 70 75 80  
 Asn Ala Thr Thr Glu Trp Leu Tyr Gln Thr Leu Leu Ala Thr Gly Tyr  
 85 90 95  
 Tyr Asp Val Tyr Lys Gln Pro Phe Val Glu Leu Phe Thr Ala Ala Thr  
 100 105 110  
 Thr Lys Phe Thr Ala Gly Gly Glu Glu Ile Pro Val Ser Tyr Met Thr  
 115 120 125  
 Phe Gly Pro Ser Gly Asp Ala Thr Ala Asn Ile Val Lys Val Asn Asn  
 130 135 140  
 Leu Gly Cys Ala Ala Glu Asp Tyr Pro Ala Ser Val Ser Gly Gln His  
 145 150 155 160  
 Ala Leu Val Ser Arg Gly Thr Cys Thr Phe Ala Gln Lys Ser Thr Leu  
 165 170 175  
 Ala Lys Ala Ala Gly Ala Val Gly Ala Leu Ile Tyr Asn Asn Glu Pro  
 180 185 190  
 Glu Gln Pro Leu Ser Gly Thr Leu Gly Gly Ala Gly Asp Tyr Ala Pro  
 195 200 205  
 Thr Val Gly Met Thr Lys Glu Ala Gly Glu Ser Leu Ile Ala Lys Leu  
 210 215 220  
 Gly Asn Gly Thr Thr Leu Glu Gly Thr Leu Phe Ile Asp Ala Ile Gln  
 225 230 235 240  
 Glu Asn Arg Thr Asn Tyr Asn Val Ile Ala Glu Thr Lys Glu Gly Asp  
 245 250 255  
 His Asn Asn Val Leu Met Ile Gly Gly His Thr Asp Ser Val Phe Gln  
 260 265 270  
 Gly Pro Gly Ile Asn Asp Asp Gly Ser Gly Thr Ile Gly Thr Leu Val  
 275 280 285  
 Thr Gly Leu Ala Leu Thr Lys Tyr Lys Ile Lys Asn Ala Val Arg Leu  
 290 295 300  
 Gly Phe Trp Gly Ala Glu Glu Phe Gly Lys Leu Gly Ser Phe Tyr Tyr  
 305 310 315 320  
 Met Lys Thr Ile Asn Gly Thr Phe Gly Gly Ser Thr Ala Glu Ala Asn  
 325 330 335  
 Lys Ile Arg Ala Tyr Leu Asn Phe Asp Met Ile Ala Ser Pro Asn Tyr  
 340 345 350  
 Val Leu Gly Ile Tyr Asp Gly Asp Gly Ser Ala Phe Asn Phe Ser Gly  
 355 360 365  
 Ala Ala Gly Ser Asp Lys Ile Glu Lys Asp Phe Glu Glu Phe Tyr Glu  
 370 375 380  
 Glu Arg Gly Leu Pro His Val Pro Ser Leu Phe Thr Leu Arg Ser Asp  
 385 390 395 400  
 Tyr Ala Ala Phe Leu Glu Asn Gly Ile Pro Ser Gly Gly Leu Phe Thr  
 405 410 415  
 Gly Ala Glu Val Leu Lys Thr Glu Glu Glu Ala Gln Leu Phe Gly Gly  
 420 425 430  
 Glu Ala Gly Lys Pro Leu Asp Gly Cys Tyr His Gln Ala Cys Asp Asp  
 435 440 445  
 Ile Asn Asn Leu Ala His Asp Ala Tyr Leu Leu Asn Thr Gln Ser Ile  
 450 455 460  
 Ala Asn Ser Val Ala Lys Tyr Ala Val Ser Phe Glu Gly Ile Pro Lys  
 465 470 475 480  
 Ala Asn Ala Thr Leu Arg Lys Arg Gly Ala Glu Ser Ala Arg Phe Met  
 485 490 495  
 Ser Arg Phe Asp His Gly Gly His Glu His Leu Gly Gln Pro Cys Gly  
 500 505 510  
 Ala Gly Lys His Ala Ile  
 515

&lt;210&gt; 222

&lt;211&gt; 1554

&lt;212&gt; DNA

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

&lt;220&gt;

&lt;221&gt; CDS

10336256.txt

&lt;222&gt; (1)...(1554)

&lt;400&gt; 222

atg agg ttc gtt cca ttc gtt gcg ctc gct gcg cct gtc ctt gcc cag	48
Met Arg Phe Val Pro Phe Val Ala Leu Ala Pro Val Leu Ala Gln	
1 5 10 15	
gtc ggt ccc aag cca aac cca aac aca aag ccc ggc aag cct cca aag	96
Val Gly Pro Lys Pro Asn Pro Asn Thr Lys Pro Gly Lys Pro Pro Lys	
20 25 30	
cct gac gac aag cct aag aag ctc gtc act ccc aag gat ctg atc aag	144
Pro Asp Asp Lys Pro Lys Lys Leu Val Thr Pro Lys Asp Leu Ile Lys	
35 40 45	
gac atc aaa ctt gag gat ctg ctc aag ggc tcc caa aag ctc caa gac	192
Asp Ile Lys Leu Glu Asp Leu Leu Lys Gly Ser Gln Lys Leu Gln Asp	
50 55 60	
att gcc gac gaa gct ggc ggt aac cgt gct ttt ggt ggc aca ggg cac	240
Ile Ala Asp Glu Ala Gly Gly Asn Arg Ala Phe Gly Gly Thr Gly His	
65 70 75 80	
aac gcg acc acc gaa tgg ttg tac cag act ttg ttg gcc act ggt tac	288
Asn Ala Thr Thr Glu Trp Leu Tyr Gln Thr Leu Leu Ala Thr Gly Tyr	
85 90 95	
tat gac gtg tac aag cag cca ttc gtt gag ctt ttc acc gct gct acg	336
Tyr Asp Val Tyr Lys Gln Pro Phe Val Glu Leu Phe Thr Ala Ala Thr	
100 105 110	
acc aag ttc act gct ggt ggt gaa gag att ccc gtc tct tac atg acc	384
Thr Lys Phe Thr Ala Gly Gly Glu Glu Ile Pro Val Ser Tyr Met Thr	
115 120 125	
ttt ggc ccc tct ggc gat gcc act gcc aac att gtc aag gtt aac aac	432
Phe Gly Pro Ser Gly Asp Ala Thr Ala Asn Ile Val Lys Val Asn Asn	
130 135 140	
ctg gga tgc gcc gcc gaa gac tac ccc gct agt gtt tct ggc caa cac	480
Leu Gly Cys Ala Ala Glu Asp Tyr Pro Ala Ser Val Ser Gly Gln His	
145 150 155 160	
gca ctc gtc tcc cga ggc aca tgt act ttt gcc caa aag tct acc ctg	528
Ala Leu Val Ser Arg Gly Thr Cys Thr Phe Ala Gln Lys Ser Thr Leu	
165 170 175	
gcc aag gct gct ggt gct gta ggc gcg ctc atc tac aac aat gag cca	576
Ala Lys Ala Ala Gly Ala Val Gly Ala Leu Ile Tyr Asn Asn Glu Pro	
180 185 190	
gag cag ccc ctc tca ggt act ctt gga ggt gca ggt gac tac gct cct	624
Glu Gln Pro Leu Ser Gly Thr Leu Gly Gly Ala Gly Asp Tyr Ala Pro	
195 200 205	
act gtc ggt atg acc aag gag gct gga gag tct ctc att gct aag ctt	672
Thr Val Gly Met Thr Lys Glu Ala Gly Glu Ser Leu Ile Ala Lys Leu	
210 215 220	
gga aac ggc act aca ctt gag gga acc ctc ttc atc gat gcc atc cag	720
Gly Asn Gly Thr Thr Leu Glu Gly Thr Leu Phe Ile Asp Ala Ile Gln	
225 230 235 240	
gaa aac cgc acc aac tac aac gtc att gct gag aca aag gag ggc gac	768
Glu Asn Arg Thr Asn Tyr Asn Val Ile Ala Glu Thr Lys Glu Gly Asp	
245 250 255	
cac aac aac gtt ctc atg att ggt ggc	816

10336256.txt

His	Asn	Asn	Val	Leu	Met	Ile	Gly	Gly	His	Thr	Asp	Ser	Val	Phe	Gln	
			260					265					270			
ggt	cct	ggt	atc	aac	gat	gac	gga	tct	ggt	act	att	ggt	act	ctg	ggt	864
Gly	Pro	Gly	Ile	Asn	Asp	Asp	Gly	Ser	Gly	Thr	Ile	Gly	Thr	Leu	Val	
		275					280					285				
act	ggt	ctt	gct	ctc	acc	aag	tac	aag	atc	aag	aac	gcc	ggt	cgt	ctt	912
Thr	Gly	Leu	Ala	Leu	Thr	Lys	Tyr	Lys	Ile	Lys	Asn	Ala	Val	Arg	Leu	
	290					295					300					
ggt	ttc	tgg	ggc	gcc	gag	gag	ttt	ggc	aag	ctt	gga	tcc	ttc	tac	tac	960
Gly	Phe	Trp	Gly	Ala	Glu	Glu	Phe	Gly	Lys	Leu	Gly	Ser	Phe	Tyr	Tyr	
305					310					315					320	
atg	aag	acc	atc	aac	ggt	act	ttc	ggc	ggc	agc	acc	gca	gag	gct	aac	1008
Met	Lys	Thr	Ile	Asn	Gly	Thr	Phe	Gly	Gly	Ser	Thr	Ala	Glu	Ala	Asn	
				325					330					335		
aag	atc	cgt	gcc	tac	ctc	aac	ttc	gac	atg	att	gcc	tcg	ccc	aac	tat	1056
Lys	Ile	Arg	Ala	Tyr	Leu	Asn	Phe	Asp	Met	Ile	Ala	Ser	Pro	Asn	Tyr	
			340					345					350			
gtc	ctc	ggt	atc	tac	gat	ggt	gat	ggc	agt	gca	ttc	aac	ttt	tct	ggc	1104
Val	Leu	Gly	Ile	Tyr	Asp	Gly	Asp	Gly	Ser	Ala	Phe	Asn	Phe	Ser	Gly	
		355					360					365				
gca	gcc	ggt	tcc	gac	aag	atc	gag	aag	gac	ttt	gaa	gag	ttt	tac	gag	1152
Ala	Ala	Gly	Ser	Asp	Lys	Ile	Glu	Lys	Asp	Phe	Glu	Glu	Phe	Tyr	Glu	
	370					375					380					
gag	cgt	ggc	ctt	cct	cac	gtc	ccc	tcc	ctc	ttt	acc	ctc	cgc	tcc	gac	1200
Glu	Arg	Gly	Leu	Pro	His	Val	Pro	Ser	Leu	Phe	Thr	Leu	Arg	Ser	Asp	
385					390					395					400	
tac	gct	gcc	ttc	ctc	gag	aac	ggt	atc	ccc	tct	ggc	ggt	ctc	ttc	acc	1248
Tyr	Ala	Ala	Phe	Leu	Glu	Asn	Gly	Ile	Pro	Ser	Gly	Gly	Leu	Phe	Thr	
				405					410					415		
ggt	gcc	gaa	gtc	ctc	aag	acc	gag	gag	gag	gcc	cag	ctc	ttc	ggc	ggt	1296
Gly	Ala	Glu	Val	Leu	Lys	Thr	Glu	Glu	Glu	Ala	Gln	Leu	Phe	Gly	Gly	
			420					425					430			
gaa	gcc	ggc	aag	ccc	ctc	gac	gga	tgc	tac	cac	cag	gcc	tgc	gac	gac	1344
Glu	Ala	Gly	Lys	Pro	Leu	Asp	Gly	Cys	Tyr	His	Gln	Ala	Cys	Asp	Asp	
		435					440					445				
atc	aac	aac	ctt	gcc	cac	gac	gcc	tac	ctc	ctc	aac	acc	cag	agc	att	1392
Ile	Asn	Asn	Leu	Ala	His	Asp	Ala	Tyr	Leu	Leu	Asn	Thr	Gln	Ser	Ile	
	450					455					460					
gcc	aac	tcc	ggt	gcc	aag	tac	gcc	gtc	tct	ttc	gag	ggt	atc	ccc	aag	1440
Ala	Asn	Ser	Val	Ala	Lys	Tyr	Ala	Val	Ser	Phe	Glu	Gly	Ile	Pro	Lys	
					470					475					480	
gcc	aac	gct	act	ctc	cgc	aaa	cgc	ggt	gct	gag	tcg	gca	agg	ttc	atg	1488
Ala	Asn	Ala	Thr	Leu	Arg	Lys	Arg	Gly	Ala	Glu	Ser	Ala	Arg	Phe	Met	
				485					490					495		
agc	agg	ttc	gac	cac	ggt	ggc	cat	gag	cac	ctt	ggt	cag	cct	tgc	ggt	1536
Ser	Arg	Phe	Asp	His	Gly	Gly	His	Glu	His	Leu	Gly	Gln	Pro	Cys	Gly	
			500					505					510			
gct	gga	aag	cac	gct	att											1554
Ala	Gly	Lys	His	Ala	Ile											
		515														

10336256.txt

<210> 223  
 <211> 518  
 <212> PRT  
 <213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<220>  
 <221> SIGNAL  
 <222> (1)...(15)

<221> DOMAIN  
 <222> (234)...(471)  
 <223> Peptidase family M28

<221> DOMAIN  
 <222> (115)...(224)  
 <223> PA (protease associate) domain

<400> 223  
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 1 5 10 15  
 Val Gly Pro Lys Pro Asn Pro Asn Thr Lys Pro Gly Lys Pro Pro Lys  
 20 25 30  
 Pro Asp Asp Lys Pro Lys Lys Leu Val Thr Pro Lys Asp Leu Ile Lys  
 35 40 45  
 Asp Ile Lys Leu Glu Asp Leu Lys Gly Ser Gln Lys Leu Gln Asp  
 50 55 60  
 Ile Ala Asp Glu Ala Gly Gly Asn Arg Ala Phe Gly Gly Thr Gly His  
 65 70 75 80  
 Asn Ala Thr Thr Glu Trp Leu Tyr Gln Thr Leu Leu Ala Thr Gly Tyr  
 85 90 95  
 Tyr Asp Val Tyr Lys Gln Pro Phe Val Glu Leu Phe Thr Ala Ala Thr  
 100 105 110  
 Thr Lys Phe Thr Ala Gly Gly Glu Glu Ile Pro Val Ser Tyr Met Thr  
 115 120 125  
 Phe Gly Pro Ser Gly Asp Ala Thr Ala Asn Ile Val Lys Val Asn Asn  
 130 135 140  
 Leu Gly Cys Ala Ala Glu Asp Tyr Pro Ala Ser Val Ser Gly Gln His  
 145 150 155 160  
 Ala Leu Val Ser Arg Gly Thr Cys Thr Phe Ala Gln Lys Ser Thr Leu  
 165 170 175  
 Ala Lys Ala Ala Gly Ala Val Gly Ala Leu Ile Tyr Asn Asn Glu Pro  
 180 185 190  
 Glu Gln Pro Leu Ser Gly Thr Leu Gly Gly Ala Gly Asp Tyr Ala Pro  
 195 200 205  
 Thr Val Gly Met Thr Lys Glu Ala Gly Glu Ser Leu Ile Ala Lys Leu  
 210 215 220  
 Gly Asn Gly Thr Thr Leu Glu Gly Thr Leu Phe Ile Asp Ala Ile Gln  
 225 230 235 240  
 Glu Asn Arg Thr Asn Tyr Asn Val Ile Ala Glu Thr Lys Glu Gly Asp  
 245 250 255  
 His Asn Asn Val Leu Met Ile Gly Gly His Thr Asp Ser Val Phe Gln  
 260 265 270  
 Gly Pro Gly Ile Asn Asp Asp Gly Ser Gly Thr Ile Gly Thr Leu Val  
 275 280 285  
 Thr Gly Leu Ala Leu Thr Lys Tyr Lys Ile Lys Asn Ala Val Arg Leu  
 290 295 300  
 Gly Phe Trp Gly Ala Glu Phe Gly Lys Leu Gly Ser Phe Tyr Tyr  
 305 310 315 320  
 Met Lys Thr Ile Asn Gly Thr Phe Gly Gly Ser Thr Ala Glu Ala Asn  
 325 330 335  
 Lys Ile Arg Ala Tyr Leu Asn Phe Asp Met Ile Ala Ser Pro Asn Tyr  
 340 345 350  
 Val Leu Gly Ile Tyr Asp Gly Asp Gly Ser Ala Phe Asn Phe Ser Gly  
 355 360 365  
 Ala Ala Gly Ser Asp Lys Ile Glu Lys Asp Phe Glu Glu Phe Tyr Glu  
 370 375 380  
 Glu Arg Gly Leu Pro His Val Pro Ser Leu Phe Thr Leu Arg Ser Asp  
 385 390 395 400

10336256.txt

Tyr Ala Ala Phe Leu Glu Asn Gly Ile Pro Ser Gly Gly Leu Phe Thr  
                   405                  410                  415  
 Gly Ala Glu Val Leu Lys Thr Glu Glu Ala Gln Leu Phe Gly Gly  
                   420                  425                  430  
 Glu Ala Gly Lys Pro Leu Asp Gly Cys Tyr His Gln Ala Cys Asp Asp  
                   435                  440                  445  
 Ile Asn Asn Leu Ala His Asp Ala Tyr Leu Leu Asn Thr Gln Ser Ile  
                   450                  455                  460  
 Ala Asn Ser Val Ala Lys Tyr Ala Val Ser Phe Glu Gly Ile Pro Lys  
                   465                  470                  475                  480  
 Ala Asn Ala Thr Leu Arg Lys Arg Gly Ala Glu Ser Ala Arg Phe Met  
                   485                  490                  495  
 Ser Arg Phe Asp His Gly Gly His Glu His Leu Gly Gln Pro Cys Gly  
                   500                  505                  510  
 Ala Gly Lys His Ala Ile  
                   515

&lt;210&gt; 224

&lt;211&gt; 3377

&lt;212&gt; DNA

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1001)...(1321)

&lt;223&gt; Exon

&lt;221&gt; CDS

&lt;222&gt; (1379)...(1536)

&lt;223&gt; Exon

&lt;221&gt; CDS

&lt;222&gt; (1589)...(1694)

&lt;223&gt; Exon

&lt;221&gt; CDS

&lt;222&gt; (1745)...(2377)

&lt;223&gt; Exon

&lt;400&gt; 224

caagactcaa	ctgcaaagga	tcagcttttg	ctgttttaaat	gctaccttgg	gtagctttca	60
tgtttgagga	acgaaaaaat	agtattgacc	ggaacgtgta	tttagtcccg	aatcgtccag	120
aacaatgcaa	ctacaaaagc	atgccacaag	gtataagcag	tgtaggtttc	ggatatctgg	180
aatcgtttgc	ataagagatg	agaaaaagag	acaagggcga	agtttcacgg	aactctttgg	240
ccgtaaaagc	atcaaaattg	catatgggta	gttttggcct	ataaaagtga	ttttctcaca	300
gcatgcctag	ctctatcaat	tgctacctaa	aacctgagcg	ctggccaaaa	aacgacaaaa	360
tcatttctct	gattggctcg	ttctaaggca	gtaatactaa	ctgttctcca	gactttgtct	420
agatatgggt	tagggtagag	cgcaggcccc	catgctcctt	ggcccttcaa	cataaccgac	480
tccagggagg	tttacatcga	ctgatattcg	ttctcagagc	gctgaaacgt	catagatcct	540
ctttagagact	gcctttttta	attacaaaac	tactggcata	gatcttccga	gacttgattc	600
agccgcgaaa	gctccaacac	aggcccacaa	aacgcgatgc	tggttcccga	gacccgtcgc	660
ttcccatact	actacggtta	aggcgctcaa	attggcaagc	gttggccgag	agaacaggga	720
tttcgcctt	cccacattcc	tattatttcc	taaatacccc	ttacgcaatt	ccttggccac	780
ccatgactcg	gaggatttta	ttaagctata	cgaatattgt	tgcagatcct	atgcccacac	840
aggcagaagt	taagaaacaa	caagacctgc	tiggatgtgg	gacttttttt	caattacaat	900
ggtctatgcg	acaacggcca	tgatgcaatt	caaaaagtgt	gtctagtcca	gcagtgttgg	960
gcaagccgcc	tctgtttccac	acgccttgcc	ttcgttcaca	atg cgc ttc ttc act		1015
				Met Arg Phe Phe Thr		
				1                  5		
cgt ttc acc gcg cta gtc aca gcc gca gct ccg ttc att gct ctt gct						1063
Arg Phe Thr Ala Leu Val Thr Ala Ala Ala Pro Phe Ile Ala Leu Ala						
	10		15		20	
gct ccc gtc gca gca cct cca gag aat gac ata att cct gga aaa tac						1111
Ala Pro Val Ala Ala Pro Pro Glu Asn Asp Ile Ile Pro Gly Lys Tyr						
	25		30		35	

## 10336256.txt

ata gtc cag ctg aag cct gat acc gat gtc gca gcg gtc gct gcc cac	1159
Ile Val Gln Leu Lys Pro Asp Thr Asp Val Ala Ala Val Ala Ala His	
40 45 50	
cat cac aaa gtg cgc agc atc cat gcc cgc aac ctg gcc cga cga ggt	1207
His His Lys Val Arg Ser Ile His Ala Arg Asn Leu Ala Arg Arg Gly	
55 60 65	
gac aat tct ccg act ggt gag cca gtg gag cgc gag tac ggg ttc ggc	1255
Asp Asn Ser Pro Thr Gly Glu Pro Val Glu Arg Glu Tyr Gly Phe Gly	
70 75 80 85	
gac ttc aaa ggc tat tct ggg ttt ttc gat gaa gca acc atc gaa gag	1303
Asp Phe Lys Gly Tyr Ser Gly Phe Phe Asp Glu Ala Thr Ile Glu Glu	
90 95 100	
ttg aaa act ctg cca gag gtaatacagg ccccttcata caatgtcaca	1351
Leu Lys Thr Leu Pro Glu	
105	
acctagcaat gctgatataa ttgttag gtg ctt gta gtt gag cca gat ttt atc	1405
Val Leu Val Val Glu Pro Asp Phe Ile	
110 115	
atg agg act tcc gca att gtg tct cag gca agc cca cca tgg ggc ctc	1453
Met Arg Thr Ser Ala Ile Val Ser Gln Ala Ser Pro Pro Trp Gly Leu	
120 125 130	
gct agt atc tcc tcc cgc aca cca gga gct gcc tct tat gtc tac gac	1501
Ala Ser Ile Ser Ser Arg Thr Pro Gly Ala Ala Ser Tyr Val Tyr Asp	
135 140 145	
gac agt gcg ggc caa ggc acc ttt tcc tac gtg at aggtaagtca	1546
Asp Ser Ala Gly Gln Gly Thr Phe Ser Tyr Val Ile	
150 155 160	
aaaacatagt gtagatcttg atttggtggt gacatattat ca a gac acg ggt gtg	1601
Asp Thr Gly Val	
cgc atc acc cac cag gac ttt ggc gga cga gcc atc tgg gga ttt aat	1649
Arg Ile Thr His Gln Asp Phe Gly Gly Arg Ala Ile Trp Gly Phe Asn	
165 170 175 180	
gcc gta aga aac agt cct gat act gat gaa gat ggc cat gga acg	1694
Ala Val Arg Asn Ser Pro Asp Thr Asp Glu Asp Gly His Gly Thr	
185 190 195	
taagccacac ttcatctcac agtggcaata ctcttctgac ataaactagt cac gtt	1750
His Val	
gct gga acc gtt ggc ggt acc aaa tat ggt gtt gcc aag aaa acc acc	1798
Ala Gly Thr Val Gly Gly Thr Lys Tyr Gly Val Ala Lys Lys Thr Thr	
200 205 210	
atc ata agt gtc aag acc ttc ggt ggt agc tca gga agt gca tca gat	1846
Ile Ile Ser Val Lys Thr Phe Gly Gly Ser Ser Gly Ser Ala Ser Asp	
215 220 225	
gtc ttc gca ggg ttc gac tgg acg gtc aac gat atc gtt tcc aag aac	1894
Val Phe Ala Gly Phe Asp Trp Thr Val Asn Asp Ile Val Ser Lys Asn	
230 235 240 245	
cga caa aac att gcc gtc atc aat atg tcg ttc ggt gga tct gcc tct	1942
Arg Gln Asn Ile Ala Val Ile Asn Met Ser Phe Gly Gly Ser Ala Ser	
250 255 260	

## 10336256.txt

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aca acg tgg gac aat gcc att act gca gct tgg aac aaa ggg gta agc      1990
Thr Thr Trp Asp Asn Ala Ile Thr Ala Ala Trp Asn Lys Gly Val Ser
265                               270                               275

atg gtc gta gca gca gga aac gaa gac gga ccc aca tcc aat cgc tcg      2038
Met Val Val Ala Ala Gly Asn Glu Asp Gly Pro Thr Ser Asn Arg Ser
280                               285                               290

cca gcc cgc tct ccc gaa gcc atc tgt gtc ggg aac gtc cag agc aac      2086
Pro Ala Arg Ser Pro Glu Ala Ile Cys Val Gly Asn Val Gln Ser Asn
295                               300                               305

aac aga agg ctc agc ggt gga gga ggc tcc aac tac ggc cct gaa gtg      2134
Asn Arg Arg Leu Ser Gly Gly Gly Ser Asn Tyr Gly Pro Glu Val
310                               315                               320                               325

gat atc ttc gct gca ggc acc ctc atc gtc tcc gca tcc cat ctg agc      2182
Asp Ile Phe Ala Ala Gly Thr Leu Ile Val Ser Ala Ser His Leu Ser
330                               335                               340

gac aca gga aca acc act aag aac ggt act tcc atg gcg gct cct cac      2230
Asp Thr Gly Thr Thr Lys Asn Gly Thr Ser Met Ala Ala Pro His
345                               350                               355

gta gct ggt ctg atc tca tac ctt cgt ggc ctt gag ggt ccc tcg act      2278
Val Ala Gly Leu Ile Ser Tyr Leu Arg Gly Leu Glu Gly Pro Ser Thr
360                               365                               370

gcg gcg gcc att aag gcg agg gtg tat caa ctg gcc acg cct ggt gtc      2326
Ala Ala Ala Ile Lys Ala Arg Val Tyr Gln Leu Ala Thr Pro Gly Val
375                               380                               385

gtg aca gac gca atg ggc tca gtc aat cta ctg gca tac aac ggt aac      2374
Val Thr Asp Ala Met Gly Ser Val Asn Leu Leu Ala Tyr Asn Gly Asn
390                               395                               400                               405

aaa taatcgcat tctcatgaac gaggatccta gaattgcggt aatctacgat      2427
Lys

tttatgattg ggatgtaatc tacttccttg cctgggctct tttctgtata tattatgtgt      2487
tgaataacta ccaattatcc gattttatcc aagtcacttt caatgcttca aagttgtagt      2547
atgacttggt tagactaacc tgtaatgttc tagaagtcac gctgtctacc aatccaactc      2607
gaactcgaca gtgactcgga aggccttcga aaacacaagc tcttgaacga agggaaacaca      2667
agcgcttcatt tttttactac tcgtctcgaa tcgattcctt cacaatgtta ttgaaaggaa      2727
caactagctc acagatgagt tacaaagcat ctcaagatat cgataattct tcaaaatctc      2787
atattagtag gtgagcaata cattgccatg ttcccacttg gtaaagggtg acttttacga      2847
aaggatatact tagcagcttg gcgcgcgtcaa aaaatgtcaa caccaaccgg acatgtcgaa      2907
tgatccactt ccaagtcac caagacggag caagtcctgc ctatcctgcc gtgaactcca      2967
gaaaacgtgt acgatcatcg gggatgatgc aaggtccatc cttgtgtcaa gagacactcg      3027
ctgtgcagag acagcttcta atccgtactt cctgaatctt ttacctatag atcttccaag      3087
ctttcggtaa tataataaag ttctaccgtc ttctcttctt cagaaatcaa gtctccagaa      3147
agcaccattg caatgttgga cttgttatcg atcgttgctc gatgcggggc gccaacatca      3207
acatccagag tgtaatgcat ggcagcgcac tacacgcagc tacatattgg ggcgaaaaat      3267
gcaaagctgg agcttcta atgtcaaaattc gatatcaagc agctccaaga tccgtacaac      3327
cagactctac tctcgtaggc tgcaggcggt ggccagcctc atactgctaa      3377

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&lt;210&gt; 225

&lt;211&gt; 107

&lt;212&gt; PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

&lt;400&gt; 225

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Met Arg Phe Phe Thr Arg Phe Thr Ala Leu Val Thr Ala Ala Ala Pro
 1           5           10           15
Phe Ile Ala Leu Ala Ala Pro Val Ala Ala Pro Pro Glu Asn Asp Ile
20           25           30
Ile Pro Gly Lys Tyr Ile Val Gln Leu Lys Pro Asp Thr Asp Val Ala

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## 10336256.txt

35 40 45  
 Ala Val Ala Ala His His His Lys Val Arg Ser Ile His Ala Arg Asn  
 50 55 60  
 Leu Ala Arg Arg Gly Asp Asn Ser Pro Thr Gly Glu Pro Val Glu Arg  
 65 70 75 80  
 Glu Tyr Gly Phe Gly Asp Phe Lys Gly Tyr Ser Gly Phe Phe Asp Glu  
 85 90 95  
 Ala Thr Ile Glu Glu Leu Lys Thr Leu Pro Glu  
 100 105

&lt;210&gt; 226

&lt;211&gt; 53

&lt;212&gt; PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

&lt;400&gt; 226

Val Leu Val Val Glu Pro Asp Phe Ile Met Arg Thr Ser Ala Ile Val  
 1 5 10 15  
 Ser Gln Ala Ser Pro Pro Trp Gly Leu Ala Ser Ile Ser Ser Arg Thr  
 20 25 30  
 Pro Gly Ala Ala Ser Tyr Val Tyr Asp Asp Ser Ala Gly Gln Gly Thr  
 35 40 45  
 Phe Ser Tyr Val Ile  
 50

&lt;210&gt; 227

&lt;211&gt; 35

&lt;212&gt; PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

&lt;400&gt; 227

Asp Thr Gly Val Arg Ile Thr His Gln Asp Phe Gly Gly Arg Ala Ile  
 1 5 10 15  
 Trp Gly Phe Asn Ala Val Arg Asn Ser Pro Asp Thr Asp Glu Asp Gly  
 20 25 30  
 His Gly Thr  
 35

&lt;210&gt; 228

&lt;211&gt; 211

&lt;212&gt; PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

&lt;400&gt; 228

His Val Ala Gly Thr Val Gly Gly Thr Lys Tyr Gly Val Ala Lys Lys  
 1 5 10 15  
 Thr Thr Ile Ile Ser Val Lys Thr Phe Gly Gly Ser Ser Gly Ser Ala  
 20 25 30  
 Ser Asp Val Phe Ala Gly Phe Asp Trp Thr Val Asn Asp Ile Val Ser  
 35 40 45  
 Lys Asn Arg Gln Asn Ile Ala Val Ile Asn Met Ser Phe Gly Gly Ser  
 50 55 60  
 Ala Ser Thr Thr Trp Asp Asn Ala Ile Thr Ala Ala Trp Asn Lys Gly  
 65 70 75 80  
 Val Ser Met Val Val Ala Ala Gly Asn Glu Asp Gly Pro Thr Ser Asn  
 85 90 95  
 Arg Ser Pro Ala Arg Ser Pro Glu Ala Ile Cys Val Gly Asn Val Gln  
 100 105 110  
 Ser Asn Asn Arg Arg Leu Ser Gly Gly Gly Gly Ser Asn Tyr Gly Pro  
 115 120 125  
 Glu Val Asp Ile Phe Ala Ala Gly Thr Leu Ile Val Ser Ala Ser His  
 130 135 140  
 Leu Ser Asp Thr Gly Thr Thr Thr Lys Asn Gly Thr Ser Met Ala Ala  
 145 150 155 160  
 Pro His Val Ala Gly Leu Ile Ser Tyr Leu Arg Gly Leu Glu Gly Pro  
 165 170 175  
 Ser Thr Ala Ala Ala Ile Lys Ala Arg Val Tyr Gln Leu Ala Thr Pro  
 180 185 190

10336256.txt

Gly Val Val Thr Asp Ala Met Gly Ser Val Asn Leu Leu Ala Tyr Asn  
 195 200 205  
 Gly Asn Lys  
 210

&lt;210&gt; 229

&lt;211&gt; 1218

&lt;212&gt; DNA

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1218)

&lt;400&gt; 229

atg cgc ttc ttc act cgt ttc acc gcg cta gtc aca gcc gca gct ccg	48
Met Arg Phe Phe Thr Arg Phe Thr Ala Leu Val Thr Ala Ala Ala Pro	
1 5 10 15	
ttc att gct ctt gct gct ccc gtc gca gca cct cca gag aat gac ata	96
Phe Ile Ala Leu Ala Ala Pro Val Ala Ala Pro Pro Glu Asn Asp Ile	
20 25 30	
att cct gga aaa tac ata gtc cag ctg aag cct gat acc gat gtc gca	144
Ile Pro Gly Lys Tyr Ile Val Gln Leu Lys Pro Asp Thr Asp Val Ala	
35 40 45	
gcg gtc gct gcc cac cat cac aaa gtg cgc agc atc cat gcc cgc aac	192
Ala Val Ala Ala His His His Lys Val Arg Ser Ile His Ala Arg Asn	
50 55 60	
ctg gcc cga cga ggt gac aat tct ccg act ggt gag cca gtg gag cgc	240
Leu Ala Arg Arg Gly Asp Asn Ser Pro Thr Gly Glu Pro Val Glu Arg	
65 70 75 80	
gag tac ggg ttc ggc gac ttc aaa ggc tat tct ggg ttt ttc gat gaa	288
Glu Tyr Gly Phe Gly Asp Phe Lys Gly Tyr Ser Gly Phe Phe Asp Glu	
85 90 95	
gca acc atc gaa gag ttg aaa act ctg cca gag gtg ctt gta gtt gag	336
Ala Thr Ile Glu Glu Leu Lys Thr Leu Pro Glu Val Leu Val Val Glu	
100 105 110	
cca gat ttt atc atg agg act tcc gca att gtg tct cag gca agc cca	384
Pro Asp Phe Ile Met Arg Thr Ser Ala Ile Val Ser Gln Ala Ser Pro	
115 120 125	
cca tgg ggc ctc gct agt atc tcc tcc cgc aca cca gga gct gcc tct	432
Pro Trp Gly Leu Ala Ser Ile Ser Ser Arg Thr Pro Gly Ala Ala Ser	
130 135 140	
tat gtc tac gac gac agt gcg ggc caa ggc acc ttt tcc tac gtg ata	480
Tyr Val Tyr Asp Asp Ser Ala Gly Gln Gly Thr Phe Ser Tyr Val Ile	
145 150 155 160	
gac acg ggt gtg cgc atc acc cac cag gac ttt ggc gga cga gcc atc	528
Asp Thr Gly Val Arg Ile Thr His Gln Asp Phe Gly Gly Arg Ala Ile	
165 170 175	
tgg gga ttt aat gcc gta aga aac agt cct gat act gat gaa gat ggc	576
Trp Gly Phe Asn Ala Val Arg Asn Ser Pro Asp Thr Asp Glu Asp Gly	
180 185 190	
cat gga acg cac gtt gct gga acc gtt ggc ggt acc aaa tat ggt gtt	624
His Gly Thr His Val Ala Gly Thr Val Gly Gly Thr Lys Tyr Gly Val	
195 200 205	
gcc aag aaa acc acc atc ata agt gtc aag acc ttc ggt ggt agc tca	672

10336256.txt

Ala	Lys	Lys	Thr	Thr	Ile	Ile	Ser	Val	Lys	Thr	Phe	Gly	Gly	Ser	Ser	
210						215					220					
gga	agt	gca	tca	gat	gtc	ttc	gca	ggg	ttc	gac	tgg	acg	gtc	aac	gat	720
Gly	Ser	Ala	Ser	Asp	Val	Phe	Ala	Gly	Phe	Asp	Trp	Thr	Val	Asn	Asp	
225					230				235						240	
atc	gtt	tcc	aag	aac	cga	caa	aac	att	gcc	gtc	atc	aat	atg	tcg	ttc	768
Ile	Val	Ser	Lys	Asn	Arg	Gln	Asn	Ile	Ala	Val	Ile	Asn	Met	Ser	Phe	
				245					250					255		
ggt	gga	tct	gcc	tct	aca	acg	tgg	gac	aat	gcc	att	act	gca	gct	tgg	816
Gly	Gly	Ser	Ala	Ser	Thr	Thr	Trp	Asp	Asn	Ala	Ile	Thr	Ala	Ala	Trp	
			260					265					270			
aac	aaa	ggg	gta	agc	atg	gtc	gta	gca	gca	gga	aac	gaa	gac	gga	ccc	864
Asn	Lys	Gly	Val	Ser	Met	Val	Val	Ala	Ala	Gly	Asn	Glu	Asp	Gly	Pro	
		275					280					285				
aca	tcc	aat	cgc	tcg	cca	gcc	cgc	tct	ccc	gaa	gcc	atc	tgt	gtc	ggg	912
Thr	Ser	Asn	Arg	Ser	Pro	Ala	Arg	Ser	Pro	Glu	Ala	Ile	Cys	Val	Gly	
	290					295				300						
aac	gtc	cag	agc	aac	aac	aga	agg	ctc	agc	ggt	gga	gga	ggc	tcc	aac	960
Asn	Val	Gln	Ser	Asn	Asn	Arg	Arg	Leu	Ser	Gly	Gly	Gly	Gly	Ser	Asn	
305					310					315					320	
tac	ggc	cct	gaa	gtg	gat	atc	ttc	gct	gca	ggc	acc	ctc	atc	gtc	tcc	1008
Tyr	Gly	Pro	Glu	Val	Asp	Ile	Phe	Ala	Ala	Gly	Thr	Leu	Ile	Val	Ser	
				325				330						335		
gca	tcc	cat	ctg	agc	gac	aca	gga	aca	acc	act	aag	aac	ggt	act	tcc	1056
Ala	Ser	His	Leu	Ser	Asp	Thr	Gly	Thr	Thr	Thr	Lys	Asn	Gly	Thr	Ser	
			340				345						350			
atg	gcg	gct	cct	cac	gta	gct	ggt	ctg	atc	tca	tac	ctt	cgt	ggc	ctt	1104
Met	Ala	Ala	Pro	His	Val	Ala	Gly	Leu	Ile	Ser	Tyr	Leu	Arg	Gly	Leu	
		355					360					365				
gag	ggt	ccc	tcg	act	gcg	gcg	gcc	att	aag	gcg	agg	gtg	tat	caa	ctg	1152
Glu	Gly	Pro	Ser	Thr	Ala	Ala	Ala	Ile	Lys	Ala	Arg	Val	Tyr	Gln	Leu	
	370					375				380						
gcc	acg	cct	ggt	gtc	gtg	aca	gac	gca	atg	ggc	tca	gtc	aat	cta	ctg	1200
Ala	Thr	Pro	Gly	Val	Val	Thr	Asp	Ala	Met	Gly	Ser	Val	Asn	Leu	Leu	
385					390					395					400	
gca	tac	aac	ggt	aac	aaa											1218
Ala	Tyr	Asn	Gly	Asn	Lys											
				405												

&lt;210&gt; 230

&lt;211&gt; 406

&lt;212&gt; PRT

&lt;213&gt; Cochliobolus heterostrophus strain C4 (ATCC 48331)

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; (1)...(21)

&lt;221&gt; DOMAIN

&lt;222&gt; (35)...(120)

&lt;223&gt; Subtilisin N-terminal region

&lt;221&gt; DOMAIN

&lt;222&gt; (134)...(397)

&lt;223&gt; Subtilase family

## 10336256.txt

&lt;400&gt; 230

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Met Arg Phe Phe Thr Arg Phe Thr Ala Leu Val Thr Ala Ala Ala Pro
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Phe Ile Ala Leu Ala Ala Pro Val Ala Ala Pro Pro Glu Asn Asp Ile
20      25      30
Ile Pro Gly Lys Tyr Ile Val Gln Leu Lys Pro Asp Thr Asp Val Ala
35      40      45
Ala Val Ala Ala His His His Lys Val Arg Ser Ile His Ala Arg Asn
50      55      60
Leu Ala Arg Arg Gly Asp Asn Ser Pro Thr Gly Glu Pro Val Glu Arg
65      70      75      80
Glu Tyr Gly Phe Gly Asp Phe Lys Gly Tyr Ser Gly Phe Phe Asp Glu
85      90      95
Ala Thr Ile Glu Glu Leu Lys Thr Leu Pro Glu Val Leu Val Val Glu
100     105     110
Pro Asp Phe Ile Met Arg Thr Ser Ala Ile Val Ser Gln Ala Ser Pro
115     120     125
Pro Trp Gly Leu Ala Ser Ile Ser Ser Arg Thr Pro Gly Ala Ala Ser
130     135     140
Tyr Val Tyr Asp Asp Ser Ala Gly Gln Gly Thr Phe Ser Tyr Val Ile
145     150     155     160
Asp Thr Gly Val Arg Ile Thr His Gln Asp Phe Gly Gly Arg Ala Ile
165     170     175
Trp Gly Phe Asn Ala Val Arg Asn Ser Pro Asp Thr Asp Glu Asp Gly
180     185     190
His Gly Thr His Val Ala Gly Thr Val Gly Gly Thr Lys Tyr Gly Val
195     200     205
Ala Lys Lys Thr Thr Ile Ile Ser Val Lys Thr Phe Gly Gly Ser Ser
210     215     220
Gly Ser Ala Ser Asp Val Phe Ala Gly Phe Asp Trp Thr Val Asn Asp
225     230     235     240
Ile Val Ser Lys Asn Arg Gln Asn Ile Ala Val Ile Asn Met Ser Phe
245     250     255
Gly Gly Ser Ala Ser Thr Thr Trp Asp Asn Ala Ile Thr Ala Ala Trp
260     265     270
Asn Lys Gly Val Ser Met Val Val Ala Ala Gly Asn Glu Asp Gly Pro
275     280     285
Thr Ser Asn Arg Ser Pro Ala Arg Ser Pro Glu Ala Ile Cys Val Gly
290     295     300
Asn Val Gln Ser Asn Asn Arg Arg Leu Ser Gly Gly Gly Gly Ser Asn
305     310     315     320
Tyr Gly Pro Glu Val Asp Ile Phe Ala Ala Gly Thr Leu Ile Val Ser
325     330     335
Ala Ser His Leu Ser Asp Thr Gly Thr Thr Lys Asn Gly Thr Ser
340     345     350
Met Ala Ala Pro His Val Ala Gly Leu Ile Ser Tyr Leu Arg Gly Leu
355     360     365
Glu Gly Pro Ser Thr Ala Ala Ile Lys Ala Arg Val Tyr Gln Leu
370     375     380
Ala Thr Pro Gly Val Val Thr Asp Ala Met Gly Ser Val Asn Leu Leu
385     390     395     400
Ala Tyr Asn Gly Asn Lys
405

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&lt;210&gt; 231

&lt;211&gt; 3206

&lt;212&gt; DNA

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (883)...(948)

&lt;223&gt; Exon

&lt;221&gt; CDS

&lt;222&gt; (1010)...(3106)

&lt;223&gt; Exon

## 10336256.txt

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gtagggtgtaa tatgctgaca cgaaaataca gtcgaatcga gccagatcta ggcctggcaa 180  
ggcaggtata gatgtcaatc tgctcacgga catgttaggc gtgcaaaagg cccaagccag 240  
accaaggatg ccaagaaata tcatgcagtc ccgcccctctc aattccgcga ggatgcattc 300  
cagcagccag ccagcgccgt ggatgtggag gatctatgtg taacctcatg ttggactttt 360  
tttcgacctg cttttttggg tgcaccgttt atccgccaca aattagttgg tgattagcgt 420  
gagctgtggg catgcgccac caatcgcat gtgggcttgg tggagctact acacaccaa 480  
gatacccacc cataaacgcc aagtcagtc atccagcgac tctcaagtgg accaagttgc 540  
gataggacga cacggaaaca tgctttcttg caatccacct aggacgagct tgtttttgtc 600  
cccgcgcatc tagccctgat cgggcaggag acatggtgca aaacgtctat cttttgacgt 660  
ctatggacta gtcgctact cattgcctat ggaatgatgg catcgctact tcaggtaacc 720  
gtcccgaag gagtggtccc actgcctgga tggcgacatg ccctgcggca ggggcctcgg 780  
gcttagctct ttgtacaaat aattcgatg ccctgcatgg ccttcttctg gtcacgcacc 840  
tcgtccaatt gagcttttac gaagctggtc gcatactgca ca atg gct cgt tac 894  
Met Ala Arg Tyr  
1

ctc agt gtt gcc gca gca ctg gct gct act ggc gcg tgc gcg ttc aca 942  
Leu Ser Val Ala Ala Ala Leu Ala Ala Thr Gly Ala Cys Ala Phe Thr 20  
5 10 15

ccc gag tgcgtctttt gtcccctaca gctacatgct cccgatgacg gcaagcta 998  
Pro Glu

aaacatacag g ttg ctt ctt agc acc gta cga cgc gct gcc gcc gat ccc 1048  
Leu Leu Leu Ser Thr Val Arg Arg Ala Ala Ala Asp Pro 35  
25 30

agt cca gat ggc tca gtc gcg ctc ttc tcg tac acg cag tac tcc ttc 1096  
Ser Pro Asp Gly Ser Val Ala Leu Phe Ser Tyr Thr Gln Tyr Ser Phe 50  
40 45

gag gaa cat gcg cgc acg gct ggc atg aac ctc atc gat ctc aag acc 1144  
Glu Glu His Ala Arg Thr Ala Gly Met Asn Leu Ile Asp Leu Lys Thr 65  
55 60

ggt gag gtc acc aag tcg ggc ctc gac ccc agc gag gtc aac gaa gtg 1192  
Gly Glu Val Thr Lys Ser Gly Leu Asp Pro Ser Glu Val Asn Glu Val 80  
70 75

gcc tgg att cct ggc acc gag acc ggt atc atc tac atc aat ggc aca 1240  
Ala Trp Ile Pro Gly Thr Glu Thr Gly Ile Ile Tyr Ile Asn Gly Thr 95  
85 90

aac gag gaa atc cca ggt ggt gtc acc ctg tgg att ggt gac atc aag 1288  
Asn Glu Glu Ile Pro Gly Gly Val Thr Leu Trp Ile Gly Asp Ile Lys 115  
100 105 110

gac cca agc gcc agc act ctt gtt gcc tcc ctg gat gca cca tac tcc 1336  
Asp Pro Ser Ala Ser Thr Leu Val Ala Ser Leu Asp Ala Pro Tyr Ser 130  
120 125

ggc ttg aag gtt gcc aac acc tct act ggt gac ttg cat ttc ttg gtc 1384  
Gly Leu Lys Val Ala Asn Thr Ser Thr Gly Asp Leu His Phe Leu Val 145  
135 140

aac agc ttg gcc tac ccc aac ggc act gca gtt aac ccc gag acc gaa 1432  
Asn Ser Leu Ala Tyr Pro Asn Gly Thr Ala Val Asn Pro Glu Thr Glu 160  
150 155

gtc aag cca act tca act gcc cgt tac tac tcg gat atc tat gtc cgc 1480  
Val Lys Pro Thr Ser Thr Ala Arg Tyr Tyr Ser Asp Ile Tyr Val Arg 175  
165 170

## 10336256.txt

cac His 180	tgg Trp	gat Asp	acc Thr	tgg Trp	cta Leu 185	act Thr	aag Lys	aac Asn	cgc Arg	tac Tyr 190	cag Gln	ctt Leu	ttt Phe	gct Ala	ggt Gly 195	1528
aca Thr	ctt Leu	tcc Ser	aag Lys	aac Asn 200	agc Ser	agt Ser	tat Tyr	gct Ala	ctc Leu 205	tct Ser	ggc Gly	gct Ala	ggc Gly	gtg Val 210	cgc Arg	1576
aac Asn	atc Ile	caa Gln	agt Ser 215	ggt Gly	atc Ile	aaa Lys	ttc Phe	acc Thr 220	gct Ala	act Thr	cag Gln	cct Pro	gag Glu 225	act Thr	ccc Pro	1624
gtc Val	cag Gln	cct Pro 230	ttt Phe	ggc Gly	gac Asp	tcg Ser	agc Ser 235	gat Asp	tat Tyr	gac Asp	atc Ile	agt Ser 240	ccc Pro	gat Asp	ggc Gly	1672
tct Ser	atg Met 245	tat Tyr	gct Ala	ttc Phe	att Ile	agc Ser 250	aag Lys	gct Ala	cct Pro	cag Gln	ctc Leu 255	aac Asn	aag Lys	gcc Ala	aac Asn	1720
tac Tyr 260	acc Thr	gcg Ala	tcc Ser	tac Tyr	cta Leu 265	tac Tyr	gtc Val	ggt Gly	gcc Ala	ttt Phe 270	gcc Ala	tcc Ser	aac Asn	gaa Glu	gct Ala 275	1768
ccc Pro	gtt Val	gct Ala	ctc Leu	aac Asn 280	ggc Gly	cct Pro	gac Asp	tct Ser	gag Glu 285	gct Ala	ttc Phe	aag Lys	gct Ala	gga Gly 290	cac His	1816
cag Gln	ggt Gly	gct Ala	tcc Ser 295	ggt Gly	cta Leu	cca Pro	tcc Ser	ttc Phe 300	tcc Ser	ggt Gly	gac Asp	agc Ser	tcg Cys 305	aag Lys	ctt Leu	1864
gca Ala	tat Tyr	gtc Val 310	caa Gln	caa Gln	gac Asp	gag Glu	gac Asp 315	tac Tyr	tat Tyr	gag Glu	tcg Ser	gac Asp 320	agg Arg	ttc Phe	aag Lys	1912
ctg Leu	tac Tyr 325	acc Thr	tac Tyr	gac Asp	gtt Val	gct Ala 330	gtc Val	gag Glu	ggc Gly	caa Gln	ggc Gly 335	gtg Val	gcc Ala	gct Ala	agc Ser	1960
aac Asn 340	tgg Trp	aag Lys	agc Ser	ttg Leu	agc Ser 345	gaa Glu	ggt Gly	ttt Phe	gac Asp	cgc Arg 350	tgg Trp	gtg Val	caa Gln	ggt Gly	ccc Pro 355	2008
att Ile	act Thr	tgg Trp	gct Ala	cac His 360	gac Asp	gat Asp	tct Ser	tca Ser	atc Ile 365	tac Tyr	gtc Val	act Thr	gct Ala	gat Asp 370	gac Asp	2056
tac Tyr	gcc Ala	cgc Arg	aac Asn 375	aag Lys	atc Ile	ttc Phe	aac Asn	ttc Phe 380	cca Pro	atc Ile	acc Thr	gcg Ala	gat Asp 385	gag Glu	aag Lys	2104
ttt Phe	gtt Val	ccc Pro 390	gag Glu	ccg Pro	cta Leu	act Thr	gga Gly 395	aac Asn	act Thr	tca Ser	gtt Val	tcg Ser 400	gcg Ala	ttt Phe	tct Ser	2152
ctg Leu	ctt Leu 405	cct Pro	gac Asp	ggt Gly	tcg Ser	ctg Leu 410	ttc Phe	gtt Val	gca Ala	gcc Ala	acc Thr 415	gct Ala	atc Ile	tgg Trp	act Thr	2200
ccc Pro 420	aac Asn	gaa Glu	tgg Trp	tac Tyr	atc Ile 425	ctc Leu	gcc Ala	gac Asp	ggc Gly	aac Asn 430	aag Lys	aag Lys	acg Thr	ctt Leu	ctt Leu 435	2248
gac Asp	gct Ala	tcc Ser	cag Gln	gtt Val 440	gac Asp	ccc Pro	aac Asn	ctg Leu	gcc Ala 445	ggt Gly	ctc Leu	agc Ser	tcc Ser	aag Lys 450	act Thr	2296

10336256.txt																
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			455					460					465			
ctt	cag	gct	tat	gtc	gtc	aag	ccc	aca	ttc	tac	caa	gag	aac	gtt	act	2392
Leu	Gln	Ala	Tyr	Val	Val	Lys	Pro	Thr	Phe	Tyr	Gln	Glu	Asn	Val	Thr	
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tac	ccc	ctt	gct	ttc	ctg	att	cac	ggg	ggg	cct	cag	ggc	aac	tgg	ggc	2440
Tyr	Pro	Leu	Ala	Phe	Leu	Ile	His	Gly	Gly	Pro	Gln	Gly	Asn	Trp	Gly	
			485			490					495					
aac	agc	tgg	tca	aac	cgc	tgg	aac	ccg	cag	gtc	tgg	gcc	gac	caa	ggc	2488
Asn	Ser	Trp	Ser	Asn	Arg	Trp	Asn	Pro	Gln	Val	Trp	Ala	Asp	Gln	Gly	
					505					510					515	
tac	atc	gtc	gtc	gca	cct	aac	ccg	act	ggg	tct	aca	agt	ttc	gga	cag	2536
Tyr	Ile	Val	Val	Ala	Pro	Asn	Pro	Thr	Gly	Ser	Thr	Ser	Phe	Gly	Gln	
				520					525					530		
tac	ctc	atc	gac	tcc	atc	cag	ggc	gag	tgg	ggc	agc	tgg	cca	tac	gaa	2584
Tyr	Leu	Ile	Asp	Ser	Ile	Gln	Gly	Glu	Trp	Gly	Ser	Trp	Pro	Tyr	Glu	
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gac	ctg	gtc	aat	gcc	tgg	aac	tac	atc	aac	tcc	acc	atg	acg	tgg	atc	2632
Asp	Leu	Val	Asn	Ala	Trp	Asn	Tyr	Ile	Asn	Ser	Thr	Met	Thr	Trp	Ile	
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gac	acc	gag	aac	ggg	atc	gcc	gcc	ggg	gcc	tcc	tac	ggg	gga	tac	atg	2680
Asp	Thr	Glu	Asn	Gly	Ile	Ala	Ala	Gly	Ala	Ser	Tyr	Gly	Gly	Tyr	Met	
			565			570				575						
acc	aac	tgg	atc	cag	tcc	aat	gac	ctc	ggc	aac	gag	ttc	aag	gct	ctc	2728
Thr	Asn	Trp	Ile	Gln	Ser	Asn	Asp	Leu	Gly	Asn	Glu	Phe	Lys	Ala	Leu	
					585				590						595	
gtc	acc	cat	gac	ggg	atc	tcc	aac	acc	gag	ggg	gcc	tgg	gcg	tcc	gag	2776
Val	Thr	His	Asp	Gly	Ile	Ser	Asn	Thr	Glu	Gly	Ala	Trp	Ala	Ser	Glu	
				600					605					610		
gag	ctc	tgg	ttc	atc	cgc	cac	gac	tac	gat	ggc	aac	atc	tgg	gac	tca	2824
Glu	Leu	Trp	Phe	Ile	Arg	His	Asp	Tyr	Asp	Gly	Asn	Ile	Trp	Asp	Ser	
			615					620					625			
ccc	gcc	tac	cgc	cag	tgg	aac	ccc	cag	aac	cac	att	gcc	aac	tgg	tcc	2872
Pro	Ala	Tyr	Arg	Gln	Trp	Asn	Pro	Gln	Asn	His	Ile	Ala	Asn	Trp	Ser	
			630				635					640				
act	ccc	cag	ttc	gtc	atc	cac	aac	acg	ctc	gac	tac	cgt	ctc	ccc	gag	2920
Thr	Pro	Gln	Phe	Val	Ile	His	Asn	Thr	Leu	Asp	Tyr	Arg	Leu	Pro	Glu	
			645			650					655					
agc	gac	ggc	atc	agc	ctg	ttc	aac	atc	ctc	cag	gcg	cgc	ggg	atc	ccc	2968
Ser	Asp	Gly	Ile	Ser	Leu	Phe	Asn	Ile	Leu	Gln	Ala	Arg	Gly	Ile	Pro	
					665					670					675	
agt	cgc	ttc	ctc	aac	ttc	ccc	gac	gag	aac	cac	tgg	gtc	ctc	aag	cag	3016
Ser	Arg	Phe	Leu	Asn	Phe	Pro	Asp	Glu	Asn	His	Trp	Val	Leu	Lys	Gln	
				680					685					690		
gag	aac	agc	ttg	gtt	tgg	cac	act	gag	att	ttc	aac	tgg	atc	aac	cac	3064
Glu	Asn	Ser	Leu	Val	Trp	His	Thr	Glu	Ile	Phe	Asn	Trp	Ile	Asn	His	
			695					700					705			
tgg	tcc	aag	ggg	gag	cct	ttg	agc	act	acc	ccg	att	ggc	aac			3106
Trp	Ser	Lys	Gly	Glu	Pro	Leu	Ser	Thr	Thr	Pro	Ile	Gly	Asn			
			710				715					720				

10336256.txt

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&lt;210&gt; 232

&lt;211&gt; 22

&lt;212&gt; PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

&lt;400&gt; 232

Met Ala Arg Tyr Leu Ser Val Ala Ala Ala Leu Ala Ala Thr Gly Ala  
 1 5 10 15  
 Cys Ala Phe Thr Pro Glu  
 20

&lt;210&gt; 233

&lt;211&gt; 699

&lt;212&gt; PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

&lt;400&gt; 233

Leu Leu Leu Ser Thr Val Arg Arg Ala Ala Ala Asp Pro Ser Pro Asp  
 1 5 10 15  
 Gly Ser Val Ala Leu Phe Ser Tyr Thr Gln Tyr Ser Phe Glu Glu His  
 20 25 30  
 Ala Arg Thr Ala Gly Met Asn Leu Ile Asp Leu Lys Thr Gly Glu Val  
 35 40 45  
 Thr Lys Ser Gly Leu Asp Pro Ser Glu Val Asn Glu Val Ala Trp Ile  
 50 55 60  
 Pro Gly Thr Glu Thr Gly Ile Ile Tyr Ile Asn Gly Thr Asn Glu Glu  
 65 70 75 80  
 Ile Pro Gly Gly Val Thr Leu Trp Ile Gly Asp Ile Lys Asp Pro Ser  
 85 90 95  
 Ala Ser Thr Leu Val Ala Ser Leu Asp Ala Pro Tyr Ser Gly Leu Lys  
 100 105 110  
 Val Ala Asn Thr Ser Thr Gly Asp Leu His Phe Leu Val Asn Ser Leu  
 115 120 125  
 Ala Tyr Pro Asn Gly Thr Ala Val Asn Pro Glu Thr Glu Val Lys Pro  
 130 135 140  
 Thr Ser Thr Ala Arg Tyr Tyr Ser Asp Ile Tyr Val Arg His Trp Asp  
 145 150 155 160  
 Thr Trp Leu Thr Lys Asn Arg Tyr Gln Leu Phe Ala Gly Thr Leu Ser  
 165 170 175  
 Lys Asn Ser Ser Tyr Ala Leu Ser Gly Ala Gly Val Arg Asn Ile Gln  
 180 185 190  
 Ser Gly Ile Lys Phe Thr Ala Thr Gln Pro Glu Thr Pro Val Gln Pro  
 195 200 205  
 Phe Gly Asp Ser Ser Asp Tyr Asp Ile Ser Pro Asp Gly Ser Met Tyr  
 210 215 220  
 Ala Phe Ile Ser Lys Ala Pro Gln Leu Asn Lys Ala Asn Tyr Thr Ala  
 225 230 235 240  
 Ser Tyr Leu Tyr Val Gly Ala Phe Ala Ser Asn Glu Ala Pro Val Ala  
 245 250 255  
 Leu Asn Gly Pro Asp Ser Glu Ala Phe Lys Ala Gly His Gln Gly Ala  
 260 265 270  
 Ser Gly Leu Pro Ser Phe Ser Gly Asp Ser Cys Lys Leu Ala Tyr Val  
 275 280 285  
 Gln Gln Asp Glu Asp Tyr Tyr Glu Ser Asp Arg Phe Lys Leu Tyr Thr  
 290 295 300  
 Tyr Asp Val Ala Val Glu Gly Gln Gly Val Ala Ala Ser Asn Trp Lys  
 305 310 315 320  
 Ser Leu Ser Glu Gly Phe Asp Arg Trp Val Gln Gly Pro Ile Thr Trp  
 325 330 335  
 Ala His Asp Asp Ser Ser Ile Tyr Val Thr Ala Asp Asp Tyr Ala Arg  
 340 345 350  
 Asn Lys Ile Phe Asn Phe Pro Ile Thr Ala Asp Glu Lys Phe Val Pro  
 355 360 365  
 Glu Pro Leu Thr Gly Asn Thr Ser Val Ser Ala Phe Ser Leu Leu Pro  
 370 375 380

## 10336256.txt

Asp Gly Ser Leu Phe Val Ala Ala Thr Ala Ile Trp Thr Pro Asn Glu  
 385 390 395 400  
 Trp Tyr Ile Leu Ala Asp Gly Asn Lys Lys Thr Leu Leu Asp Ala Ser  
 405 410 415  
 Gln Val Asp Pro Asn Leu Ala Gly Leu Ser Ser Lys Thr Val Ser Glu  
 420 425 430  
 Ile Phe Phe Asn Gly Ser Asn Pro Asp Leu Lys Gln Gln Leu Gln Ala  
 435 440 445  
 Tyr Val Val Lys Pro Thr Phe Tyr Gln Glu Asn Val Thr Tyr Pro Leu  
 450 455 460  
 Ala Phe Leu Ile His Gly Gly Pro Gln Gly Asn Trp Gly Asn Ser Trp  
 465 470 475 480  
 Ser Asn Arg Trp Asn Pro Gln Val Trp Ala Asp Gln Gly Tyr Ile Val  
 485 490 495  
 Val Ala Pro Asn Pro Thr Gly Ser Thr Ser Phe Gly Gln Tyr Leu Ile  
 500 505 510  
 Asp Ser Ile Gln Gly Glu Trp Gly Ser Trp Pro Tyr Glu Asp Leu Val  
 515 520 525  
 Asn Ala Trp Asn Tyr Ile Asn Ser Thr Met Thr Trp Ile Asp Thr Glu  
 530 535 540  
 Asn Gly Ile Ala Ala Gly Ala Ser Tyr Gly Gly Tyr Met Thr Asn Trp  
 545 550 555 560  
 Ile Gln Ser Asn Asp Leu Gly Asn Glu Phe Lys Ala Leu Val Thr His  
 565 570 575  
 Asp Gly Ile Ser Asn Thr Glu Gly Ala Trp Ala Ser Glu Glu Leu Trp  
 580 585 590  
 Phe Ile Arg His Asp Tyr Asp Gly Asn Ile Trp Asp Ser Pro Ala Tyr  
 595 600 605  
 Arg Gln Trp Asn Pro Gln Asn His Ile Ala Asn Trp Ser Thr Pro Gln  
 610 615 620  
 Phe Val Ile His Asn Thr Leu Asp Tyr Arg Leu Pro Glu Ser Asp Gly  
 625 630 635 640  
 Ile Ser Leu Phe Asn Ile Leu Gln Ala Arg Gly Ile Pro Ser Arg Phe  
 645 650 655  
 Leu Asn Phe Pro Asp Glu Asn His Trp Val Leu Lys Gln Glu Asn Ser  
 660 665 670  
 Leu Val Trp His Thr Glu Ile Phe Asn Trp Ile Asn His Trp Ser Lys  
 675 680 685  
 Gly Glu Pro Leu Ser Thr Thr Pro Ile Gly Asn  
 690 695

&lt;210&gt; 234

&lt;211&gt; 2163

&lt;212&gt; DNA

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(2163)

&lt;400&gt; 234

atg gct cgt tac ctc agt gtt gcc gca gca ctg gct gct act ggc gcg 48  
 Met Ala Arg Tyr 5 Leu Ala Ala 10 Leu Ala Ala Thr Gly Ala 15

tgc gcg ttc aca ccc gag ttg ctt ctt agc acc gta cga cgc gct gcc 96  
 Cys Ala Phe Thr 20 Pro Glu Leu Leu 25 Ser Thr Val Arg 30 Ala Ala

gcc gat ccc agt cca gat ggc tca gtc gcg ctc ttc tcg tac acg cag 144  
 Ala Asp Pro 35 Ser Pro Asp Gly Ser Val Ala Leu Phe Ser Tyr Thr Gln 45

tac tcc ttc gag gaa cat gcg cgc acg gct ggc atg aac ctc atc gat 192  
 Tyr Ser 50 Phe Glu Glu His Ala Arg Thr Ala Gly Met 60 Asn Leu Ile Asp

ctc aag acc ggt gag gtc acc aag tcg ggc ctc gac ccc agc gag gtc 240  
 Page 230

10336256.txt

Leu 65	Lys	Thr	Gly	Glu	Val 70	Thr	Lys	Ser	Gly	Leu 75	Asp	Pro	Ser	Glu	Val 80	
aac Asn	gaa Glu	gtg Val	gcc Ala	tgg Trp 85	att Ile	cct Pro	ggc Gly	acc Thr	gag Glu 90	acc Thr	ggt Gly	atc Ile	atc Ile	tac Tyr 95	atc Ile	288
aat Asn	ggc Gly	aca Thr	aac Asn 100	gag Glu	gaa Glu	atc Ile	cca Pro	ggt Gly 105	ggt Gly	gtc Val	acc Thr	ctg Leu	tgg Trp 110	att Ile	ggt Gly	336
gac Asp	atc Ile	aag Lys 115	gac Asp	cca Pro	agc Ser	gcc Ala	agc Ser 120	act Thr	ctt Leu	ggt Val	gcc Ala	tcc Ser 125	ctg Leu	gat Asp	gca Ala	384
cca Pro	tac Tyr 130	tcc Ser	ggc Gly	ttg Leu	aag Lys	gtt Val 135	gcc Ala	aac Asn	acc Thr	tct Ser	act Thr 140	ggt Gly	gac Asp	ttg Leu	cat His	432
ttc Phe 145	ttg Leu	gtc Val	aac Asn	agc Ser	ttg Leu 150	gcc Ala	tac Tyr	ccc Pro	aac Asn	ggc Gly 155	act Thr	gca Ala	ggt Val	aac Asn	ccc Pro 160	480
gag Glu	acc Thr	gaa Glu	gtc Val	aag Lys 165	cca Pro	act Thr	tca Ser	act Thr	gcc Ala 170	cgt Arg	tac Tyr	tac Tyr	tcg Ser	gat Asp 175	atc Ile	528
tat Tyr	gtc Val	cgc Arg	cac His 180	tgg Trp	gat Asp	acc Thr	tgg Trp	cta Leu 185	act Thr	aag Lys	aac Asn	cgc Arg	tac Tyr 190	cag Gln	ctt Leu	576
ttt Phe	gct Ala	ggt Gly 195	aca Thr	ctt Leu	tcc Ser	aag Lys	aac Asn 200	agc Ser	agt Ser	tat Tyr	gct Ala	ctc Leu 205	tct Ser	ggc Gly	gct Ala	624
ggc Gly	gtg Val 210	cgc Arg	aac Asn	atc Ile	caa Gln	agt Ser 215	ggt Gly	atc Ile	aaa Lys	ttc Phe	acc Thr 220	gct Ala	act Thr	cag Gln	cct Pro	672
gag Glu 225	act Thr	ccc Pro	gtc Val	cag Gln	cct Pro 230	ttt Phe	ggc Gly	gac Asp	tcg Ser	agc Ser 235	gat Asp	tat Tyr	gac Asp	atc Ile	agt Ser 240	720
ccc Pro	gat Asp	ggc Gly	tct Ser	atg Met 245	tat Tyr	gct Ala	ttc Phe	att Ile	agc Ser 250	aag Lys	gct Ala	cct Pro	cag Gln	ctc Leu 255	aac Asn	768
aag Lys	gcc Ala	aac Asn	tac Tyr 260	acc Thr	gcg Ala	tcc Ser	tac Tyr	cta Leu 265	tac Tyr	gtc Val	ggt Gly	gcc Ala	ttt Phe 270	gcc Ala	tcc Ser	816
aac Asn	gaa Glu	gct Ala 275	ccc Pro	gtt Val	gct Ala	ctc Leu	aac Asn 280	ggc Gly	cct Pro	gac Asp	tct Ser	gag Glu 285	gct Ala	ttc Phe	aag Lys	864
gct Ala	gga Gly 290	cac His	cag Gln	ggt Gly	gct Ala	tcc Ser 295	ggt Gly	cta Leu	cca Pro	tcc Ser	ttc Phe 300	tcc Ser	ggt Gly	gac Asp	agc Ser	912
tgc Cys 305	aag Lys	ctt Leu	gca Ala	tat Tyr	gtc Val 310	caa Gln	caa Gln	gac Asp	gag Glu	gac Asp 315	tac Tyr	tat Tyr	gag Glu	tcg Ser	gac Asp 320	960
agg Arg	ttc Phe	aag Lys	ctg Leu	tac Tyr 325	acc Thr	tac Tyr	gac Asp	gtt Val	gct Ala 330	gtc Val	gag Glu	ggc Gly	caa Gln	ggc Gly 335	gtg Val	1008
gcc	gct	agc	aac	tgg	aag	agc	ttg	agc	gaa	ggt	ttt	gac	cgc	tgg	gtg	1056

10336256.txt															
Ala	Ala	Ser	Asn 340	Trp	Lys	Ser	Leu	Ser 345	Glu	Gly	Phe	Asp	Arg 350	Trp	Val
caa Gln	ggt Gly	ccc Pro 355	att Ile	act Thr	tgg Trp	gct Ala	cac His 360	gac Asp	gat Asp	tct Ser	tca Ser	atc Ile 365	tac Tyr	gtc Val	act Thr
gct Ala	gat Asp 370	gac Asp	tac Tyr	gcc Ala	cgc Arg	aac Asn 375	aag Lys	atc Ile	ttc Phe	aac Asn	ttc Phe 380	cca Pro	atc Ile	acc Thr	gcg Ala
gat Asp 385	gag Glu	aag Lys	ttt Phe	gtt Val	ccc Pro 390	gag Glu	ccg Pro	cta Leu	act Thr	gga Gly 395	aac Asn	act Thr	tca Ser	gtt Val	tcg Ser 400
gcg Ala	ttt Phe	tct Ser	ctg Leu	ctt Leu 405	cct Pro	gac Asp	ggt Gly	tcg Ser	ctg Leu 410	ttc Phe	gtt Val	gca Ala	gcc Ala	acc Thr 415	gct Ala
atc Ile	tgg Trp	act Thr	ccc Pro 420	aac Asn	gaa Glu	tgg Trp	tac Tyr	atc Ile 425	ctc Leu	gcc Ala	gac Asp	ggc Gly 430	aac Asn	aag Lys	aag Lys
acg Thr	ctt Leu	ctt Leu 435	gac Asp	gct Ala	tcc Ser	cag Gln	gtt Val 440	gac Asp	ccc Pro	aac Asn	ctg Leu	gcc Ala 445	ggc Gly	ctc Leu	agc Ser
tcc Ser	aag Lys 450	act Thr	gtc Val	tct Ser	gag Glu	att Ile 455	ttc Phe	ttc Phe	aat Asn	ggc Gly	tcc Ser 460	aac Asn	ccc Pro	gat Asp	ctc Leu
aag Lys 465	caa Gln	caa Gln	ctt Leu	cag Gln	gct Ala 470	tat Tyr	gtc Val	gtc Val	aag Lys	ccc Pro 475	aca Thr	ttc Phe	tac Tyr	caa Gln	gag Glu 480
aac Asn	gtt Val	act Thr	tac Tyr	ccc Pro 485	ctt Leu	gct Ala	ttc Phe	ctg Leu	att Ile 490	cac His	ggt Gly	ggt Gly	cct Pro	cag Gln 495	ggc Gly
aac Asn	tgg Trp	ggc Gly	aac Asn 500	agc Ser	tgg Trp	tca Ser	aac Asn	cgc Arg 505	tgg Trp	aac Asn	ccg Pro	cag Gln	gtc Val 510	tgg Trp	gcc Ala
gac Asp	caa Gln	ggc Gly 515	tac Tyr	atc Ile	gtc Val	gtc Val	gca Ala 520	cct Pro	aac Asn	ccg Pro	act Thr	ggt Gly 525	tct Ser	aca Thr	agt Ser
ttc Phe	gga Gly 530	cag Gln	tac Tyr	ctc Leu	atc Ile	gac Asp 535	tcc Ser	atc Ile	cag Gln	ggc Gly	gag Glu 540	tgg Trp	ggc Gly	agc Ser	tgg Trp
cca Pro 545	tac Tyr	gaa Glu	gac Asp	ctg Leu	gtc Val 550	aat Asn	gcc Ala	tgg Trp	aac Asn	tac Tyr 555	atc Ile	aac Asn	tcc Ser	acc Thr	atg Met 560
acg Thr	tgg Trp	atc Ile	gac Asp	acc Thr 565	gag Glu	aac Asn	ggt Gly	atc Ile	gcc Ala 570	gcc Ala	ggt Gly	gcc Ala	tcg Ser	tac Tyr 575	ggt Gly
gga Gly	tac Tyr	atg Met	acc Thr 580	aac Asn	tgg Trp	atc Ile	cag Gln	tcc Ser 585	aat Asn	gac Asp	ctc Leu	ggc Gly	aac Asn 590	gag Glu	ttc Phe
aag Lys	gct Ala	ctc Leu 595	gtc Val	acc Thr	cat His	gac Asp	ggt Gly 600	atc Ile	tcc Ser	aac Asn	acc Thr	gag Glu 605	ggt Gly	gcc Ala	tgg Trp
gcg	tcc	gag	gag	ctc	tgg	ttc	atc	cgc	cac	gac	tac	gat	ggc	aac	atc

10336256.txt

Ala 610	Ser	Glu	Glu	Leu	Trp	Phe 615	Ile	Arg	His	Asp 620	Tyr	Asp	Gly	Asn	Ile	
tgg 625	gac Trp	tca Asp	ccc Ser	gcc Pro	tac Ala	cgc Tyr 630	cag Arg	tgg Gln	aac Trp	ccc Asn 635	cag Pro	aac Gln	cac Asn	att His	gcc Ile 640	1920
aac 645	tgg Asn	tcc Trp	act Ser	ccc Thr	cag Pro 645	ttc Gln	gtc Phe	atc Val	cac Ile	aac His 650	acg Asn	ctc Thr	gac Leu	tac Asp	cgt Tyr 655	1968
ctc 660	ccc Leu	gag Pro	agc Glu	gac Ser 660	ggc Asp	atc Gly	agc Ile	ctg Ser	ttc Leu 665	aac Phe	atc Asn	ctc Ile	cag Leu	gcg Ala 670	cg Arg	2016
ggt 680	atc Gly	ccc Ile	agt Pro	cg Ser 675	ttc Arg	ctc Phe	aac Leu	ttc Asn 680	ccc Phe	gac Pro	gag Asp	aac Glu	cac Asn 685	tgg His	gtc Trp Val	2064
ctc 690	aag Leu	cag Lys	gag Gln	aac Glu	agc Asn	ttg Ser	ggt Leu 695	tgg Val	cac Trp	act His	gag Thr	att Glu 700	ttc Ile	aac Phe	tgg Asn Trp	2112
atc 705	aac Ile	cac Asn	tgg His	tcc Trp	aag Ser 710	ggt Lys	gag Gly	cct Glu	ttg Pro	agc Leu 715	act Ser	acc Thr	ccg Thr	att Pro	ggc Ile Gly 720	2160
aac 725	Asn															2163

&lt;210&gt; 235

&lt;211&gt; 721

&lt;212&gt; PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

&lt;400&gt; 235

Met 1	Ala	Arg	Tyr	Leu 5	Ser	Val	Ala	Ala	Ala 10	Leu	Ala	Ala	Thr	Gly 15	Ala
Cys	Ala	Phe	Thr 20	Pro	Glu	Leu	Leu	Leu 25	Ser	Thr	Val	Arg	Arg 30	Ala	Ala
Ala	Asp	Pro 35	Ser	Pro	Asp	Gly	Ser 40	Val	Ala	Leu	Phe	Ser 45	Tyr	Thr	Gln
Tyr	Ser	Phe 50	Glu	Glu	His	Ala 55	Arg	Thr	Ala	Gly	Met 60	Asn	Leu	Ile	Asp
Leu 65	Lys	Thr	Gly	Glu	Val 70	Thr	Lys	Ser	Gly	Leu 75	Asp	Pro	Ser	Glu	Val 80
Asn	Glu	Val	Ala	Trp 85	Ile	Pro	Gly	Thr	Glu 90	Thr	Gly	Ile	Ile	Tyr 95	Ile
Asn	Gly	Thr	Asn 100	Glu	Glu	Ile	Pro	Gly 105	Gly	Val	Thr	Leu	Trp 110	Ile	Gly
Asp	Ile	Lys 115	Asp	Pro	Ser	Ala	Ser 120	Thr	Leu	Val	Ala	Ser 125	Leu	Asp	Ala
Pro	Tyr 130	Ser	Gly	Leu	Lys	Val 135	Ala	Asn	Thr	Ser	Thr 140	Gly	Asp	Leu	His
Phe 145	Leu	Val	Asn	Ser	Leu 150	Ala	Tyr	Pro	Asn	Gly 155	Thr	Ala	Val	Asn	Pro 160
Glu	Thr	Glu	Val	Lys 165	Pro	Thr	Ser	Thr	Ala 170	Arg	Tyr	Tyr	Ser	Asp 175	Ile
Tyr	Val	Arg	His 180	Trp	Asp	Thr	Trp	Leu 185	Thr	Lys	Asn	Arg	Tyr 190	Gln	Leu
Phe	Ala	Gly 195	Thr	Leu	Ser	Lys	Asn 200	Ser	Ser	Tyr	Ala	Leu 205	Ser	Gly	Ala
Gly	Val 210	Arg	Asn	Ile	Gln	Ser 215	Gly	Ile	Lys	Phe	Thr 220	Ala	Thr	Gln	Pro
Glu 225	Thr	Pro	Val	Gln	Pro 230	Phe	Gly	Asp	Ser	Ser 235	Asp	Tyr	Asp	Ile	Ser 240

10336256.txt

Pro	Asp	Gly	Ser	Met	Tyr	Ala	Phe	Ile	Ser	Lys	Ala	Pro	Gln	Leu	Asn
				245					250					255	
Lys	Ala	Asn	Tyr	Thr	Ala	Ser	Tyr	Leu	Tyr	Val	Gly	Ala	Phe	Ala	Ser
			260					265					270		
Asn	Glu	Ala	Pro	Val	Ala	Leu	Asn	Gly	Pro	Asp	Ser	Glu	Ala	Phe	Lys
		275					280					285			
Ala	Gly	His	Gln	Gly	Ala	Ser	Gly	Leu	Pro	Ser	Phe	Ser	Gly	Asp	Ser
	290					295					300				
Cys	Lys	Leu	Ala	Tyr	Val	Gln	Gln	Asp	Glu	Asp	Tyr	Tyr	Glu	Ser	Asp
305					310					315					320
Arg	Phe	Lys	Leu	Tyr	Thr	Tyr	Asp	Val	Ala	Val	Glu	Gly	Gln	Gly	Val
				325					330					335	
Ala	Ala	Ser	Asn	Trp	Lys	Ser	Leu	Ser	Glu	Gly	Phe	Asp	Arg	Trp	Val
			340					345					350		
Gln	Gly	Pro	Ile	Thr	Trp	Ala	His	Asp	Asp	Ser	Ser	Ile	Tyr	Val	Thr
		355					360					365			
Ala	Asp	Asp	Tyr	Ala	Arg	Asn	Lys	Ile	Phe	Asn	Phe	Pro	Ile	Thr	Ala
	370					375					380				
Asp	Glu	Lys	Phe	Val	Pro	Glu	Pro	Leu	Thr	Gly	Asn	Thr	Ser	Val	Ser
385					390					395					400
Ala	Phe	Ser	Leu	Leu	Pro	Asp	Gly	Ser	Leu	Phe	Val	Ala	Ala	Thr	Ala
				405					410					415	
Ile	Trp	Thr	Pro	Asn	Glu	Trp	Tyr	Ile	Leu	Ala	Asp	Gly	Asn	Lys	Lys
			420					425					430		
Thr	Leu	Leu	Asp	Ala	Ser	Gln	Val	Asp	Pro	Asn	Leu	Ala	Gly	Leu	Ser
		435					440					445			
Ser	Lys	Thr	Val	Ser	Glu	Ile	Phe	Phe	Asn	Gly	Ser	Asn	Pro	Asp	Leu
	450					455					460				
Lys	Gln	Gln	Leu	Gln	Ala	Tyr	Val	Val	Lys	Pro	Thr	Phe	Tyr	Gln	Glu
465					470					475					480
Asn	Val	Thr	Tyr	Pro	Leu	Ala	Phe	Leu	Ile	His	Gly	Gly	Pro	Gln	Gly
				485					490					495	
Asn	Trp	Gly	Asn	Ser	Trp	Ser	Asn	Arg	Trp	Asn	Pro	Gln	Val	Trp	Ala
			500					505					510		
Asp	Gln	Gly	Tyr	Ile	Val	Val	Ala	Pro	Asn	Pro	Thr	Gly	Ser	Thr	Ser
		515					520					525			
Phe	Gly	Gln	Tyr	Leu	Ile	Asp	Ser	Ile	Gln	Gly	Glu	Trp	Gly	Ser	Trp
	530					535					540				
Pro	Tyr	Glu	Asp	Leu	Val	Asn	Ala	Trp	Asn	Tyr	Ile	Asn	Ser	Thr	Met
545					550					555					560
Thr	Trp	Ile	Asp	Thr	Glu	Asn	Gly	Ile	Ala	Ala	Gly	Ala	Ser	Tyr	Gly
				565					570					575	
Gly	Tyr	Met	Thr	Asn	Trp	Ile	Gln	Ser	Asn	Asp	Leu	Gly	Asn	Glu	Phe
			580					585					590		
Lys	Ala	Leu	Val	Thr	His	Asp	Gly	Ile	Ser	Asn	Thr	Glu	Gly	Ala	Trp
		595					600					605			
Ala	Ser	Glu	Glu	Leu	Trp	Phe	Ile	Arg	His	Asp	Tyr	Asp	Gly	Asn	Ile
	610					615					620				
Trp	Asp	Ser	Pro	Ala	Tyr	Arg	Gln	Trp	Asn	Pro	Gln	Asn	His	Ile	Ala
625					630					635					640
Asn	Trp	Ser	Thr	Pro	Gln	Phe	Val	Ile	His	Asn	Thr	Leu	Asp	Tyr	Arg
				645					650					655	
Leu	Pro	Glu	Ser	Asp	Gly	Ile	Ser	Leu	Phe	Asn	Ile	Leu	Gln	Ala	Arg
			660					665					670		
Gly	Ile	Pro	Ser	Arg	Phe	Leu	Asn	Phe	Pro	Asp	Glu	Asn	His	Trp	Val
		675					680					685			
Leu	Lys	Gln	Glu	Asn	Ser	Leu	Val	Trp	His	Thr	Glu	Ile	Phe	Asn	Trp
	690					695					700				
Ile	Asn	His	Trp	Ser	Lys	Gly	Glu	Pro	Leu	Ser	Thr	Thr	Pro	Ile	Gly
705					710					715					720
Asn															

&lt;210&gt; 236

&lt;211&gt; 3434

&lt;212&gt; DNA

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

10336256.txt

<220>  
 <221> CDS  
 <222> (1001)... (1318)  
 <223> Exon

<221> CDS  
 <222> (1382)... (1645)  
 <223> Exon

<221> CDS  
 <222> (1711)... (1887)  
 <223> Exon

<221> CDS  
 <222> (1940)... (2437)  
 <223> Exon

<221> misc\_feature  
 <222> (1)... (3434)  
 <223> n = A,T,C or G

<400> 236  
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 ttgtcagggt gtggcgctgg ggggtgcaggg tcctgctagt ggcagtactg gcgagggaca 120  
 tgcaagtggg catggtgggg ggagtgcatt tgaggataag gatgaggggt cggtagtgaa 180  
 ggggtatagg gcgagttatt ggctcatggt tgggtatatg gtggtgtgca tggggattgc 240  
 gggtgtgggg ttgaggaagg cgggtaagggt tgggctgaag aaggagtgaagg acttagat 300  
 gttttgccct tgtgtattct gctaccatgt cgtatgtaat actagcatct acctcgacg 360  
 cagcactttc agcaccttct cagcccacat cctgacaccg atccgtactc cacagctaca 420  
 cccggtccct ccacgcgcaa aggggaagggt cgcagtccgc ctccaccgat gcgtcaccgg 480  
 taccattcca tcttccacag catacttatg ggcccacacg tacagtatcc ccgcaagtca 540  
 ttcgcacatc gcaggcgtag cctacatggt gcgcgttacc caatgtggca gttggctggt 600  
 ctgccaaggc gcaaattccc tgcagatcac catctaggca cataaggctt gagctggacc 660  
 acccaggctt atctcgacg aagcaacgat attactacc tgcccggccat gtcgacccaa 720  
 tacctacaca gaatatggga gaccagcttc ccaagcaagg ttgctgcccc ggccagcggc 780  
 caaggccagt cgggcagggt tgaggggaatg gtaggctgtc caaggcccaa tgtggaatga 840  
 agccgtcgtg ctgcatcggc gggcatgtac ttttgtcatg agagcaattt gactttgttt 900  
 cgaggcgatt atatattaga gggtaggcga agcctgagaa tgttctttcc tcaggccacg 960  
 cttctccctc tcacctttct ctgtcttcaa tctttagacc atg aag ctc ctc agc 1015  
 Met Lys Leu Leu Ser  
 1 5

gtc acc ctg gcc tcg ctg ggc ctc gcc tcc gcc gcc acc gtt gcc aag 1063  
 Val Thr Leu Ala Ser Leu Gly Leu Ala Ser Ala Ala Thr Val Ala Lys  
 10 15 20

aaa gtg acc tac gac gac tgg aag gtc gtc cgt gtc aat gtc ggc gca 1111  
 Lys Val Thr Tyr Asp Asp Trp Lys Val Val Arg Val Asn Val Gly Ala  
 25 30 35

gac gct gct aag ctc gaa aat gta atg agc aag ctg cag ctt gag ctg 1159  
 Asp Ala Ala Lys Leu Glu Asn Val Met Ser Lys Leu Gln Leu Glu Leu  
 40 45 50

tgg aag ggc aag cct gcg tca agc gat gtc gtc gat gtt atg gtg ccg 1207  
 Trp Lys Gly Lys Pro Ala Ser Ser Asp Val Val Asp Val Met Val Pro  
 55 60 65

ccg tcg tcg gtc aag gac ttt gag gct cag act cag ggt ttc gaa aca 1255  
 Pro Ser Ser Val Lys Asp Phe Glu Ala Gln Thr Gln Gly Phe Glu Thr  
 70 75 80 85

aaa gtc atg cat gag aat ctt ggc ctt tct atc gca gac gag cag agt 1303  
 Lys Val Met His Glu Asn Leu Gly Leu Ser Ile Ala Asp Glu Gln Ser  
 90 95 100

ttt ggc aca tat gcc ggtacgcttg ttttccccgc cctgtaaatt gaagaggtga 1358  
 Phe Gly Thr Tyr Ala

10336256.txt

105

catgggaagt cctaactctg tca gct ggt ctt gca cca aac tcg acg tgg ttt 1411  
 Ala Gly Leu Ala Pro Asn Ser Thr Trp Phe  
 110 115

aac tcc tac cac tcc att gct gat cac atg caa tgg att agc gat ctt 1459  
 Asn Ser Tyr His Ser Ile Ala Asp His Met Gln Trp Ile Ser Asp Leu  
 120 125 130

gcg gct gca tac ccc aag aac gca gaa gtc att tct gca ggc aag tcg 1507  
 Ala Ala Ala Tyr Pro Lys Asn Ala Glu Val Ile Ser Ala Gly Lys Ser  
 135 140 145

gtt gag ggc cgt gat atc aag ggt atc cac atc tgg ggt agt ggt ggt 1555  
 Val Glu Gly Arg Asp Ile Lys Gly Ile His Ile Trp Gly Ser Gly Gly  
 150 155 160

aag gga tct cag aag ggt gta gta tgg cac ggc act gtg cac gca cgt 1603  
 Lys Gly Ser Gln Lys Gly Val Val Trp His Gly Thr Val His Ala Arg  
 165 170 175 180

gaa tgg atc acg aca atg gta aat tcc ctt ttc aaa aaa aaa 1645  
 Glu Trp Ile Thr Thr Met Val Asn Ser Leu Phe Lys Lys Lys  
 185 190

aacaggaaca aaggaaagga agaattgtgc taacacactt acaggtgggc gaatatgcag 1705  
 catac caa ctc ctt acc tcc act gac gcc aca acc gcc ggc ttc aaa gac 1755  
 Gln Leu Leu Thr Ser Thr Asp Ala Thr Thr Ala Gly Phe Lys Asp  
 195 200 205

tcg tac gac ttc tac atc ttc ccc atc gtc aac cca gat ggc ttc gcc 1803  
 Ser Tyr Asp Phe Tyr Ile Phe Pro Ile Val Asn Pro Asp Gly Phe Ala  
 210 215 220 225

tac agt cag acc acc gac cgc atg tgg cgc aag aac cgc cag act act 1851  
 Tyr Ser Gln Thr Thr Asp Arg Met Trp Arg Lys Asn Arg Gln Thr Thr  
 230 235 240

ccc agc gcc tca tgc gta ggc cgg gac atc aac cgt aagttctctc 1897  
 Pro Ser Ala Ser Cys Val Gly Arg Asp Ile Asn Arg  
 245 250

ccgtcccccc aagcatatat acatctaacc gatcatcaag gc aac tgg ccc tct 1951  
 Asn Trp Pro Ser  
 255

cac tgg aac cag gcc aac ggt gcc tcc acc tcg ccc tgc gac caa gac 1999  
 His Trp Asn Gln Ala Asn Gly Ala Ser Thr Ser Pro Cys Asp Gln Asp  
 260 265 270

tac aaa ggc ccc tca gcc ggc gac ggc gta gaa acc aaa gcc ctg aaa 2047  
 Tyr Lys Gly Pro Ser Ala Gly Asp Gly Val Glu Thr Lys Ala Leu Lys  
 275 280 285

gcg cac ctc gac agc atc gcc gcc ggc aaa ggc ata acc ctc tac atg 2095  
 Ala His Leu Asp Ser Ile Ala Ala Gly Lys Gly Ile Thr Leu Tyr Met  
 290 295 300 305

gac atc cac gcc tac agc caa ctc tgg atg tac ccc tac ggc tac acc 2143  
 Asp Ile His Ala Tyr Ser Gln Leu Trp Met Tyr Pro Tyr Gly Tyr Thr  
 310 315 320

tgc tcc ggc gct ctc ccc aac tcc gca aag tac tct tcg ctg acc aac 2191  
 Cys Ser Gly Ala Leu Pro Asn Ser Ala Lys Tyr Ser Ser Leu Thr Asn  
 325 330 335

ggt gcc att gcc gcg gtc aag gca gtg cat gga acg gcg ttc acg ggc 2239

10336256.txt

Gly Ala Ile Ala Ala Val Lys Ala Val His Gly Thr Ala Phe Thr Gly  
 340 345 350

ggc ccg att tgc aat acc atc tat cag gtt agt ggc gat agt gtg gat 2287  
 Gly Pro Ile Cys Asn Thr Ile Tyr Gln Val Ser Gly Asp Ser Val Asp  
 355 360 365

tat gcg ttt gag gtc gca aag gcg acg tat agt atg acg gtc gag ttg 2335  
 Tyr Ala Phe Glu Val Ala Lys Ala Thr Tyr Ser Met Thr Val Glu Leu  
 370 375 380 385

agg gat acg ggt aag tat ggg ttt gtc ctg ccg aaa gag cag att gtg 2383  
 Arg Asp Thr Gly Lys Tyr Gly Phe Val Leu Pro Lys Glu Gln Ile Val  
 390 400

ccg agt gcc gag gag atg tgg gct ggt ttg agg tac ttg gtg aag aat 2431  
 Pro Ser Ala Glu Glu Met Trp Ala Gly Leu Arg Tyr Leu Val Lys Asn  
 405 410 415

atg taa ggtggtagag gggaatatat gtatatatcga gtgtggggat gtattttttt 2487  
 Met \*

tggtgggctg gggggccttct ggaagatttt gagttggcgg ggggagcccc attgtagata 2547  
 tatttttctag aggatgaaaa atcttgagag cagagagaga gagaattggc gttaaaaaag 2607  
 gtcttttgag gaaggggttg cctttcttat ttctgtgatc ttgatgatac gaggagagga 2667  
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 aagaatggag tggtaatagt accaaaaagt gtgtacacct cttgaaagggt atgcacctat 2787  
 caggtagcat aatcaaatta atcatgattg cgatgaacgt aactgaatag caaactatgg 2847  
 ttgcaacaag gacacgcagt gcagcaaagc attccaatca atgcctataa attcgcaata 2907  
 tcttccgtct atctctccca tcttatcacc agccacaaat tcattggacc tccatatctc 2967  
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 aaccaccaat caagccgctt acatctctta aaaaaccact ataccattcc tctccaccac 3087  
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 caccctcacc acccgccacc tctgctccct ccaacacccc accaacctcc ccccatgcac 3207  
 cgtttccaac ctaggccaga cctctgccc caccacacc agcgacagct acatcttcca 3267  
 gtgcaacgcc gcgacccctc actggcacgt catgcccaga tgcacgtcgg ccaacgcgcc 3327  
 ctgctccaac acgacctgca cgctctcac agacgcctgc gtagaatcct ccacgcaatg 3387  
 cgcgacactg ctctcgcacg gctacaacgg catcgccgtg tgccgcg 3434

&lt;210&gt; 237

&lt;211&gt; 106

&lt;212&gt; PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

&lt;400&gt; 237

Met Lys Leu Leu Ser Val Thr Leu Ala Ser Leu Gly Leu Ala Ser Ala  
 1 5 10 15

Ala Thr Val Ala Lys Lys Val Thr Tyr Asp Asp Trp Lys Val Val Arg  
 20 25 30

Val Asn Val Gly Ala Asp Ala Ala Lys Leu Glu Asn Val Met Ser Lys  
 35 40 45

Leu Gln Leu Glu Leu Trp Lys Gly Lys Pro Ala Ser Ser Asp Val Val  
 50 55 60

Asp Val Met Val Pro Pro Ser Ser Val Lys Asp Phe Glu Ala Gln Thr  
 65 70 75 80

Gln Gly Phe Glu Thr Lys Val Met His Glu Asn Leu Gly Leu Ser Ile  
 85 90 95

Ala Asp Glu Gln Ser Phe Gly Thr Tyr Ala  
 100 105

&lt;210&gt; 238

&lt;211&gt; 88

&lt;212&gt; PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

&lt;400&gt; 238

Ala Gly Leu Ala Pro Asn Ser Thr Trp Phe Asn Ser Tyr His Ser Ile

## 10336256.txt

1 5 10 15  
 Ala Asp His Met Gln Trp Ile Ser Asp Leu Ala Ala Tyr Pro Lys  
 20 25 30  
 Asn Ala Glu Val Ile Ser Ala Gly Lys Ser Val Glu Gly Arg Asp Ile  
 35 40 45  
 Lys Gly Ile His Ile Trp Gly Ser Gly Gly Lys Gly Ser Gln Lys Gly  
 50 55 60  
 Val Val Trp His Gly Thr Val His Ala Arg Glu Trp Ile Thr Thr Met  
 65 70 75 80  
 Val Asn Ser Leu Phe Lys Lys Lys  
 85

&lt;210&gt; 239

&lt;211&gt; 59

&lt;212&gt; PRT

&lt;213&gt; Cochliobolus heterostrophus strain C4 (ATCC 48331)

&lt;400&gt; 239

Gln Leu Leu Thr Ser Thr Asp Ala Thr Thr Ala Gly Phe Lys Asp Ser  
 1 5 10 15  
 Tyr Asp Phe Tyr Ile Phe Pro Ile Val Asn Pro Asp Gly Phe Ala Tyr  
 20 25 30  
 Ser Gln Thr Thr Asp Arg Met Trp Arg Lys Asn Arg Gln Thr Thr Pro  
 35 40 45  
 Ser Ala Ser Cys Val Gly Arg Asp Ile Asn Arg  
 50 55

&lt;210&gt; 240

&lt;211&gt; 165

&lt;212&gt; PRT

&lt;213&gt; Cochliobolus heterostrophus strain C4 (ATCC 48331)

&lt;400&gt; 240

Asn Trp Pro Ser His Trp Asn Gln Ala Asn Gly Ala Ser Thr Ser Pro  
 1 5 10 15  
 Cys Asp Gln Asp Tyr Lys Gly Pro Ser Ala Gly Asp Gly Val Glu Thr  
 20 25 30  
 Lys Ala Leu Lys Ala His Leu Asp Ser Ile Ala Ala Gly Lys Gly Ile  
 35 40 45  
 Thr Leu Tyr Met Asp Ile His Ala Tyr Ser Gln Leu Trp Met Tyr Pro  
 50 55 60  
 Tyr Gly Tyr Thr Cys Ser Gly Ala Leu Pro Asn Ser Ala Lys Tyr Ser  
 65 70 75 80  
 Ser Leu Thr Asn Gly Ala Ile Ala Ala Val Lys Ala Val His Gly Thr  
 85 90 95  
 Ala Phe Thr Gly Gly Pro Ile Cys Asn Thr Ile Tyr Gln Val Ser Gly  
 100 105 110  
 Asp Ser Val Asp Tyr Ala Phe Glu Val Ala Lys Ala Thr Tyr Ser Met  
 115 120 125  
 Thr Val Glu Leu Arg Asp Thr Gly Lys Tyr Gly Phe Val Leu Pro Lys  
 130 135 140  
 Glu Gln Ile Val Pro Ser Ala Glu Glu Met Trp Ala Gly Leu Arg Tyr  
 145 150 155 160  
 Leu Val Lys Asn Met  
 165

&lt;210&gt; 241

&lt;211&gt; 1254

&lt;212&gt; DNA

&lt;213&gt; Cochliobolus heterostrophus strain C4 (ATCC 48331)

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1254)

&lt;400&gt; 241

atg aag ctc ctc agc gtc acc ctg gcc tcg ctg ggc ctc gcc tcc gcc  
 Met Lys Leu Leu Ser Val Thr Leu Ala Ser Leu Gly Leu Ala Ser Ala

10336256.txt																
1			5			10			15							
gcc Ala	acc Thr	gtt Val	gcc Ala 20	aag Lys	aaa Lys	gtg Val	acc Thr	tac Tyr 25	gac Asp	gac Asp	tgg Trp	aag Lys	gtc Val 30	gtc Val	cgt Arg	96
gtc Val	aat Asn	gtc Val 35	ggc Gly	gca Ala	gac Asp	gct Ala	gct Ala 40	aag Lys	ctc Leu	gaa Glu	aat Asn	gta Val 45	atg Met	agc Ser	aag Lys	144
ctg Leu	cag Gln 50	ctt Leu	gag Glu	ctg Leu	tgg Trp	aag Lys 55	ggc Gly	aag Lys	cct Pro	gcg Ala	tca Ser 60	agc Ser	gat Asp	gtc Val	gtc Val	192
gat Asp 65	gtt Val	atg Met	gtg Val	ccg Pro	ccg Pro 70	tcg Ser	tcg Ser	gtc Val	aag Lys	gac Asp 75	ttt Phe	gag Glu	gct Ala	cag Gln	act Thr 80	240
cag Gln	ggg Gly	ttc Phe	gaa Glu	aca Thr 85	aaa Lys	gtc Val	atg Met	cat His	gag Glu 90	aat Asn	ctt Leu	ggc Gly	ctt Leu	tct Ser 95	atc Ile	288
gca Ala	gac Asp	gag Glu	cag Gln 100	agt Ser	ttt Phe	ggc Gly	aca Thr	tat Tyr 105	gcc Ala	gct Ala	ggg Gly	ctt Leu	gca Ala 110	cca Pro	aac Asn	336
tcg Ser	acg Thr	tgg Trp 115	ttt Phe	aac Asn	tcc Ser	tac Tyr	cac His 120	tcc Ser	att Ile	gct Ala	gat Asp	cac His 125	atg Met	caa Gln	tgg Trp	384
att Ile 130	agc Ser	gat Asp	ctt Leu	gcg Ala	gct Ala	gca Ala 135	tac Tyr	ccc Pro	aag Lys	aac Asn	gca Ala 140	gaa Glu	gtc Val	att Ile	tct Ser	432
gca Ala 145	ggc Gly	aag Lys	tcg Ser	gtt Val	gag Glu 150	ggc Gly	cgt Arg	gat Asp	atc Ile	aag Lys 155	ggg Gly	atc Ile	cac His	atc Ile	tgg Trp 160	480
ggg Gly	agt Ser	ggg Gly	ggg Gly	aag Lys 165	gga Gly	tct Ser	cag Gln	aag Lys	ggg Gly 170	gta Val	gta Val	tgg Trp	cac His	ggc Gly 175	act Thr	528
gtg Val	cac His	gca Ala	cgt Arg 180	gaa Glu	tgg Trp	atc Ile	acg Thr	aca Thr 185	atg Met	gta Val	aat Asn	tcc Ser	ctt Leu 190	ttc Phe	aaa Lys	576
aaa Lys	aaa Lys	caa Gln 195	ctc Leu	ctt Leu	acc Thr	tcc Ser	act Thr 200	gac Asp	gcc Ala	aca Thr	acc Thr	gcc Ala 205	ggc Gly	ttc Phe	aaa Lys	624
gac Asp	tcg Ser 210	tac Tyr	gac Asp	ttc Phe	tac Tyr	atc Ile 215	ttc Phe	ccc Pro	atc Ile	gtc Val	aac Asn 220	cca Pro	gat Asp	ggc Gly	ttc Phe	672
gcc Ala 225	tac Tyr	agt Ser	cag Gln	acc Thr	acc Thr 230	gac Asp	cgc Arg	atg Met	tgg Trp	cgc Arg 235	aag Lys	aac Asn	cgc Arg	cag Gln	act Thr 240	720
act Thr	ccc Pro	agc Ser	gcc Ala	tca Ser 245	tgc Cys	gta Val	ggc Gly	cgg Arg	gac Asp 250	atc Ile	aac Asn	cgt Arg	aac Asn	tgg Trp 255	ccc Pro	768
tct Ser	cac His	tgg Trp	aac Asn 260	cag Gln	gcc Ala	aac Asn	ggg Gly	gcc Ala 265	tcc Ser	acc Thr	tcg Ser	ccc Pro	tgc Cys 270	gac Asp	caa Gln	816
gac Asp	tac Tyr	aaa Lys	ggc Gly	ccc Pro	tca Ser	gcc Ala	ggc Gly	gac Asp	ggc Gly	gta Val	gaa Glu	acc Thr	aaa Lys	gcc Ala	ctg Leu	864

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10336256.txt

275	280	285	
aaa gcg cac ctc gac agc atc gcc gcc ggc aaa ggc ata acc ctc tac Lys Ala His Leu Asp Ser Ile Ala Ala Gly Lys Gly Ile Thr Leu Tyr			912
	290	300	
atg gac atc cac gcc tac agc caa ctc tgg atg tac ccc tac ggc tac Met Asp Ile His Ala Tyr Ser Gln Leu Trp Met Tyr Pro Tyr Gly Tyr			960
	305	315	
acc tgc tcc ggc gct ctc ccc aac tcc gca aag tac tct tcg ctg acc Thr Cys Ser Gly Ala Leu Pro Asn Ser Ala Lys Tyr Ser Ser Leu Thr			1008
	325	330	
aac ggt gcc att gcc gcg gtc aag gca gtg cat gga acg gcg ttc acg Asn Gly Ala Ile Ala Ala Val Lys Ala Val His Gly Thr Ala Phe Thr			1056
	340	345	
ggc ggc ccg att tgc aat acc atc tat cag gtt agt ggc gat agt gtg Gly Gly Pro Ile Cys Asn Thr Ile Tyr Gln Val Ser Gly Asp Ser Val			1104
	355	360	
gat tat gcg ttt gag gtc gca aag gcg acg tat agt atg acg gtc gag Asp Tyr Ala Phe Glu Val Ala Lys Ala Thr Tyr Ser Met Thr Val Glu			1152
	370	375	
ttg agg gat acg ggt aag tat ggg ttt gtc ctg ccg aaa gag cag att Leu Arg Asp Thr Gly Lys Tyr Gly Phe Val Leu Pro Lys Glu Gln Ile			1200
	385	390	
gtg ccg agt gcc gag gag atg tgg gct ggt ttg agg tac ttg gtg aag Val Pro Ser Ala Glu Glu Met Trp Ala Gly Leu Arg Tyr Leu Val Lys			1248
	405	410	
aat atg Asn Met			1254

<210> 242  
 <211> 418  
 <212> PRT  
 <213> Cochliobolus heterostrophus strain C4 (ATCC 48331)

<220>  
 <221> SIGNAL  
 <222> (1)...(20)

<221> DOMAIN  
 <222> (117)...(321)  
 <223> Zinc carboxypeptidase

<400> 242  
 Met Lys Leu Leu Ser Val Thr Leu Ala Ser Leu Gly Leu Ala Ser Ala  
 -20 -15 -10 -5  
 Ala Thr Val Ala Lys Lys Val Thr Tyr Asp Asp Trp Lys Val Val Arg  
 1 10  
 Val Asn Val Gly Ala Asp Ala Ala Lys Leu Glu Asn Val Met Ser Lys  
 15 20 25  
 Leu Gln Leu Glu Leu Trp Lys Gly Lys Pro Ala Ser Ser Asp Val Val  
 30 35 40  
 Asp Val Met Val Pro Pro Ser Ser Val Lys Asp Phe Glu Ala Gln Thr  
 45 50 55 60  
 Gln Gly Phe Glu Thr Lys Val Met His Glu Asn Leu Gly Leu Ser Ile  
 65 70 75  
 Ala Asp Glu Gln Ser Phe Gly Thr Tyr Ala Ala Gly Leu Ala Pro Asn  
 80 85 90  
 Ser Thr Trp Phe Asn Ser Tyr His Ser Ile Ala Asp His Met Gln Trp

## 10336256.txt

95 100 105  
 Ile Ser Asp Leu Ala Ala Ala Tyr Pro Lys Asn Ala Glu Val Ile Ser  
 110 115 120  
 Ala Gly Lys Ser Val Glu Gly Arg Asp Ile Lys Gly Ile His Ile Trp  
 125 130 135 140  
 Gly Ser Gly Gly Lys Gly Ser Gln Lys Gly Val Val Trp His Gly Thr  
 145 150 155  
 Val His Ala Arg Glu Trp Ile Thr Thr Met Val Asn Ser Leu Phe Lys  
 160 165 170  
 Lys Lys Gln Leu Leu Thr Ser Thr Asp Ala Thr Thr Ala Gly Phe Lys  
 175 180 185  
 Asp Ser Tyr Asp Phe Tyr Ile Phe Pro Ile Val Asn Pro Asp Gly Phe  
 190 195 200  
 Ala Tyr Ser Gln Thr Thr Asp Arg Met Trp Arg Lys Asn Arg Gln Thr  
 205 210 215 220  
 Thr Pro Ser Ala Ser Cys Val Gly Arg Asp Ile Asn Arg Asn Trp Pro  
 225 230 235  
 Ser His Trp Asn Gln Ala Asn Gly Ala Ser Thr Ser Pro Cys Asp Gln  
 240 245 250  
 Asp Tyr Lys Gly Pro Ser Ala Gly Asp Gly Val Glu Thr Lys Ala Leu  
 255 260 265  
 Lys Ala His Leu Asp Ser Ile Ala Ala Gly Lys Gly Ile Thr Leu Tyr  
 270 275 280  
 Met Asp Ile His Ala Tyr Ser Gln Leu Trp Met Tyr Pro Tyr Gly Tyr  
 285 290 295 300  
 Thr Cys Ser Gly Ala Leu Pro Asn Ser Ala Lys Tyr Ser Ser Leu Thr  
 305 310 315  
 Asn Gly Ala Ile Ala Ala Val Lys Ala Val His Gly Thr Ala Phe Thr  
 320 325 330  
 Gly Gly Pro Ile Cys Asn Thr Ile Tyr Gln Val Ser Gly Asp Ser Val  
 335 340 345  
 Asp Tyr Ala Phe Glu Val Ala Lys Ala Thr Tyr Ser Met Thr Val Glu  
 350 355 360  
 Leu Arg Asp Thr Gly Lys Tyr Gly Phe Val Leu Pro Lys Glu Gln Ile  
 365 370 375 380  
 Val Pro Ser Ala Glu Met Trp Ala Gly Leu Arg Tyr Leu Val Lys  
 385 390 395  
 Asn Met

<210> 243  
 <211> 4594  
 <212> DNA  
 <213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<220>  
 <221> CDS  
 <222> (1692)...(1873)  
 <223> Exon

<221> CDS  
 <222> (2057)...(2509)  
 <223> Exon

<221> CDS  
 <222> (2593)...(2768)  
 <223> Exon

<221> CDS  
 <222> (2834)...(3597)  
 <223> Exon

<400> 243  
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 ctcccgcaca cctgttctgg aacgggtcag agacgccgaa gttgaggtat ttgcccgga 180  
 ccgaaagcgt ctggtcctcg atcttgaagg tgaaatctgg cagtgtggcg ttgcatggga 240  
 aggtattact accgccaagt gtcaactcgt agtctggaac ctgactgtag tagttggcga 300

## 10336256.txt

cgaccggatc agggaggtag atgagcggag aaccagagtc gacagtggta ttaccgatga 360  
 tggccgggtcc aaaggttttg ttgccgcgc cactactctcc aactgctatg gtccaatgct 420  
 tcatgttgctc gaccacaggc gtatatgtga tgcgccaggt gtatttggaat ttgtcgagat 480  
 agccaaagtc ccaagaacca ttgccctcgg gcctcaagtt tgctgcaaag acttttttct 540  
 tcagtgtcgg tgcgacggtt tcgaagaagg tgctttgttg cacaggcttt acctgggtga 600  
 tgatgccgaa cgcaagacct atgataccat ccgagtcgat atcgctgggg acatagggtg 660  
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 caatgccatt ggccgaggag ccgcctgagt aggtgatggg ccaattatag ttgggcaaca 780  
 gctgtgcaga cgacgatggg aagtagtagg ttttgctcgg accctgcata gttgatgtct 840  
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 ttccaataat ggtaggggta aagtaggtga tgccagggtc gtcggggcact acagtgcagg 960  
 acccttctctg ttggcctgca acattggctt gtctcttgct gacagtttcc gtggtaggat 1020  
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 cggcgtcgac actataggca gcgccggagc gttctggtag aagagcgag gcagaagagg 1140  
 cgagtatggc gagtgcgagc ttggctgtca ttgttggtgac atgtgacatt gtgtttgtgt 1200  
 gaatagtaga gagaagatgg tggagtaaag aggggtgtcac ccggcaaatg ctgtgtagcc 1260  
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 tggcatgatg tcaacaaggt cgtattgaga agcaaagacg atgagttcac aggggaggtt 1560  
 gaccgaaata gcaaaaacga tgtatgcatt gcccatcccg gtagtctata aaaagtaaga 1620  
 gcttgcttga cgtgggaaat ggggtgccga tccagagcgt gcattaatgt gaaagtggac 1680  
 taggagagaa g atg gcg cca atc aag ttg gtc ggg tgg aaa tgg cgg act 1730  
 Met Ala Pro Ile Lys Leu Val Gly Trp Lys Trp Arg Thr  
 1 5 10

ggc tgg ccg ggg ata att cgg cta gcg ggc tgg gag agg aag gag ctc 1778  
 Gly Trp Pro Gly Ile Ile Arg Leu Ala Gly Trp Glu Arg Lys Glu Leu  
 15 20 25

gtg ttg aca cga tgc agc gtc cac ttt ggc atc cat gaa aca cgc atc 1826  
 Val Leu Thr Arg Cys Ser Val His Phe Gly Ile His Glu Thr Arg Ile  
 30 35 40 45

cga tat att gtt ctc caa aaa ccg gga ccc ccg caa acc cac aag cc 1873  
 Arg Tyr Ile Val Leu Gln Lys Pro Gly Pro Pro Gln Thr His Lys Pro  
 50 55 60

gtcaagataa gtacacacct gcacaacggc aaagacaagg tacagtggtc cgtgccacac 1933  
 acacagcata gccaaactca aatccatcgt actcgtattg ctacattccc ggcacggccc 1993  
 gactcagtca gtagccaact taccatgtag cgttgtaata agctttggcc actctcttgg 2053  
 cag t gca tac gct ctg gag atc aca gtc gac cgt cca cac ccc aca ctc 2102  
 Ala Tyr Ala Leu Glu Ile Thr Val Asp Arg Pro His Pro Thr Leu  
 65 70 75

agg agt gcc ctg ggt cgg tca gcc gag aga cag gca tct ggt act cac 2150  
 Arg Ser Ala Leu Gly Arg Ser Ala Glu Arg Gln Ala Ser Gly Thr His  
 80 85 90

ata aag acc tgc cat ggc tcc gtc ttc cct tgc ctt gcc cgc atc tgc 2198  
 Ile Lys Thr Cys His Gly Ser Val Phe Pro Cys Leu Ala Arg Ile Cys  
 95 100 105

gca atc ttg ctc tca cac tca aca atc atg cct gat tcc aag atg gtc 2246  
 Ala Ile Leu Leu Ser His Ser Thr Ile Met Pro Asp Ser Lys Met Val  
 110 115 120

tca cgc gcc ctt ctc gcc gcc ctt gca ctc cct gct gtc tct gcc gag 2294  
 Ser Arg Ala Leu Leu Ala Ala Leu Ala Leu Pro Ala Val Ser Ala Glu  
 125 130 135 140

ctt ccc cca ggc gcc att gct gtg ccc ctg atc cga gac gcc gaa ctc 2342  
 Leu Pro Pro Gly Ala Ile Ala Val Pro Leu Ile Arg Asp Ala Glu Leu  
 145 150 155

gac gca tac tac gca gag ttc cag gtc gga acg ccc ccg cag aag gaa 2390  
 Asp Ala Tyr Tyr Ala Glu Phe Gln Val Gly Thr Pro Pro Gln Lys Glu

10336256.txt																	
160				165				170									
tac	ctc	aaa	gtc	gat	act	ggc	agc	cca	cga	tat	tcc	ttt	ctt	aac	ccg	2438	
Tyr	Leu	Lys	Val	Asp	Thr	Gly	Ser	Pro	Arg	Tyr	Ser	Phe	Leu	Asn	Pro		
		175					180					185					
cgc	aac	caa	gaa	tgt	gtc	tcg	gat	cca	gcg	tca	tgc	act	act	ttt	ggc	2486	
Arg	Asn	Gln	Glu	Cys	Val	Ser	Asp	Pro	Ala	Ser	Cys	Thr	Thr	Phe	Gly		
	190					195					200						
act	ttt	gac	aac	ttg	acc	tct	tc	gtaagtaatc atctttggct tcttttttta								2539	
Thr	Phe	Asp	Asn	Leu	Thr	Ser	Ser										
205					210												
ttaaaaaaag aagcccccaa aaagattgca agcgctaatt ctacatcttc cag a act																2596	
														Thr			
tgt	cgt	tat	gaa	gga	cct	ggc	ttc	tac	gat	gaa	ctc	tac	gca	tta	gga	2644	
Cys	Arg	Tyr	Glu	Gly	Pro	Gly	Phe	Tyr	Asp	Glu	Leu	Tyr	Ala	Leu	Gly		
	215					220					225						
ttt	ggc	gat	tac	ctc	agt	gac	acc	ttg	gtc	ctg	ggc	ggg	gtc	acc	atg	2692	
Phe	Gly	Asp	Tyr	Leu	Ser	Asp	Thr	Leu	Val	Leu	Gly	Gly	Val	Thr	Met		
230					235					240					245		
ccc	aac	atg	tat	ttc	ggg	tac	acg	tcc	aat	tat	acg	gcc	gga	aaa	gta	2740	
Pro	Asn	Met	Tyr	Phe	Gly	Tyr	Thr	Ser	Asn	Tyr	Thr	Ala	Gly	Lys	Val		
				250					255					260			
gtt	cca	gaa	cca	att	caa	act	att	ctg	g	gtatgtcaag acacccgtgt							2788
Val	Pro	Glu	Pro	Ile	Gln	Thr	Ile	Leu									
			265					270									
tcttcgtgca cgactgcagt ctaactgttt gattgcgaaa tctag gc ctg tct ctc																2844	
											Gly	Leu	Ser	Leu			
gaa	tgt	tat	ccg	gag	gag	cct	gac	tgc	atg	tcc	aaa	ggg	gca	tat	ttt	2892	
Glu	Cys	Tyr	Pro	Glu	Glu	Pro	Asp	Cys	Met	Ser	Lys	Gly	Ala	Tyr	Phe		
275					280					285					290		
cta	cca	gag	ttg	aag	aac	gcc	tca	ctg	att	gac	gtc	atg	gca	aca	agt	2940	
Leu	Pro	Glu	Leu	Lys	Asn	Ala	Ser	Leu	Ile	Asp	Val	Met	Ala	Thr	Ser		
				295					300					305			
atg	tac	ctt	ggg	ccg	gat	gaa	ttc	aac	gtc	acc	aat	gcc	cag	atg	atc	2988	
Met	Tyr	Leu	Gly	Pro	Asp	Glu	Phe	Asn	Val	Thr	Asn	Ala	Gln	Met	Ile		
			310					315				320					
att	ggg	ggc	gcc	tat	gac	aag	gca	aag	gtg	gac	ggg	gac	atg	ttc	acg	3036	
Ile	Gly	Gly	Ala	Tyr	Asp	Lys	Ala	Lys	Val	Asp	Gly	Asp	Met	Phe	Thr		
		325					330				335						
ctg	gag	atg	gtg	gat	cca	ttc	tcc	aca	ctc	acc	ggc	gaa	caa	acg	aac	3084	
Leu	Glu	Met	Val	Asp	Pro	Phe	Ser	Thr	Leu	Thr	Gly	Glu	Gln	Thr	Asn		
		340				345					350						
tac	gtg	aac	gtc	act	gca	atg	gaa	gtt	gta	ctt	gac	ggc	ggc	aac	cgc	3132	
Tyr	Val	Asn	Val	Thr	Ala	Met	Glu	Val	Val	Leu	Asp	Gly	Gly	Asn	Arg		
355					360				365						370		
acg	tca	caa	acc	ttt	gga	gat	aag	ggg	gtt	ggg	gtc	ccc	atc	ttg	ctc	3180	
Thr	Ser	Gln	Thr	Phe	Gly	Asp	Lys	Gly	Val	Gly	Val	Pro	Ile	Leu	Leu		
				375					380					385			
gac	acg	ggc	att	gca	acc	tgg	tac	gtg	act	gat	acc	att	ttc	ggc	gcc	3228	
Asp	Thr	Gly	Ile	Ala	Thr	Trp	Tyr	Val	Thr	Asp	Thr	Ile	Phe	Gly	Ala		

10336256.txt

390	395	400	
gtc tcc tac gga ttg ggt att acc gcc ttc caa cct gga aaa cag gtg Val Ser Tyr 405 Gly Leu Gly Ile Thr 410 Ala Phe Gln Pro Gly Lys Gln Val			3276
acc tct gtt gac tgc aag tac cgg gac ccc aac aat gcc aag ggc tac Thr 420 Ser Val Asp Cys Lys Tyr 425 Arg Asp Pro Asn Asn 430 Ala Lys Gly Tyr			3324
atc tct gtc gaa ttc ggc gct agt ggc aag att gac gtt ccg ctg cac Ile 435 Ser Val Glu Phe Gly 440 Ala Ser Gly Lys Ile 445 Asp Val Pro Leu His 450			3372
gaa att atc tct ctg ttt gct aat agc acg tgt ggc gtc tac atg gag Glu Ile Ile Ser Leu 455 Phe Ala Asn Ser Thr 460 Cys Gly Val Tyr Met 465 Glu			3420
cct cgc tcg gaa acc gat att ggc gta ctc gca gac ccc ttt att cgt Pro Arg Ser Glu 470 Thr Asp Ile Gly Val 475 Leu Ala Asp Pro Phe Ile Arg 480			3468
gca att tac gca atc ttc gac cag acc cac agg acc atc aca atg ggc Ala Ile Tyr 485 Ala Ile Phe Asp Gln Thr His Arg Thr Ile 495 Thr Met Gly			3516
aaa gca aaa tac aca act gag cag aac att gtg ccc ttc ccc gag gga Lys Ala Lys Tyr Thr Thr Glu 505 Gln Asn Ile Val Pro Phe Pro Glu Gly 510			3564
ggg ttc aca gtg ggc tcc aag gtc agc tct tag Gly Phe Thr Val Gly Ser 520 Lys Val Ser Ser *	acacggcaca	tgtatatatt	3617
tgtaatccgg ttagaatgta catattcaag ttgggattgt gagatccaag cgctcttatg caagaggaaa cgcgacagat gatgtttaat gatgtcgtgg ttaccaatct tgacacattc caatgatgca tttcaactcg taaagattta tttcaagttg ttgaggccat atctacattt ccatgataca taccaaagcg ggtccactag aaatggacaa cacagcagtg ccaagaaaat gattacaacg aatacagagtc aagacactga actctgtagt gaagattagt gctgaccttt gttgataatg gacatgaact acgttggcgc tgcggggcgg aatatccaca tattaagaga catctttacct cccgtaataa ggcttaattg atgggtgcatt acaagcccac ctatgactct tgtctggaag aaagtgccta gatttgcgct ttagctgcaa aggctattta gtctgactgt actactcgtt ctatgtagca aggggtgcgta tggttaagtag atgtcgcgtg agaatcgcgc taacgtaaca cggagatccc tgtcaactag gtaagagtg ggagagcaag tggcagtaga gtttggagct actagtatgt aaattctaatt tcttcgtgca accaaagccc tggggggagc atggatacgg ggcagggtact gtgaacataa tgtcgcgaatt atattcatca tgtcgttact atagccggca atgaactgat taacaagcaa ccccgcgatg atatcatctt atagctcccc acccctcagt caaccccatc cattaacacc ccagccatgg caacggtcag tgaggcggag gcgccacagc ctagggaagg tgcctttgat ctaccaactg cagatgggtac atcccaagcc accgttactt tacaagaaaa tgaagatgcc accaaaccgc ccctgctact cgacatcacc aaacgagctc tcgaccc			3677 3737 3797 3857 3917 3977 4037 4097 4157 4217 4277 4337 4397 4457 4517 4577 4594

&lt;210&gt; 244

&lt;211&gt; 61

&lt;212&gt; PRT

&lt;213&gt; Cochliobolus heterostrophus strain C4 (ATCC 48331)

&lt;400&gt; 244

Met Ala Pro Ile Lys Leu Val Gly Trp Lys Trp Arg Thr Gly Trp Pro  
 1 5 10 15  
 Gly Ile Ile Arg Leu Ala Gly Trp Glu Arg Lys Glu Leu Val Leu Thr  
 20 25 30  
 Arg Cys Ser Val His Phe Gly Ile His Glu Thr Arg Ile Arg Tyr Ile  
 35 40 45  
 Val Leu Gln Lys Pro Gly Pro Pro Gln Thr His Lys Pro  
 50 55 60

&lt;210&gt; 245

10336256.txt

&lt;211&gt; 151

&lt;212&gt; PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

&lt;400&gt; 245

```

Ala Tyr Ala Leu Glu Ile Thr Val Asp Arg Pro His Pro Thr Leu Arg
 1      5      10      15
Ser Ala Leu Gly Arg Ser Ala Glu Arg Gln Ala Ser Gly Thr His Ile
 20      25      30
Lys Thr Cys His Gly Ser Val Phe Pro Cys Leu Ala Arg Ile Cys Ala
 35      40      45
Ile Leu Leu Ser His Ser Thr Ile Met Pro Asp Ser Lys Met Val Ser
 50      55      60
Arg Ala Leu Leu Ala Ala Leu Ala Leu Pro Ala Val Ser Ala Glu Leu
 65      70      75      80
Pro Pro Gly Ala Ile Ala Val Pro Leu Ile Arg Asp Ala Glu Leu Asp
 85      90      95
Ala Tyr Tyr Ala Glu Phe Gln Val Gly Thr Pro Pro Gln Lys Glu Tyr
100      105      110
Leu Lys Val Asp Thr Gly Ser Pro Arg Tyr Ser Phe Leu Asn Pro Arg
115      120      125
Asn Gln Glu Cys Val Ser Asp Pro Ala Ser Cys Thr Thr Phe Gly Thr
130      135      140
Phe Asp Asn Leu Thr Ser Ser
145      150

```

&lt;210&gt; 246

&lt;211&gt; 58

&lt;212&gt; PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

&lt;400&gt; 246

```

Thr Cys Arg Tyr Glu Gly Pro Gly Phe Tyr Asp Glu Leu Tyr Ala Leu
 1      5      10      15
Gly Phe Gly Asp Tyr Leu Ser Asp Thr Leu Val Leu Gly Gly Val Thr
 20      25      30
Met Pro Asn Met Tyr Phe Gly Tyr Thr Ser Asn Tyr Thr Ala Gly Lys
 35      40      45
Val Val Pro Glu Pro Ile Gln Thr Ile Leu
 50      55

```

&lt;210&gt; 247

&lt;211&gt; 254

&lt;212&gt; PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

&lt;400&gt; 247

```

Gly Leu Ser Leu Glu Cys Tyr Pro Glu Glu Pro Asp Cys Met Ser Lys
 1      5      10      15
Gly Ala Tyr Phe Leu Pro Glu Leu Lys Asn Ala Ser Leu Ile Asp Val
 20      25      30
Met Ala Thr Ser Met Tyr Leu Gly Pro Asp Glu Phe Asn Val Thr Asn
 35      40      45
Ala Gln Met Ile Ile Gly Gly Ala Tyr Asp Lys Ala Lys Val Asp Gly
 50      55      60
Asp Met Phe Thr Leu Glu Met Val Asp Pro Phe Ser Thr Leu Thr Gly
 65      70      75      80
Glu Gln Thr Asn Tyr Val Asn Val Thr Ala Met Glu Val Val Leu Asp
 85      90      95
Gly Gly Asn Arg Thr Ser Gln Thr Phe Gly Asp Lys Gly Val Gly Val
100      105      110
Pro Ile Leu Leu Asp Thr Gly Ile Ala Thr Trp Tyr Val Thr Asp Thr
115      120      125
Ile Phe Gly Ala Val Ser Tyr Gly Leu Gly Ile Thr Ala Phe Gln Pro
130      135      140
Gly Lys Gln Val Thr Ser Val Asp Cys Lys Tyr Arg Asp Pro Asn Asn
145      150      155      160
Ala Lys Gly Tyr Ile Ser Val Glu Phe Gly Ala Ser Gly Lys Ile Asp
Page 245

```

## 10336256.txt

Val Pro Leu His 165 Glu Ile Ile Ser Leu Phe Ala Asn Ser Thr 175 Cys Gly  
 Val Tyr Met 180 Glu Pro Arg Ser Glu 185 Thr Asp Ile Gly Val 190 Leu Ala Asp  
 Pro Phe Ile 195 Arg Ala Ile Tyr 200 Ala Ile Phe Asp Gln 205 Thr His Arg Thr  
 Ile Thr Met Gly Lys Ala 215 Tyr Thr Thr Glu 220 Gln Asn Ile Val Pro  
 225 Phe Pro Glu Gly Gly 230 Phe Thr Val Gly Ser 235 Lys Val Ser Ser 240  
 245

&lt;210&gt; 248

&lt;211&gt; 1575

&lt;212&gt; DNA

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1575)

&lt;400&gt; 248

atg gcg cca atc aag ttg gtc ggg tgg aaa tgg cgg act ggc tgg ccg	48
Met Ala Pro Ile Lys 5 Leu Val Gly Trp 10 Lys Trp Arg Thr Gly Trp Pro 15	
ggg ata att cgg cta gcg ggc tgg gag agg aag gag ctc gtg ttg aca	96
Gly Ile Ile Arg 20 Leu Ala Gly Trp 25 Glu Arg Lys Glu Leu Val 30 Leu Thr	
cga tgc agc gtc cac ttt ggc atc cat gaa aca cgc atc cga tat att	144
Arg Cys Ser 35 Val His Phe Gly 40 His Glu Thr Arg Ile 45 Arg Tyr Ile	
gtt ctc caa aaa ccg gga ccc ccg caa acc cac aag cct gca tac gct	192
Val Leu 50 Gln Lys Pro Gly Pro 55 Gln Thr His Lys 60 Pro Ala Tyr Ala	
ctg gag atc aca gtc gac cgt cca cac ccc aca ctc agg agt gcc ctg	240
Leu 65 Glu Ile Thr Val Asp 70 Arg Pro His Pro Thr 75 Leu Arg Ser Ala Leu 80	
ggt cgg tca gcc gag aga cag gca tct ggt act cac ata aag acc tgc	288
Gly Arg Ser Ala Glu 85 Arg Gln Ala Ser Gly 90 Thr His Ile Lys Thr 95 Cys	
cat ggc tcc gtc ttc cct tgc ctt gcc cgc atc tgc gca atc ttg ctc	336
His Gly Ser Val 100 Phe Pro Cys Leu Ala 105 Arg Ile Cys Ala Ile 110 Leu Leu	
tca cac tca aca atc atg cct gat tcc aag atg gtc tca cgc gcc ctt	384
Ser His Ser 115 Thr Ile Met Pro Asp 120 Ser Lys Met Val Ser 125 Arg Ala Leu	
ctc gcc gcc ctt gca ctc cct gct gtc tct gcc gag ctt ccc cca ggc	432
Leu Ala Ala Leu Ala Leu Pro 135 Ala Val Ser Ala Glu Leu Pro Pro Gly	
gcc att gct gtg ccc ctg atc cga gac gcc gaa ctc gac gca tac tac	480
Ala Ile Ala Val Pro Leu 150 Ile Arg Asp Ala Glu 155 Leu Asp Ala Tyr Tyr 160	
gca gag ttc cag gtc gga acg ccc ccg cag aag gaa tac ctc aaa gtc	528
Ala Glu Phe Gln Val 165 Gly Thr Pro Pro Gln Lys Glu Tyr Leu 175 Lys Val	
gat act ggc agc cca cga tat tcc ttt ctt aac ccg cgc aac caa gaa	576
Asp Thr Gly Ser Pro Arg Tyr Ser Phe Leu Asn Pro Arg Asn Gln Glu	

10336256.txt																
180						185						190				
tgt Cys	gtc Val	tcg Ser 195	gat Asp	cca Pro	gcg Ala	tca Ser	tgc Cys 200	act Thr	act Thr	ttt Phe	ggc Gly	act Thr 205	ttt Phe	gac Asp	aac Asn	624
ttg Leu	acc Thr 210	tct Ser	tca Ser	act Thr	tgt Cys	cgt Arg 215	tat Tyr	gaa Glu	gga Gly	cct Pro	ggc Gly 220	ttc Phe	tac Tyr	gat Asp	gaa Glu	672
ctc Leu 225	tac Tyr	gca Ala	tta Leu	gga Gly	ttt Phe 230	ggc Gly	gat Asp	tac Tyr	ctc Leu	agt Ser 235	gac Asp	acc Thr	ttg Leu	gtc Val	ctg Leu 240	720
ggc Gly	ggt Gly	gtc Val	acc Thr	atg Met 245	ccc Pro	aac Asn	atg Met	tat Tyr	ttc Phe 250	ggg Gly	tac Tyr	acg Thr	tcc Ser	aat Asn 255	tat Tyr	768
acg Thr	gcc Ala	gga Gly	aaa Lys 260	gta Val	gtt Val	cca Pro	gaa Glu	cca Pro 265	att Ile	caa Gln	act Thr	att Ile	ctg Leu 270	ggc Gly	ctg Leu	816
tct Ser	ctc Leu	gaa Glu 275	tgt Cys	tat Tyr	ccg Pro	gag Glu	gag Glu 280	cct Pro	gac Asp	tgc Cys	atg Met	tcc Ser 285	aaa Lys	ggg Gly	gca Ala	864
tat Tyr	ttt Phe 290	cta Leu	cca Pro	gag Glu	ttg Leu	aag Lys 295	aac Asn	gcc Ala	tca Ser	ctg Leu	att Ile 300	gac Asp	gtc Val	atg Met	gca Ala	912
aca Thr 305	agt Ser	atg Met	tac Tyr	ctt Leu	ggg Gly 310	ccg Pro	gat Asp	gaa Glu	ttc Phe	aac Asn 315	gtc Val	acc Thr	aat Asn	gcc Ala	cag Gln 320	960
atg Met	atc Ile	att Ile	ggt Gly	ggc Gly 325	gcc Ala	tat Tyr	gac Asp	aag Lys	gca Ala 330	aag Lys	gtg Val	gac Asp	ggt Gly	gac Asp 335	atg Met	1008
ttc Phe	acg Thr	ctg Leu	gag Glu 340	atg Met	gtg Val	gat Asp	cca Pro	ttc Phe 345	tcc Ser	aca Thr	ctc Leu	acc Thr	ggc Gly 350	gaa Glu	caa Gln	1056
acg Thr	aac Asn	tac Tyr 355	gtg Val	aac Asn	gtc Val	act Thr	gca Ala 360	atg Met	gaa Glu	gtt Val	gta Val	ctt Leu 365	gac Asp	ggc Gly	ggc Gly	1104
aac Asn	cgc Arg 370	acg Thr	tca Ser	caa Gln	acc Thr	ttt Phe 375	gga Gly	gat Asp	aag Lys	ggt Gly	gtt Val 380	ggt Gly	gtc Val	ccc Pro	atc Ile	1152
ttg Leu 385	ctc Leu	gac Asp	acg Thr	ggc Gly	att Ile 390	gca Ala	acc Thr	tgg Trp	tac Tyr	gtg Val 395	act Thr	gat Asp	acc Thr	att Ile	ttc Phe 400	1200
ggc Gly	gcc Ala	gtc Val	tcc Ser	tac Tyr 405	gga Gly	ttg Leu	ggt Gly	att Ile	acc Thr 410	gcc Ala	ttc Phe	caa Gln	cct Pro	gga Gly 415	aaa Lys	1248
cag Gln	gtg Val	acc Thr	tct Ser 420	gtt Val	gac Asp	tgc Cys	aag Lys	tac Tyr 425	cgg Arg	gac Asp	ccc Pro	aac Asn	aat Asn 430	gcc Ala	aag Lys	1296
ggc Gly	tac Tyr	atc Ile 435	tct Ser	gtc Val	gaa Glu	ttc Phe	ggc Gly 440	gct Ala	agt Ser	ggc Gly	aag Lys	att Ile 445	gac Asp	gtt Val	ccg Pro	1344
ctg Leu	cac His	gaa Glu	att Ile	atc Ile	tct Ser	ctg Leu	ttt Phe	gct Ala	aat Asn	agc Ser	acg Thr	tgt Cys	ggc Gly	gtc Val	tac Tyr	1392

10336256.txt  
460

450	atg gag cct cgc tcg gaa acc gat att ggc gta ctc gca gac ccc ttt	1440
	Met Glu Pro Arg Ser Glu Thr Asp Ile Gly Val Leu Ala Asp Pro Phe	
465		470
455	att cgt gca att tac gca atc ttc gac cag acc cac agg acc atc aca	1488
	Ile Arg Ala Ile Tyr Ala Ile Phe Asp Gln Thr His Arg Thr Ile Thr	
		485
	atg ggc aaa gca aaa tac aca act gag cag aac att gtg ccc ttc ccc	1536
	Met Gly Lys Ala Lys Tyr Thr Thr Glu Gln Asn Ile Val Pro Phe Pro	
		500
	gag gga ggt ttc aca gtg ggc tcc aag gtc agc tct tag	1575
	Glu Gly Gly Phe Thr Val Gly Ser Lys Val Ser Ser *	
		515
		520

&lt;210&gt; 249

&lt;211&gt; 524

&lt;212&gt; PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

&lt;220&gt;

&lt;221&gt; DOMAIN

&lt;222&gt; (104)...(500)

&lt;223&gt; Eukaryotic aspartyl protease

&lt;400&gt; 249

Met	Ala	Pro	Ile	Lys	Leu	Val	Gly	Trp	Lys	Trp	Arg	Thr	Gly	Trp	Pro
1				5					10				15		
Gly	Ile	Ile	Arg	Leu	Ala	Gly	Trp	Glu	Arg	Lys	Glu	Leu	Val	Leu	Thr
			20					25					30		
Arg	Cys	Ser	Val	His	Phe	Gly	Ile	His	Glu	Thr	Arg	Ile	Arg	Tyr	Ile
		35					40					45			
Val	Leu	Gln	Lys	Pro	Gly	Pro	Pro	Gln	Thr	His	Lys	Pro	Ala	Tyr	Ala
	50				55						60				
Leu	Glu	Ile	Thr	Val	Asp	Arg	Pro	His	Pro	Thr	Leu	Arg	Ser	Ala	Leu
65				70						75					80
Gly	Arg	Ser	Ala	Glu	Arg	Gln	Ala	Ser	Gly	Thr	His	Ile	Lys	Thr	Cys
			85						90				95		
His	Gly	Ser	Val	Phe	Pro	Cys	Leu	Ala	Arg	Ile	Cys	Ala	Ile	Leu	Leu
			100					105				110			
Ser	His	Ser	Thr	Ile	Met	Pro	Asp	Ser	Lys	Met	Val	Ser	Arg	Ala	Leu
		115					120					125			
Leu	Ala	Ala	Leu	Ala	Leu	Pro	Ala	Val	Ser	Ala	Glu	Leu	Pro	Pro	Gly
	130					135					140				
Ala	Ile	Ala	Val	Pro	Leu	Ile	Arg	Asp	Ala	Glu	Leu	Asp	Ala	Tyr	Tyr
145				150						155					160
Ala	Glu	Phe	Gln	Val	Gly	Thr	Pro	Pro	Gln	Lys	Glu	Tyr	Leu	Lys	Val
			165						170					175	
Asp	Thr	Gly	Ser	Pro	Arg	Tyr	Ser	Phe	Leu	Asn	Pro	Arg	Asn	Gln	Glu
		180						185					190		
Cys	Val	Ser	Asp	Pro	Ala	Ser	Cys	Thr	Thr	Phe	Gly	Thr	Phe	Asp	Asn
		195					200					205			
Leu	Thr	Ser	Ser	Thr	Cys	Arg	Tyr	Glu	Gly	Pro	Gly	Phe	Tyr	Asp	Glu
	210					215					220				
Leu	Tyr	Ala	Leu	Gly	Phe	Gly	Asp	Tyr	Leu	Ser	Asp	Thr	Leu	Val	Leu
225				230						235					240
Gly	Gly	Val	Thr	Met	Pro	Asn	Met	Tyr	Phe	Gly	Tyr	Thr	Ser	Asn	Tyr
			245						250					255	
Thr	Ala	Gly	Lys	Val	Val	Pro	Glu	Pro	Ile	Gln	Thr	Ile	Leu	Gly	Leu
		260						265					270		
Ser	Leu	Glu	Cys	Tyr	Pro	Glu	Glu	Pro	Asp	Cys	Met	Ser	Lys	Gly	Ala
		275					280					285			
Tyr	Phe	Leu	Pro	Glu	Leu	Lys	Asn	Ala	Ser	Leu	Ile	Asp	Val	Met	Ala
		290				295					300				

10336256.txt

Thr	Ser	Met	Tyr	Leu	Gly	Pro	Asp	Glu	Phe	Asn	Val	Thr	Asn	Ala	Gln
305					310					315					320
Met	Ile	Ile	Gly	Gly	Ala	Tyr	Asp	Lys	Ala	Lys	Val	Asp	Gly	Asp	Met
			325						330					335	
Phe	Thr	Leu	Glu	Met	Val	Asp	Pro	Phe	Ser	Thr	Leu	Thr	Gly	Glu	Gln
			340					345					350		
Thr	Asn	Tyr	Val	Asn	Val	Thr	Ala	Met	Glu	Val	Val	Leu	Asp	Gly	Gly
		355					360					365			
Asn	Arg	Thr	Ser	Gln	Thr	Phe	Gly	Asp	Lys	Gly	Val	Gly	Val	Pro	Ile
	370					375					380				
Leu	Leu	Asp	Thr	Gly	Ile	Ala	Thr	Trp	Tyr	Val	Thr	Asp	Thr	Ile	Phe
385					390					395					400
Gly	Ala	Val	Ser	Tyr	Gly	Leu	Gly	Ile	Thr	Ala	Phe	Gln	Pro	Gly	Lys
			405						410					415	
Gln	Val	Thr	Ser	Val	Asp	Cys	Lys	Tyr	Arg	Asp	Pro	Asn	Asn	Ala	Lys
			420					425					430		
Gly	Tyr	Ile	Ser	Val	Glu	Phe	Gly	Ala	Ser	Gly	Lys	Ile	Asp	Val	Pro
		435					440					445			
Leu	His	Glu	Ile	Ile	Ser	Leu	Phe	Ala	Asn	Ser	Thr	Cys	Gly	Val	Tyr
	450					455					460				
Met	Glu	Pro	Arg	Ser	Glu	Thr	Asp	Ile	Gly	Val	Leu	Ala	Asp	Pro	Phe
465					470					475					480
Ile	Arg	Ala	Ile	Tyr	Ala	Ile	Phe	Asp	Gln	Thr	His	Arg	Thr	Ile	Thr
			485						490					495	
Met	Gly	Lys	Ala	Lys	Tyr	Thr	Thr	Glu	Gln	Asn	Ile	Val	Pro	Phe	Pro
			500					505					510		
Glu	Gly	Gly	Phe	Thr	Val	Gly	Ser	Lys	Val	Ser	Ser				
		515					520								

<210> 250  
 <211> 6066  
 <212> DNA  
 <213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

<220>  
 <221> CDS  
 <222> (3361)...(3553)  
 <223> Exon

<221> CDS  
 <222> (3608)...(3767)  
 <223> Exon

<221> CDS  
 <222> (3821)...(5108)  
 <223> Exon

<400> 250							
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## 10336256.txt

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atg aag ctc ctt tcg gtc ttc ggt tca ttt ctc tgt gct tca gca gct 3408
Met Lys Leu Leu Ser Val Phe Gly Ser Phe Leu Cys Ala Ser Ala Ala
1 5 10 15

ctc gct gca aat gcc cct cgc ttt ctc aga cct aac aga gtc cat cgc 3456
Leu Ala Ala Asn Ala Pro Arg Phe Leu Arg Pro Asn Arg Val His Arg
20 25 30

ccc aat cca gtc att gag aag cgt gtc cct gga cag gac ttt cag aac 3504
Pro Asn Pro Val Ile Glu Lys Arg Val Pro Gly Gln Asp Phe Gln Asn
35 40 45

cca gag atc aac aag aga gct cat acc ttc ctc aac gca aag acc caa 3552
Pro Glu Ile Asn Lys Arg Ala His Thr Phe Leu Asn Ala Lys Thr Gln
50 55 60

c gtgagtaccg atcttgttgt cttatgtata cagacatata ctcatgtcct 3603
ttag cc ttt gct gtc gat ggc aag aat gtc ccc ttg gcc aat ttc gac 3651
Pro Phe Ala Val Asp Gly Lys Asn Val Pro Leu Ala Asn Phe Asp
65 70 75

tta ggt gag agt tat gct ggc tta cta ccc atc tcc aac gac aaa aac 3699
Leu Gly Glu Ser Tyr Ala Gly Leu Leu Pro Ile Ser Asn Asp Lys Asn
80 85 90 95

gaa acg cgc aag ctt ttt ttc tgg ttc ttt cca tct acc cag gcc aag 3747
Glu Thr Arg Lys Leu Phe Phe Trp Phe Phe Pro Ser Thr Gln Ala Lys
100 105 110

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Thr Pro Glu Glu Ile Val Met
115

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## 10336256.txt

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				120						125			
ctc	agc	ggt	ttg	ctc	caa	gag	aac	ggc	ccg	ttc	ttg	tgg	3896
Leu	Ser	Gly	Leu	Leu	Gln	Glu	Asn	Gly	Pro	Phe	Leu	Trp	
		130					135					140	
act	ctt	gcc	cca	act	cag	aac	cct	tat	tca	tgg	cac	aac	3944
Thr	Leu	Ala	Pro	Thr	Gln	Asn	Pro	Tyr	Ser	Trp	His	Asn	
	145					150					155		
atg	ctt	tgg	gtc	gaa	cag	cct	ggt	ggt	gtc	ggc	tat	tcg	3992
Met	Leu	Trp	Val	Glu	Gln	Pro	Val	Gly	Val	Gly	Tyr	Ser	
160					165					170			
ccc	gat	atc	agc	aac	gaa	tac	gaa	ctc	agt	gac	caa	ttc	4040
Pro	Asp	Ile	Ser	Asn	Glu	Tyr	Glu	Leu	Ser	Asp	Gln	Phe	
				180					185				
tac	aag	aac	ttt	gtc	gat	ctc	ttt	ggt	gtc	tgg	aac	tgg	4088
Tyr	Lys	Asn	Phe	Val	Asp	Leu	Phe	Gly	Val	Trp	Asn	Trp	
			195					200					
ggt	acc	gga	gag	tca	tat	gct	ggc	ttt	tac	ggt	cct	tac	4136
Val	Thr	Gly	Glu	Ser	Tyr	Ala	Gly	Phe	Tyr	Val	Pro	Tyr	
		210					215					220	
agc	ttc	atc	cgt	gcc	aat	gac	aag	aaa	tac	ttc	aat	ctt	4184
Ser	Phe	Ile	Arg	Ala	Asn	Asp	Lys	Lys	Tyr	Phe	Asn	Leu	
	225					230					235		
gca	atc	aac	gac	ccc	atc	atc	ggt	act	gat	act	gtc	caa	4232
Ala	Ile	Asn	Asp	Pro	Ile	Ile	Gly	Thr	Asp	Thr	Val	Gln	
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gtc	atc	cgg	ccc	tac	gtc	gaa	ttc	tgg	caa	aat	gtc	ttc	4280
Val	Ile	Arg	Pro	Tyr	Val	Glu	Phe	Trp	Gln	Asn	Val	Phe	
				260					265				
cag	act	ttc	tta	gaa	aga	gcc	cga	aag	cgc	gac	ctg	gaa	4328
Gln	Thr	Phe	Leu	Glu	Arg	Ala	Arg	Lys	Arg	Asp	Leu	Glu	
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acc	cag	tat	tat	gaa	aaa	tac	ttc	aaa	ttc	cct	ccg	cca	4376
Thr	Gln	Tyr	Tyr	Glu	Lys	Tyr	Phe	Lys	Phe	Pro	Pro	Pro	
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ttc	cca	aat	ctc	cct	gac	cca	ttc	gac	agt	acg	ggt	gat	4424
Phe	Pro	Asn	Leu	Pro	Asp	Pro	Phe	Asp	Ser	Thr	Gly	Asp	
	305					310					315		
tgc	gac	cag	ttc	gat	aac	tac	gcc	caa	gcc	att	gcc	gag	4472
Cys	Asp	Gln	Phe	Asp	Asn	Tyr	Ala	Gln	Ala	Ile	Ala	Glu	
320					325					330			
tgc	ttt	gac	gtc	tac	cac	atc	acc	gaa	acc	tgt	ccg	ttc	4520
Cys	Phe	Asp	Val	Tyr	His	Ile	Thr	Glu	Thr	Cys	Pro	Phe	
				340					345				
ccg	ctc	ggt	gga	acc	aac	cca	gga	gat	tat	gtc	gca	cca	4568
Pro	Leu	Gly	Gly	Thr	Asn	Pro	Gly	Asp	Tyr	Val	Ala	Pro	
			355					360					
gtc	tat	ttt	gac	cgc	gca	gat	gtc	aag	aag	gct	ctt	cat	4616
Val	Tyr	Phe	Asp	Arg	Ala	Asp	Val	Lys	Lys	Ala	Leu	His	
		370					375					380	

## 10336256.txt

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ggc gta aac ggc tca gac acg tct gtc cca ccc gcc aac agc ggc gtc Gly Val Asn Gly Ser Asp Thr Ser Val Pro Pro Ala Asn Ser Gly Val 400 405 410 415	4712
ctc caa aac gtt att gaa aaa aca aac aac gtc atg atc ggc tct gga Leu Gln Asn Val Ile Glu Lys Thr Asn Asn Val Met Ile Gly Ser Gly 420 425 430	4760
gac ctc gac ata ctt ctc agc aca aac ggc acc ctc ctc gcc ctt caa Asp Leu Asp Ile Leu Leu Ser Thr Asn Gly Thr Leu Leu Ala Leu Gln 435 440 445	4808
aac atg act tgg aac ggc gca caa ggt cta acc aga tac ccc tcc caa Asn Met Thr Trp Asn Gly Ala Gln Gly Leu Thr Arg Tyr Pro Ser Gln 450 455 460	4856
aac ctc tac gtg cct tac cac ccc gaa ttc aac ggc ggt gca cta gct Asn Leu Tyr Val Pro Tyr His Pro Glu Phe Asn Gly Gly Ala Leu Ala 465 470 475	4904
ggc gct gga tac cag ggc tta tgg acc aaa gaa cgc ggt ctg acc ttc Gly Ala Gly Tyr Gln Gly Leu Trp Thr Lys Glu Arg Gly Leu Thr Phe 480 485 490 495	4952
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acc gat ctc tat tagtagacga gtaggataacc tagcattacc tgtttttcgc Thr Asp Leu Tyr 545	5148
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&lt;210&gt; 251

&lt;211&gt; 64

&lt;212&gt; PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

&lt;400&gt; 251

10336256.txt

Met Lys Leu Leu Ser Val Phe Gly Ser Phe Leu Cys Ala Ser Ala Ala  
 1 5 10 15  
 Leu Ala Ala Asn Ala Pro Arg Phe Leu Arg Pro Asn Arg Val His Arg  
 20 25 30  
 Pro Asn Pro Val Ile Glu Lys Arg Val Pro Gly Gln Asp Phe Gln Asn  
 35 40 45  
 Pro Glu Ile Asn Lys Arg Ala His Thr Phe Leu Asn Ala Lys Thr Gln  
 50 55 60

&lt;210&gt; 252

&lt;211&gt; 54

&lt;212&gt; PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

&lt;400&gt; 252

Pro Phe Ala Val Asp Gly Lys Asn Val Pro Leu Ala Asn Phe Asp Leu  
 1 5 10 15  
 Gly Glu Ser Tyr Ala Gly Leu Leu Pro Ile Ser Asn Asp Lys Asn Glu  
 20 25 30  
 Thr Arg Lys Leu Phe Phe Trp Phe Phe Pro Ser Thr Gln Ala Lys Thr  
 35 40 45  
 Pro Glu Glu Ile Val Met  
 50

&lt;210&gt; 253

&lt;211&gt; 429

&lt;212&gt; PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

&lt;400&gt; 253

Leu Asn Gly Gly Pro Gly Cys Ser Ser Leu Ser Gly Leu Leu Gln Glu  
 1 5 10 15  
 Asn Gly Pro Phe Leu Trp Gln Asp Gly Thr Leu Ala Pro Thr Gln Asn  
 20 25 30  
 Pro Tyr Ser Trp His Asn Leu Thr Asn Met Leu Trp Val Glu Gln Pro  
 35 40 45  
 Val Gly Val Gly Tyr Ser Glu Gly Glu Pro Asp Ile Ser Asn Glu Tyr  
 50 55 60  
 Glu Leu Ser Asp Gln Phe Arg Gly Phe Tyr Lys Asn Phe Val Asp Leu  
 65 70 75 80  
 Phe Gly Val Trp Asn Trp Lys Thr Tyr Val Thr Gly Glu Ser Tyr Ala  
 85 90 95  
 Gly Phe Tyr Val Pro Tyr Ile Ala Asp Ser Phe Ile Arg Ala Asn Asp  
 100 105 110  
 Lys Lys Tyr Phe Asn Leu Gly Gly Ile Ala Ile Asn Asp Pro Ile Ile  
 115 120 125  
 Gly Thr Asp Thr Val Gln Gln Gln Ile Val Ile Arg Pro Tyr Val Glu  
 130 135 140  
 Phe Trp Gln Asn Val Phe Tyr Leu Asn Gln Thr Phe Leu Glu Arg Ala  
 145 150 155 160  
 Arg Lys Arg Asp Leu Glu Cys Gly Tyr Thr Gln Tyr Tyr Glu Lys Tyr  
 165 170 175  
 Phe Lys Phe Pro Pro Lys Gly Pro Phe Pro Asn Leu Pro Asp Pro  
 180 185 190  
 Phe Asp Ser Thr Gly Asp Val Pro Ile Cys Asp Gln Phe Asp Asn Tyr  
 195 200 205  
 Ala Gln Ala Ile Ala Glu Val Asn Pro Cys Phe Asp Val Tyr His Ile  
 210 215 220  
 Thr Glu Thr Cys Pro Phe Lys Ser Thr Pro Leu Gly Gly Thr Asn Pro  
 225 230 235 240  
 Gly Asp Tyr Val Ala Pro Gly Thr Glu Val Tyr Phe Asp Arg Ala Asp  
 245 250 255  
 Val Lys Lys Ala Leu His Ala Ser Pro Asn Ser Thr Trp Met Leu Cys  
 260 265 270  
 Thr Asp Lys Asn Val Phe Ala Gly Ala Gly Val Asn Gly Ser Asp Thr  
 275 280 285  
 Ser Val Pro Pro Ala Asn Ser Gly Val Leu Gln Asn Val Ile Glu Lys  
 290 295 300

## 10336256.txt

Thr Asn Asn Val Met Ile Gly Ser Gly Asp Leu Asp Ile Leu Leu Ser  
 305 310 315 320  
 Thr Asn Gly Thr Leu Ala Leu Gln Asn Met Thr Trp Asn Gly Ala  
 325 330 335  
 Gln Gly Leu Thr Arg Tyr Pro Ser Gln Asn Leu Tyr Val Pro Tyr His  
 340 345 350  
 Pro Glu Phe Asn Gly Gly Ala Leu Ala Gly Tyr Gln Gly Leu  
 355 360 365  
 Trp Thr Lys Glu Arg Gly Leu Thr Phe Tyr Thr Ala Arg Leu Ala Gly  
 370 375 380  
 His Glu Leu Pro Gly Tyr Thr Pro Gly Val Gly Tyr Arg Met Leu Glu  
 385 390 395 400  
 Ile Leu Leu Gly Arg Ile Ser Asp Phe Ser Thr Arg Asp Phe Thr  
 405 410 415  
 Thr Gln Thr Gly Asn Phe Thr Gly Thr Thr Asp Leu Tyr  
 420 425

&lt;210&gt; 254

&lt;211&gt; 1644

&lt;212&gt; DNA

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1644)

&lt;400&gt; 254

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Met Lys Leu Leu Ser Val Phe Gly Ser Phe Leu Cys Ala Ser Ala Ala	
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ctc gct gca aat gcc cct cgc ttt ctc aga cct aac aga gtc cat cgc	96
Leu Ala Ala Asn Ala Pro Arg Phe Leu Arg Pro Asn Arg Val His Arg	
20 25 30	
ccc aat cca gtc att gag aag cgt gtc cct gga cag gac ttt cag aac	144
Pro Asn Pro Val Ile Glu Lys Arg Val Pro Gly Gln Asp Phe Gln Asn	
35 40 45	
cca gag atc aac aag aga gct cat acc ttc ctc aac gca aag acc caa	192
Pro Glu Ile Asn Lys Arg Ala His Thr Phe Leu Asn Ala Lys Thr Gln	
50 55 60	
ccc ttt gct gtc gat ggc aag aat gtc ccc ttg gcc aat ttc gac tta	240
Pro Phe Ala Val Asp Gly Lys Asn Val Pro Leu Ala Asn Phe Asp Leu	
65 70 75 80	
ggt gag agt tat gct ggc tta cta ccc atc tcc aac gac aaa aac gaa	288
Gly Glu Ser Tyr Ala Gly Leu Leu Pro Ile Ser Asn Asp Lys Asn Glu	
85 90 95	
acg cgc aag ctt ttt ttc tgg ttc ttt cca tct acc cag gcc aag aca	336
Thr Arg Lys Leu Phe Phe Trp Phe Phe Pro Ser Thr Gln Ala Lys Thr	
100 105 110	
ccg gag gaa atc gtc atg ctt aat ggt ggc cct gga tgt agt tca ctc	384
Pro Glu Glu Ile Val Met Leu Asn Gly Gly Pro Gly Cys Ser Ser Leu	
115 120 125	
agc ggt ttg ctc caa gag aac ggc ccg ttc ttg tgg caa gac ggc act	432
Ser Gly Leu Leu Gln Glu Asn Gly Pro Phe Leu Trp Gln Asp Gly Thr	
130 135 140	
ctt gcc cca act cag aac cct tat tca tgg cac aac ctc acc aac atg	480
Leu Ala Pro Thr Gln Asn Pro Tyr Ser Trp His Asn Leu Thr Asn Met	
145 150 155 160	
ctt tgg gtc gaa cag cct gtt ggt gtc ggc tat tcg gaa ggc gag ccc	528

10336256.txt															
Leu	Trp	Val	Glu	Gln	Pro	Val	Gly	Val	Gly	Tyr	Ser	Glu	Gly	Glu	Pro
				165					170					175	
gat	atc	agc	aac	gaa	tac	gaa	ctc	agt	gac	caa	ttc	cgc	ggc	ttt	tac
Asp	Ile	Ser	Asn	Glu	Tyr	Glu	Leu	Ser	Asp	Gln	Phe	Arg	Gly	Phe	Tyr
			180					185					190		
aag	aac	ttt	gtc	gat	ctc	ttt	ggg	gtc	tgg	aac	tgg	aag	act	tat	gtt
Lys	Asn	Phe	Val	Asp	Leu	Phe	Gly	Val	Trp	Asn	Trp	Lys	Thr	Tyr	Val
		195					200					205			
acc	gga	gag	tca	tat	gct	ggc	ttt	tac	gtt	cct	tac	att	gct	gac	agc
Thr	Gly	Glu	Ser	Tyr	Ala	Gly	Phe	Tyr	Val	Pro	Tyr	Ile	Ala	Asp	Ser
	210					215					220				
ttc	atc	cgt	gcc	aat	gac	aag	aaa	tac	ttc	aat	ctt	ggg	ggc	atc	gca
Phe	Ile	Arg	Ala	Asn	Asp	Lys	Lys	Tyr	Phe	Asn	Leu	Gly	Gly	Ile	Ala
	225				230					235					240
atc	aac	gac	ccc	atc	atc	ggg	act	gat	act	gtc	caa	cag	cag	atc	gtc
Ile	Asn	Asp	Pro	Ile	Ile	Gly	Thr	Asp	Thr	Val	Gln	Gln	Gln	Ile	Val
				245					250					255	
atc	cgg	ccc	tac	gtc	gaa	ttc	tgg	caa	aat	gtc	ttc	tac	ttg	aac	cag
Ile	Arg	Pro	Tyr	Val	Glu	Phe	Trp	Gln	Asn	Val	Phe	Tyr	Leu	Asn	Gln
			260					265					270		
act	ttc	tta	gaa	aga	gcc	cga	aag	cgc	gac	ctg	gaa	tgc	ggg	tac	acc
Thr	Phe	Leu	Glu	Arg	Ala	Arg	Lys	Arg	Asp	Leu	Glu	Cys	Gly	Tyr	Thr
		275					280					285			
cag	tat	tat	gaa	aaa	tac	ttc	aaa	ttc	cct	ccg	cca	aag	ggg	ccc	ttc
Gln	Tyr	Tyr	Glu	Lys	Tyr	Phe	Lys	Phe	Pro	Pro	Pro	Lys	Gly	Pro	Phe
	290					295					300				
cca	aat	ctc	cct	gac	cca	ttc	gac	agt	acg	ggg	gat	gtc	cca	att	tgc
Pro	Asn	Leu	Pro	Asp	Pro	Phe	Asp	Ser	Thr	Gly	Asp	Val	Pro	Ile	Cys
	305				310					315					320
gac	cag	ttc	gat	aac	tac	gcc	caa	gcc	att	gcc	gag	gta	aat	cct	tgc
Asp	Gln	Phe	Asp	Asn	Tyr	Ala	Gln	Ala	Ile	Ala	Glu	Val	Asn	Pro	Cys
				325					330					335	
ttt	gac	gtc	tac	cac	atc	acc	gaa	acc	tgt	ccg	ttc	aag	tcg	acg	ccg
Phe	Asp	Val	Tyr	His	Ile	Thr	Glu	Thr	Cys	Pro	Phe	Lys	Ser	Thr	Pro
			340					345					350		
ctc	ggg	gga	acc	aac	cca	gga	gat	tat	gtc	gca	cca	ggc	acg	gaa	gtc
Leu	Gly	Gly	Thr	Asn	Pro	Gly	Asp	Tyr	Val	Ala	Pro	Gly	Thr	Glu	Val
		355				360						365			
tat	ttt	gac	cgc	gca	gat	gtc	aag	aag	gct	ctt	cat	gcc	agt	cct	aac
Tyr	Phe	Asp	Arg	Ala	Asp	Val	Lys	Lys	Ala	Leu	His	Ala	Ser	Pro	Asn
	370					375					380				
agc	aca	tgg	atg	ttg	tgc	aca	gat	aag	aac	gtc	ttc	gcc	ggg	gcc	ggc
Ser	Thr	Trp	Met	Leu	Cys	Thr	Asp	Lys	Asn	Val	Phe	Ala	Gly	Ala	Gly
					390					395					400
gta	aac	ggc	tca	gac	acg	tct	gtc	cca	ccc	gcc	aac	agc	ggc	gtc	ctc
Val	Asn	Gly	Ser	Asp	Thr	Ser	Val	Pro	Pro	Ala	Asn	Ser	Gly	Val	Leu
				405					410					415	
caa	aac	gtt	att	gaa	aaa	aca	aac	aac	gtc	atg	atc	ggc	tct	gga	gac
Gln	Asn	Val	Ile	Glu	Lys	Thr	Asn	Asn	Val	Met	Ile	Gly	Ser	Gly	Asp
			420					425					430		
ctc	gac	ata	ctt	ctc	agc	aca	aac	ggc	acc	ctc	ctc	gcc	ctt	caa	aac
									Page 255						

## 10336256.txt

Leu Asp Ile Leu Leu Ser Thr Asn Gly Thr Leu Leu Ala Leu Gln Asn  
 435 440 445  
 atg act tgg aac ggc gca caa ggt cta acc aga tac ccc tcc caa aac 1392  
 Met Thr Trp Asn Gly Ala Gln Gly Leu Thr Arg Tyr Pro Ser Gln Asn 450 455 460  
 ctc tac gtg cct tac cac ccc gaa ttc aac ggc ggt gca cta gct ggc 1440  
 Leu Tyr Val Pro Tyr His Pro Glu Phe Asn Gly Gly Ala Leu Ala Gly 465 470 475 480  
 gct gga tac cag ggc tta tgg acc aaa gaa cgc ggt ctg acc ttc tac 1488  
 Ala Gly Tyr Gln Gly Leu Trp Thr Lys Glu Arg Gly Leu Thr Phe Tyr 485 490 495  
 act gcg cgt ctt gca ggt cat gag ttg cca ggt tac acg cct ggc gtc 1536  
 Thr Ala Arg Leu Ala Gly His Glu Leu Pro Gly Tyr Thr Pro Gly Val 500 505 510  
 gga tac cgc atg ttg gag att ctg ctc ggt cgc atc tcc gat ttt agc 1584  
 Gly Tyr Arg Met Leu Glu Ile Leu Leu Gly Arg Ile Ser Asp Phe Ser 515 520 525  
 agc acc cgc gat ttc acc acc caa aca ggt aat ttt act ggt acc acc 1632  
 Ser Thr Arg Asp Phe Thr Thr Gln Thr Gly Asn Phe Thr Gly Thr Thr 530 535 540  
 gat ctc tat tag 1644  
 Asp Leu Tyr \* 545

&lt;210&gt; 255

&lt;211&gt; 547

&lt;212&gt; PRT

<213> *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; (1)...(18)

&lt;221&gt; DOMAIN

&lt;222&gt; (74)...(522)

&lt;223&gt; Serine carboxypeptidase

&lt;400&gt; 255

Met Lys Leu Leu Ser Val Phe Gly Ser Phe Leu Cys Ala Ser Ala Ala  
 1 5 10 15  
 Leu Ala Ala Asn Ala Pro Arg Phe Leu Arg Pro Asn Arg Val His Arg  
 20 25 30  
 Pro Asn Pro Val Ile Glu Lys Arg Val Pro Gly Gln Asp Phe Gln Asn  
 35 40 45  
 Pro Glu Ile Asn Lys Arg Ala His Thr Phe Leu Asn Ala Lys Thr Gln  
 50 55 60  
 Pro Phe Ala Val Asp Gly Lys Asn Val Pro Leu Ala Asn Phe Asp Leu  
 65 70 75 80  
 Gly Glu Ser Tyr Ala Gly Leu Leu Pro Ile Ser Asn Asp Lys Asn Glu  
 85 90 95  
 Thr Arg Lys Leu Phe Phe Trp Phe Phe Pro Ser Thr Gln Ala Lys Thr  
 100 105 110  
 Pro Glu Glu Ile Val Met Leu Asn Gly Gly Pro Gly Cys Ser Ser Leu  
 115 120 125  
 Ser Gly Leu Leu Gln Glu Asn Gly Pro Phe Leu Trp Gln Asp Gly Thr  
 130 135 140  
 Leu Ala Pro Thr Gln Asn Pro Tyr Ser Trp His Asn Leu Thr Asn Met  
 145 150 155 160  
 Leu Trp Val Glu Gln Pro Val Gly Val Gly Tyr Ser Glu Gly Glu Pro  
 165 170 175

10336256.txt

Asp Ile Ser Asn Glu Tyr Glu Leu Ser Asp Gln Phe Arg Gly Phe Tyr  
 180 185 190  
 Lys Asn Phe Val Asp Leu Phe Gly Val Trp Asn Trp Lys Thr Tyr Val  
 195 200 205  
 Thr Gly Glu Ser Tyr Ala Gly Phe Tyr Val Pro Tyr Ile Ala Asp Ser  
 210 215 220  
 Phe Ile Arg Ala Asn Asp Lys Lys Tyr Phe Asn Leu Gly Gly Ile Ala  
 225 230 235 240  
 Ile Asn Asp Pro Ile Ile Gly Thr Asp Thr Val Gln Gln Gln Ile Val  
 245 250 255  
 Ile Arg Pro Tyr Val Glu Phe Trp Gln Asn Val Phe Tyr Leu Asn Gln  
 260 265 270  
 Thr Phe Leu Glu Arg Ala Arg Lys Arg Asp Leu Glu Cys Gly Tyr Thr  
 275 280 285  
 Gln Tyr Tyr Glu Lys Tyr Phe Lys Phe Pro Pro Pro Lys Gly Pro Phe  
 290 295 300  
 Pro Asn Leu Pro Asp Pro Phe Asp Ser Thr Gly Asp Val Pro Ile Cys  
 305 310 315 320  
 Asp Gln Phe Asp Asn Tyr Ala Gln Ala Ile Ala Glu Val Asn Pro Cys  
 325 330 335  
 Phe Asp Val Tyr His Ile Thr Glu Thr Cys Pro Phe Lys Ser Thr Pro  
 340 345 350  
 Leu Gly Gly Thr Asn Pro Gly Asp Tyr Val Ala Pro Gly Thr Glu Val  
 355 360 365  
 Tyr Phe Asp Arg Ala Asp Val Lys Lys Ala Leu His Ala Ser Pro Asn  
 370 375 380  
 Ser Thr Trp Met Leu Cys Thr Asp Lys Asn Val Phe Ala Gly Ala Gly  
 385 390 395 400  
 Val Asn Gly Ser Asp Thr Ser Val Pro Pro Ala Asn Ser Gly Val Leu  
 405 410 415  
 Gln Asn Val Ile Glu Lys Thr Asn Asn Val Met Ile Gly Ser Gly Asp  
 420 425 430  
 Leu Asp Ile Leu Leu Ser Thr Asn Gly Thr Leu Leu Ala Leu Gln Asn  
 435 440 445  
 Met Thr Trp Asn Gly Ala Gln Gly Leu Thr Arg Tyr Pro Ser Gln Asn  
 450 455 460  
 Leu Tyr Val Pro Tyr His Pro Glu Phe Asn Gly Gly Ala Leu Ala Gly  
 465 470 475 480  
 Ala Gly Tyr Gln Gly Leu Trp Thr Lys Glu Arg Gly Leu Thr Phe Tyr  
 485 490 495  
 Thr Ala Arg Leu Ala Gly His Glu Leu Pro Gly Tyr Thr Pro Gly Val  
 500 505 510  
 Gly Tyr Arg Met Leu Glu Ile Leu Leu Gly Arg Ile Ser Asp Phe Ser  
 515 520 525  
 Ser Thr Arg Asp Phe Thr Thr Gln Thr Gly Asn Phe Thr Gly Thr Thr  
 530 535 540  
 Asp Leu Tyr  
 545